

STIC-Biotech/ChemLib

78693

From: Zeman, Mary  
Sent: Friday, October 25, 2002 8:12 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search 09/970966

Please run a regular search and an oligo search of the following sequences from 09/970966

SEQ ID NO: 199, 210, 211 and 214

please make the minimum window in the oligo searches 10 nucleotides.

please include interference files

Paper printout please.

Thank you,

Mary K. Zeman

Examiner, 1631

305-7133

CM1 12A17

mailbox: CM1 12D01

199 - EFD 09/656,668  
9/7/2000

Point of Contact:

Thomas G. Larson, Ph.D.  
703-308-7309  
CM1, Rm. 6 B 01

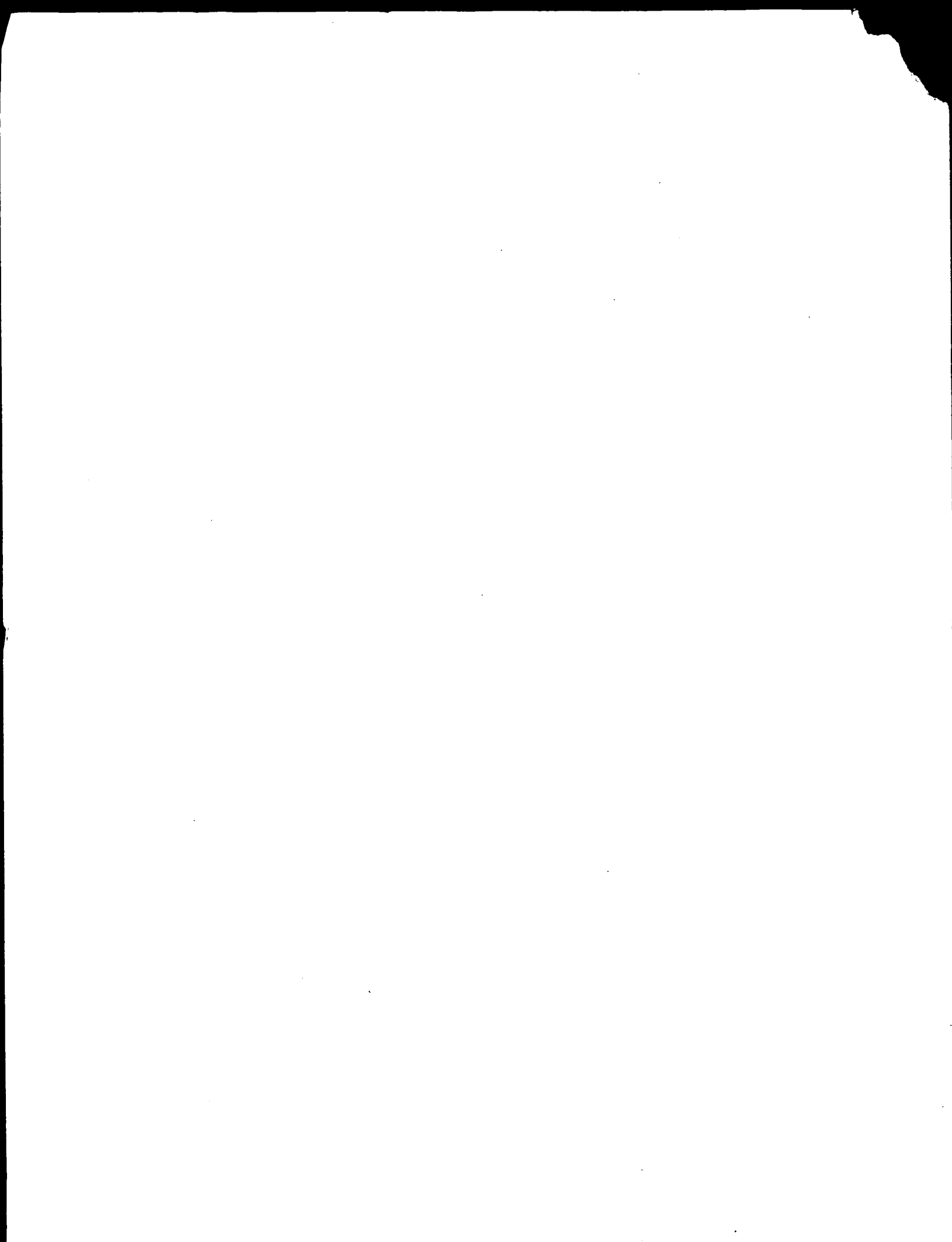
Searcher: Larson  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 11/08/02  
Searcher Prep/Review: 40  
Clerical: \_\_\_\_\_  
Online time: 40

TYPE OF SEARCH:

NA Sequences: 4  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: AB5503  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 938.618 Seconds

(without alignments)  
11441.218 Million cell updates/sec

Title: US-09-970-966-199

Sequence: 1 ggcacacttttgcgagattgt.....tggtccgcacacacacatcct 369

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Capext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 965615

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
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8: gb\_pl: \*  
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12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
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32: em\_hlg\_other: \*  
33: em\_hlg\_mus: \*  
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37: em\_hlg\_vrt: \*  
38: em\_sy: \*  
39: em\_hlg\_hum: \*  
40: em\_hlg\_mus: \*  
41: em\_hlg\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	6	AX093381
2	315	85.4	946	6	BC017318
3	315	85.4	1234	6	AX358762
4	315	85.4	1524	6	AX362255
5	315	85.4	1832	6	AX094501
6	315	85.4	1890	6	AX136281
7	314	85.1	2528	6	AX139944
8	281	76.2	396	6	AX093191
9	221	59.9	591	6	AX136556
10	175	47.4	129676	6	AC079773
11	142	38.5	147131	9	AC010974
12	47	12.7	209885	2	AC124493
13	38	10.3	1797	10	AB041649
14	22	6.0	113920	9	AL512284
15	22	6.0	161084	9	AC118794
16	20	5.4	157042	9	AC024061
17	20	5.4	171146	10	AC068808
18	20	5.4	180339	9	AC099049
19	20	5.4	190914	2	AC025029
20	20	5.4	205606	10	AL596204
21	19	5.1	2080	6	AX392969
22	19	5.1	2222	6	AX392971
23	19	5.1	2300	6	AX463719
24	19	5.1	2349	8	AF213399
25	19	5.1	2901	3	D49515
26	19	5.1	3914	10	AB017043
27	19	5.1	22752	9	AC104530
28	19	5.1	37635	9	AC004152
29	19	5.1	142329	2	AC128189
30	19	5.1	148571	9	AC105316
31	19	5.1	154693	9	AC084750
32	19	5.1	154772	2	AC106955
33	19	5.1	156128	2	AC113265
34	19	5.1	157533	9	AL354709
35	19	5.1	163041	2	AC116273
36	19	5.1	165873	9	AC066593
37	19	5.1	177070	2	AC018875
38	19	5.1	177426	2	AC021222
39	19	5.1	185551	2	AC112477
40	19	5.1	188172	9	AP003041
41	19	5.1	194769	2	AC113489
42	19	5.1	209418	2	AC122259
43	19	5.1	238472	9	AC010290
44	19	5.1	239904	2	AC096319
45	19	5.1	247865	2	AC097172

## ALIGNMENTS

RESULT 1  
LOCUS AX093381 369 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 199 from Patent WO0118046.  
ACCESSION AX093381  
VERSION AX093381.1 GI:13509829  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 369)  
Xu, J. and Stolk, J.A.  
Ovarian tumor sequences and methods of use therefor  
Patent: WO 0118046-A 199 15-MAR-2001;  
JOURNAL

FEATURES CORIMA CORPORATION (US)  
Location/Qualifiers  
source 1..369  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
misc\_feature 1..369  
/note="n = A,T,C or G"

BASE COUNT 82 a 109 c 90 g 86 t 2 others  
ORIGIN

Query Match 100.0%; Score 369; DB 6; Length 369;  
Best Local Similarity 100.0%; Pred. No. 4,4e-211;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTGTGAAGATTTCAGCTGGAACAGACTGCTCTCCCGAGTTGATTTGAAATGGAC 120  
D 61 GTGTGAAGATTTCAGCTGGAACAGACTGCTCTCCCGAGTTGATTTGAAATGGAC 120  
QY 121 GGTAAGCTTCAAGCATGTGTGCAAGAAAGAGTATGAGAGAGTGGAGATCATGTA 180  
D 121 GGTAAGCTTCAAGCATGTGTGCAAGAAAGAGTATGAGAGAGTGGAGATCATGTA 180  
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACAGTCTT 240  
D 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTGCGGGTACAGTCTT 240  
QY 241 CTGTCTCCCGAGGAACTGAACTGATTTGATCAAGTGTGCAACACCTCTTTTGA 300  
D 241 CTGTCTCCCGAGGAACTGAACTGATTTGATCAAGTGTGCAACACCTCTTTTGA 300  
QY 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTTGCTCGGCCCTTCANCCATGCTCCGAC 360  
D 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTTGCTCGGCCCTTCANCCATGCTCCGAC 360  
QY 361 CACCATCT 369  
D 361 CACCATCT 369

RESULT 2  
BC017318 946 bp mRNA linear PRI 09-NOV-2001  
LOCUS  
DEFINITION Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.  
ACCESSION BC017318  
VERSION BC017318.1 GI:16878239  
KEYWORDS MGC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 946)  
Strausberg, R.  
Direct Submission  
Submitted (05-NOV-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,

FEATURES  
source  
Location/Qualifiers  
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/clone="MGC:29643 IMAGE:3641660"  
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/clone\_id="NIH\_MGC\_39"  
/lab\_host="DH10B-R"  
/note="Vector: pOTB7"  
261..686  
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BASE COUNT 197 a 292 c 261 g 196 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.9e-178;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGCGCTCAAAATCCAGTGTACAGTGTGAAGAAATTCAGTGAACAGACT 89  
D 310 CAGGCTTTGCGCTCAAAATCCAGTGTACAGTGTGAAGAAATTCAGTGAACAGACT 369  
QY 90 GCTCTCCCCCGAGTTGATTTGATGACAGGTTGACAGTGTGTGCAAG 149  
D 370 GCTCTCCCCCGAGTTGATTTGATGACAGGTTGACAGTGTGTGCAAG 429  
QY 150 AAGTATGAGCAAGTGCAGGATGATGATGATGATGATGATGATGATGATGATGAT 209  
D 430 AAGTATGAGCAAGTGCAGGATGATGATGATGATGATGATGATGATGATGATGAT 489  
QY 210 GTCTCATGCTGCTGCGGGGTACAGTCTCTCCCGAGGAAATGAACTCAGTTT 269  
D 490 GTCTCATGCTGCTGCGGGGTACAGTCTCTCTCCCGAGGAAATGAACTCAGTTT 549  
QY 270 GCATCAGCTGTGTGAACACCCCTTTTGTAAAGGCGCCCAAGAAAGGGAAGTT 329  
D 550 GCATCAGCTGTGTGAACACCCCTTTTGTAAAGGCGCCCAAGAAAGGGAAGTT 609  
QY 330 CTGCTCGGCGCTCA 344  
D 610 CTGCTCGGCGCTCA 624

RESULT 3  
AX358762 1524 bp DNA linear PAT 13-FEB-2002  
LOCUS  
DEFINITION Sequence 15 from Patent WO0193983.  
ACCESSION AX358762  
VERSION AX358762.1 GI:16875282  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	1	Baker, K. P., Desnoyers, L., Gerritsen, M. E., Goddard, A., Godowski, P. J., Grimaldi, J. C., Gurney, A. L., Smith, V., Stephan, J. P., Watanabe, C. K., and Wood, W. I.
AUTHORS		Secreted and transmembrane polypeptides and nucleic acids encoding the same
TITLE		Patent: WO 0193983-A 15 13-DEC-2001;
JOURNAL		Genentech Inc. (US)
FEATURES		Location/Qualifiers
SOURCE		1..1524
BASE COUNT	321 a 433 c 435 g 335 t	/organism="Homo sapiens" /db_xref="taxon:9606"
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Best Local Similarity	100.0%:	Pred. NO. 1.9e-178; Indels 0; Gaps 0;
Matches 315; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
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Db	170	CAGGCTTTGCGGTGCAAAATCCAGTGTCTACGATGGAAGAAATTCAGCTGAACAAGCACT 229
QY	90	GCTCTCTCCCGAGTTCATTTGGAATTCGACGGTGAACGTTCAAGACATGTGTGAGAAG 149
Db	230	GCTCTCTCCCGAGTTCATTTGGAATTCGACGGTGAACGTTCAAGACATGTGTGAGAAG 289
QY	150	AAGTATGATGAGCAAAAGTCCCGGATCAGTACCCGAACTCTGTGTCATCATCAGCGGCT 209
Db	290	AAGTATGATGAGCAAAAGTCCCGGATCAGTACCCGAACTCTGTGTCATCATCAGCGGCT 349
QY	210	GTCTCATGCGCTCTGCGGGGTACCAAGTCTTGTGCTCCCGACGAACTGAACACTGATT 269
Db	350	GTCTCATGCGCTCTGCGGGGTACCAAGTCTTGTGCTCCCGACGAACTGAACACTGATT 409
QY	270	GGATCAGCGTGGCAACACAGCCCTCTTTGTAAGGGGCCAAGGCCCAAGAAAGGGGAAGTT 329
Db	410	GGATCAGCGTGGCAACACAGCCCTCTTTGTAAGGGGCCAAGGCCCAAGAAAGGGGAAGTT 469
QY	330	CTGCTCTGGGCGCTCA 344
Db	470	CTGCTCTGGGCGCTCA 484
RESULT 4		
AX362255		
LOCUS	AX362255	1524 bp DNA linear PAT 15-FEB-2002
DEFINITION	Sequence 15 from Patent WO0208288.	
ACCESSION	AX362255	
VERSION	AX362255.1	GI:18694585
KEYWORDS		
SOURCE		human.
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
AUTHORS	1	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE		Baker, K. P., Desnoyers, L., Gerritsen, M. E., Goddard, A., Godowski, P. J., Grimaldi, J. C., Gurney, A. L., Smith, V., Stephan, J. P., Watanabe, C. K., and Wood, W. I.
JOURNAL		Secreted and transmembrane polypeptides and nucleic acids encoding the same
FEATURES		Patent: WO 0208288-A 15 31-JAN-2002;
SOURCE		Genentech, Inc. (US)
BASE COUNT	321 a 433 c 435 g 335 t	Location/Qualifiers
ORIGIN		1..1524
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Best Local Similarity	100.0%:	Pred. NO. 1.9e-178; Indels 0; Gaps 0;
Matches 315; Conservative	0; Mismatches	0; Indels 0; Gaps 0;

Oy	30	CAGGTTTGGCCTCAATCATCGTCACGCAGTGTCGAAGAATTCCACTGAAACAACACT	89
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Oy	90	GCTCCTCCCCGAGTTCAATTGTGAATTGCACAGGTGAACGTTCAAGACATGTGCAGAAG	149
Db	230	GCTCCTCCCCGAGTTCAATTGTGAATTGCACAGGTGAACGTTCAAGACATGTGCAGAAG	289
Oy	150	AAGTGTATGGACAAAGTGTCCGGGATCATGTACGCCAAGTCTGTGCATCACACGGCCT	209
Db	290	AAGTGTATGGACAAAGTGTCCGGGATCATGTACGCCAAGTCTGTGCATCACACGGCCT	349
Oy	210	GTCATCAGCTCTGCGCGGTATCAGTCCTCTGCTCCCGGAAAATGAACTGACATTT	269
Db	350	GTCATCAGCTCTGCGCGGTATCAGTCCTCTGCTCCCGGAAAATGAACTGACATTT	409
Oy	270	GCATCAGCTGTGCACACCCCCTCTTTGTAAAGGCCAGGCCCAAGAAAAGGGAAATT	329
Db	410	GCATCAGCTGTGCACACCCCCTCTTTGTAAAGGCCAGGCCCAAGAAAAGGGAAATT	469
Oy	330	CGCCTCGGCGCTCA	344
Db	470	CGCCTCGGCGCTCA	484
RESULT 5			
LOCUS	AK094501	1832 bp	mRNA linear PRI 15-JUL-2002
DEFINITION	Homo sapiens cDNA FLJ37182 fls, clone BRAZL2001350, weakly similar to Homo sapiens Gz-selective GTPase-activating protein (RGS20) mRNA.		
ACCESSION	AK094501		
VERSION	AK094501.1	GI:21753575	
KEYWORDS	oligo capping; fls (full insert sequence).		
SOURCE	Homo sapiens alzheimer cortex cdna to mRNA, clone_1lb:BRAZL2 clone:BRAZL2001350.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Iseno,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Watsutsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Naghari,K., Masuno,Y., Negai,K. and Isogai,T.		
TITLE	NEDO human cdna sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1832)		
AUTHORS	Isogai,T. and Yamamoto,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genominfo@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cdna sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.		
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	/note="Cloning vector: pHEBSPFLJ3"		
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Best Local Similarity 100.0%; Pred. No. 1.9e-178;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D 264 CAGGCTTTGGCGTCAAAATCCAGTCTACAGTGTGAAGAAATTCAGTGAACAACGACT 323
QY 90 GCTCTCTCCCGAGATTGTTGTAATTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 149
D 324 GCTCTCTCCCGAGATTGTTGTAATTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 383
QY 150 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
D 384 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 443
QY 210 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACCTAGTTT 269
D 444 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACCTAGTTT 503
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAAGTT 329
D 504 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAAGTT 563
QY 330 CTGCTCGGGCCCTCA 344
D 564 CTGCTCGGGCCCTCA 578

RESULT 6
AX136281
LOCUS      AX136281      1890 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 203 from Patent EP1067182.
ACCESSION  AX136281
VERSION     AX136281.1  GI:14272687
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 1890)
AUTHORS     Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
TITLE       Secretory protein of membrane protein
JOURNAL     Patent: EP 1067182-A 203 10-JAN-2001;
            Helix Research Institute (Jp)
FEATURES
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            TPLNGRPKRRSSASALRPLRTTLFLKALFSAHC"
            PHLPE"
BASE COUNT      419 a      528 c      533 g      410 t
ORIGIN

Query Match      85.4%; Score 315; DB 6; Length 1890;

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Best Local Similarity 100.0%; Pred. No. 1.9e-178;
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D 323 CAGGCTTTGGCGTCAAAATCCAGTCTACAGTGTGAAGAAATTCAGTGAACAACGACT 382
QY 90 GCTCTCTCCCGAGATTGTTGTAATTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 149
D 383 GCTCTCTCCCGAGATTGTTGTAATTCACAGGTGAACGTTCAAGACATGTGTCAAGAA 442
QY 150 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
D 443 AAGTATGAGCAAAAGTCCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 502
QY 210 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACCTAGTTT 269
D 503 GTCTCATCGCTCTGCGGGATCACAGTCTCTGCTCCCGAGGAACTGAACCTAGTTT 562
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAAGTT 329
D 563 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGGCAAGGCCCAAGAAAAGGGAAGTT 622
QY 330 CTGCTCGGGCCCTCA 344
D 623 CTGCTCGGGCCCTCA 637

RESULT 7
AX319944/c
AX319944
LOCUS      AX319944      2528 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0181634.
ACCESSION  AX319944
VERSION     AX319944.1  GI:17901491
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Galvin,K.A. and Rudolph-Owen,L.A.
TITLE       Methods and compositions for the diagnosis and treatment of
            cardiovascular and tumorigenic disease using 4941
JOURNAL     Patent: WO 0181634-A 3 01-NOV-2001;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES
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            /note="unnamed protein product"
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            /db_xref="GI:17901492"
            /translation="MASPSLPGSDSQIIDSHVPEFEVATWIKITLILVYLIIYWG
            LIGNSATIRYTOVLQKRGYLOKEVTDHNVSLASDILVFLIGPMDFEYIIMPLITS
            SYTLSCKLHTEFEACSYATILVLFSEFYIAIHPREYKASPCQVKLIGFW
            VTSALVALPLLEFMGTREYPLVNVSHRGILNCSSTRHHDEPSTMSICTNLSRWT
            VROSTIEGAEVYVYLVILSVAPCMNMKQVIMKSOGLSAGGTRPQLKRSBESRT
            ARQTIIFRLRLVYTLAVCMNPQIRIMAAKPKHDMTRSTFRAYMILPSETFEY
            LSSVNPPLTYVSSQGRFVQVLCRLSLDHANHEKRLRVHAHSTDSAREVQPL
            LFASRROSSARREKIEFLSTFQSEARPOSKSLSTLESLEPNSGAKPANSAAENGFOE
            HEV"
BASE COUNT      516 a      766 c      677 g      567 t      2 others
ORIGIN

Query Match      85.1%; Score 314; DB 6; Length 2528;
Best Local Similarity 100.0%; Pred. No. 7.8e-178;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTTGGCGTCAAAATCCAGTCTACAGTGTGAAGAAATTCAGTGAACAACGACTG 90
D 2217 AGGCTTTGGCGTCAAAATCCAGTCTACAGTGTGAAGAAATTCAGTGAACAACGACTG 2158

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QY 91 CTCCTCCCCGAGTCAATGTGAATTCGACGGGGAACGTTCAAGACATGTCAGAGAAGA 150  
 Db 2157 CTCCTCCCCGAGTCAATGTGAATTCGACGGGGAACGTTCAAGACATGTCAGAGAAGA 2098  
 QY 151 AGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCTG 210  
 Db 2097 AGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCTG 2038  
 QY 211 TCTCATGCGCTCTGCGGGTACCAAGTCTTCTGCTCCCAAGGAACTGACATCAGTTTG 270  
 Db 2037 TCTCATGCGCTCTGCGGGTACCAAGTCTTCTGCTCCCAAGGAACTGACATCAGTTTG 1978  
 QY 271 CATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAGGCCCCAAGAAAGGGAGTTTC 330  
 Db 1977 CATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAGGCCCCAAGAAAGGGAGTTTC 1918  
 QY 331 TGCCCTCGGCGCTCA 344  
 Db 1917 TGCCCTCGGCGCTCA 1904

RESULT 8  
 AX093191 396 bp DNA linear PAT 30-MAR-2001  
 LOCUS AX093191  
 DEFINITION Sequence 9 from Patent WO0118046.  
 ACCESSION AX093191  
 VERSION AX093191.1 GI:13509640  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 1 (bases 1 to 396)  
 Xu, J. and Stolk, J. A.  
 Ovarian tumor sequences and methods of use therefor  
 Patent: WO 0118046-A 9 15-MAR-2001;  
 JOURNAL CORIXA CORPORATION (US)

FEATURES  
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 /db\_xref="taxon:9606"  
 misc\_feature 1..396  
 /note="n = A,T,C or G"

BASE COUNT 90 a 117 c 95 g 92 t 2 others  
 ORIGIN

Query Match 76.2%; Score 281; DB 6; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-158;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCGTGCAGAAATTCAGTGCACAGTGTGAAGATTCACAGTGAACAAGACT 89  
 Db 40 CAGGCTTTGGCGTGCAGAAATTCAGTGCACAGTGTGAAGATTCACAGTGAACAAGACT 99  
 QY 90 GCTCCTCCCCGAGTTCATGTGAATTCAGCGGTGAAGAGTTCAGACATGTGTCAAGAAG 149  
 Db 100 GCTCCTCCCCGAGTTCATGTGAATTCAGCGGTGAAGAGTTCAGACATGTGTCAAGAAG 159  
 QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCT 209  
 Db 160 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGGCT 219  
 QY 210 GTCTCATGCGCTCTGCGGGTACCAAGTCTTCTGCTCCCAAGGAACTGAACTCAGTTT 269  
 Db 220 GTCTCATGCGCTCTGCGGGTACCAAGTCTTCTGCTCCCAAGGAACTGAACTCAGTTT 279  
 QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAAAG 310  
 Db 280 GCATCAGCTGCTCAACACCCCTCTTTGTAACGGGGCCAAAG 320

RESULT 9

AX136556  
 LOCUS AX136556 591 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 478 from Patent EP1067182.  
 ACCESSION AX136556  
 VERSION AX136556.1 GI:14272960  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 1 (bases 1 to 591)  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and  
 Hayashi, K.  
 TITLE Secretory protein or membrane protein  
 JOURNAL Patent: EP 1067182-A 478 10-JAN-2001;  
 Helix Research Institute (JP)

FEATURES  
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 Best Local Similarity 100.0%; Pred. No. 1.2e-121;  
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 AC079773/c 129676 bp DNA linear PRI 09-JAN-2002  
 LOCUS AC079773

DEFINITION Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.  
 ACCESSION AC079773  
 VERSION AC079773.8 GI:15145561  
 KEYWORDS  
 SOURCE HTG.

ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 1 (bases 1 to 129676)  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Auston, J. E. and Waterston, R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE  
 PUBMED  
 99063792  
 9847074

REFERENCE  
 2 (bases 1 to 129676)  
 Shah, N., Meyer, R., Boyer, E. and Dignan, G.  
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17  
 JOURNAL Unpublished (2001)

REFERENCE  
 3 (bases 1 to 129676)  
 Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington

UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108 USA  
 4 (bases 1 to 129676)

REFERENCE  
 4 (bases 1 to 129676)  
 Waterston, R.H.

TITLE Direct Submission  
JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 129676)

REFERENCE 5 (bases 1 to 129676)  
Waterston, R.  
Direct Submission  
Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Aug 9, 2001 this sequence version replaced g1:1448358.

COMMENT  
-----  
Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [saplens@wustl.edu](mailto:saplens@wustl.edu)  
-----  
Summary Statistics  
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Center project name: H\_NH0258B17  
-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RPCL11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)  
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-1L22; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

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488..779  
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941..1253  
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1397..3331  
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2346..2370  
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repeat\_region  
repeat\_region  
repeat\_region

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repeat\_region 17238..17381  
/rpt\_family="MaLR"  
repeat\_region 17508..17966  
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repeat\_region 18933..19074  
/rpt\_family="ERV1"  
repeat\_region 19144..19250  
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Best Local Similarity 100.0%; Pred. No. 8.2e-94;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGTCCGGG 229
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Db 120741 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTGTCCGGG 120682
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QY 230 TACCAAGTCTTGTCTCCCGGAGGAAGTCACTAGTCTGATCATGCTCTGCACACC 289
      |||||||
Db 120661 TACCAAGTCTTGTCTCCCGGAGGAAGTCACTAGTCTGATCATGCTCTGCACACC 120622
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QY 290 CCTCTTGTACGGGCAAGGCGGCAAGGGAAGTCTGCTGCGGCTCTCA 344
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Db 120621 CCTCTTGTACGGGCAAGGCGGCAAGGGAAGTCTGCTGCGGCTCTCA 120567
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RESULT 11
AC010974/c      147131 bp      DNA      linear      PRI 01-MAR-2002
LOCUS
DEFINITION      Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION      AC010974
VERSION      AC010974.9 GI:19033964
KEYWORDS      HTG.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      1 (bases 1 to 147131)
              Sulston, J.E. and Waterston, R.
TITLE      Toward a complete human genome sequence
JOURNAL      Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE      99063792
PUBMED      9847074
REFERENCE
PUBMED      2 (bases 1 to 147131)
AUTHORS      Vanbrunt, A. and Stromatt, C.
TITLE      The sequence of Homo sapiens BAC clone RP11-159N20
JOURNAL      Unpublished (2001)
REFERENCE
AUTHORS      3 (bases 1 to 147131)
              Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (28-SEP-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108 USA
REFERENCE
              4 (bases 1 to 147131)

```

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AUTHORS      Waterston, R.H.
TITLE      Direct Submission
JOURNAL      Submitted (23-MAR-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE
AUTHORS      5 (bases 1 to 147131)
              Waterston, R.
TITLE      Direct Submission
JOURNAL      Submitted (01-MAR-2002) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              On Mar 1, 2002 this sequence version replaced g1:33435273.
COMMENT
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu/gsc
              Contact: saplens@wustl.wustl.edu
              Summary Statistics
              Center project name: H_NH0159N20

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Teleno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the right is RP11-458A7, 200 bp overlap; the clone sequenced to the right is RP11-258B17. Actual start of this clone is at base position 1 of RP11-159N20; actual end is at base position 147131 of RP11-159N20.

There are polymorphic base differences in the overlap between the clone RP11-159N20 and RP11-258B17.

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    991..1176
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repeat\_region 5738..5757  
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repeat\_region 6131..6178  
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misc\_feature 8810..9257  
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misc\_feature 19498..19795  
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misc\_feature 19873..20090  
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misc\_feature 19926..20089  
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Best Local Similarity 100.0%; Pred. No. 7.2e-74;  
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 30 CAGGCTTGGCGTCAATTCAGTGTACACAGTGAAGATTCCAGCTGACACAGACT 89  
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DB 15324 CAGGCTTGGCGTCAATTCAGTGTACACAGTGAAGATTCCAGCTGACACAGACT 15265  
QY 90 GCTCTCCCGGAGTCAATTCAGTGAAGCTGAAGCTGACATGTGCAGAGAAG 149  
|||||  
DB 15264 GCTCTCCCGGAGTCAATTCAGTGAAGCTGAAGCTGACATGTGCAGAGAAG 15205  
QY 150 AAGTATGAGCAAGTCCCG 171  
|||||  
DB 15204 AAGTATGAGCAAGTCCCG 15183  
  
RESULT 12  
AC124493 209885 bp DNA linear HTG 05-JUL-2002  
LOCUS AC124493/c  
DEFINITION Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT  
ACCESSION AC124493  
VERSION AC124493.2 GI:21699722  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 209885)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 209885)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
SUBMITTED (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
3 (bases 1 to 209885)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
SUBMITTED (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
COMMENT On Jul 5, 2002 this sequence version replaced gi:21426614.



```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0462P13
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: Plasmid; 100%
Chemistry: Dye-Primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 208484 bases at least Q40
Consensus quality: 208911 bases at least Q30
Consensus quality: 209285 bases at least Q20
Insert size: 20600; agarose-1p
Insert size: 212112; sum-of-ctigs
Quality coverage: 0.00 in Q20 bases; agarose-1p
Quality coverage: 11.62 in Q20 bases; sum-of-ctigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 11331: contig of 11331 bp in length
* 11332 11431: gap of unknown length
* 11432 28617: contig of 17186 bp in length
* 28618 28717: gap of unknown length
* 28718 49454: contig of 20737 bp in length
* 49455 49554: gap of unknown length
* 49555 107384: contig of 57830 bp in length
* 107385 107484: gap of unknown length
* 107485 209885: contig of 102401 bp in length.
*
* Location/Qualifiers
*   .1.209885 "Mus musculus"
*   /db_xref="taxon:10090"
*   /chromosome="UNK"
*   /clone="RP23-462P13"
*   1.11331
*   /note="assembly_name:Contig98"
*   11432..28617
*   /note="assembly_name:Contig99"
*   28718..49454
*   /note="assembly_name:Contig10"
*   49555..107384
*   /note="assembly_name:Contig11"
*   107485..209885
*   /note="assembly_name:Contig12"
*
BASE COUNT 59789 a 44784 c 46164 g 58745 t 403 others
ORIGIN
Query Match 12.7%; Score 47; DB 2; Length 209885;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 122 GTGAACGTTCAAGACATGTGTCAAGAAAGAAAGTGGAGCAAGATGC 168
DB 103249 GTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGACAAATGTC 103203
RESULT 13
AB041649 AB041649 1797 bp mRNA linear ROD 30-JUN-2000
LOCUS Mus musculus brain cDNA, clone MNCB-0671.
DEFINITION
ACCESSION AB041649

```

KEYWORDS AB041649.1 GI:76704499  
 VERSIONS fis (full insert sequence).  
 SOURCE Mus musculus (strain:C57BL) adult female cDNA to mRNA,  
 clone\_11b:Sugano mouse brain mncb clone:MNcb-0671.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (sites)  
 Osada,N., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Sugano,S. and  
 Hashimoto,K.  
 TITLE Isolation of full-length cDNA clones from mouse brain cDNA library  
 made by oligo-capping method  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1797)  
 Hashimoto,K., Osada,N., Kusuda,J. and Sugano,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-APR-2000) Katsuyuki Hashimoto, National Institute of  
 Infectious Diseases, Division of Genetic Resources, 23-1, Toyama  
 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
 (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,  
 Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)  
 URL: http://www.nih.go.jp/yoken/genebank/  
 COMMENT Lib Name: Sugano mouse brain mncb  
 Lab host: TOP10  
 Vector: pME18S-FL3  
 1st strand cDNA was primed with an oligo(dT) primer  
 [ATGGGCCCTTTTCTTTTTTTTTT]; double-stranded cDNA was synthesized  
 using specific 5' and 3' primers and amplified by PCR. The PCR  
 product was digested with SfiI and size selection was performed to  
 exclude fragments <1.5kb. The SfiI-digested PCR product was cloned  
 into distinct prairi sites of pME18S-FL3. XhoI sites just outside  
 the DraIII sites can be used to isolate the cDNA insert. Library  
 was constructed by Sugano et al.(University of Tokyo, Institute of  
 Medical Science). Custom primer used for sequencing ( 5' end primer  
 [CTTGTGCTCTAAAGCTGCG]; 3' end primer  
 [CGACCTGCAGCTCGACACA] ).  
 A part of this sequence is reported in AU035640.  
 FEATURES  
 source  
 location/Qualifiers  
 1..1797  
 /organism="Mus musculus"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone="MNcb-0671"  
 /sex="female"  
 /clone\_11b="Sugano mouse brain mncb"  
 /dev\_stage="adult"  
 325..750  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="BAA95101.1"  
 /db\_xref="GI:7670500"  
 /translation="MNVVIGIAATPCGILFWLPGIALQIOCYOCSEFPOLNDCSPSEFIV  
 NCTVNVQDMCKREYVEQSGAGITVRRKSCASACILASAGSCSPGKLNVSICSCN  
 TPLCNGPRPKRGSSASAIREFLITLTLFHLALCLAHK"  
 CDS  
 BASE COUNT 391 a 487 c 511 g 408 t  
 ORIGIN  
 Query Match 10.3%; Score 38; DB 10; Length 1797;  
 Best Local Similarity 100.0%; Pred. No. 5e-11;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 50 CAGTGTACCACTGTGAGAGATTCAGCTGACACGA 87  
 ||||||||||||||||||||||||||||||||||||  
 Db 394 CAGTGTACCACTGTGAGAGATTCAGCTGACACGA 431  
 RESULT 14  
 LOCUS AL512284 113920 bp DNA linear PRI 31-JAN-2002  
 DEFINITION Human DNA sequence from clone Rp11-248M22 on chromosome 10,  
 complete sequence.  
 ACCESSION AL512284  
 VERSION AL512284.20 GI:18477310

KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 113920)  
TITLE Rattus norvegicus  
JOURNAL Submitted (31-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humgen@sanger.ac.uk  
COMMENT On Feb 1, 2002 this sequence version replaced g1:18476636. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWSR; Tr, TRIMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/projects/C_elegans/wormpep). This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>. RP11-248M22 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/dacpac/home.htm>.  
VECTOR: pBAC3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-248M22. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-248M22 is at 1 in this sequence. The true left end of clone RP11-495F22 is at 111921 in this sequence. The true right end of clone RP11-481F7 is at 53678 in this sequence.  
FEATURES  
source  
location/Qualifiers  
1..113920  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/clone="RP11-248M22"  
/clone\_1fb="RPCT-11.1"  
20242..20503  
/note="Sequence from overlapping clone RP11-481F7 (AL603717). Assembly confirmed by restriction digest."  
BASE COUNT 28142 a 25061 c 27839 g 32878 t  
ORIGIN  
Query Match 5 0%; Score 22; DB 9; Length 113920;  
Best Local Similarity 100.0%; Pred. No. 0.24;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 233 CAGTCTCTGCTGCCAGGGA 254  
|||||  
Db 38431 CAGTCTCTGCTGCCAGGGA 38410  
RESULT 15  
AC118794 161084 bp DNA linear HTG 18-JUL-2002  
LOCUS AC118794  
DEFINITION Rattus norvegicus clone CH230-179C24, \*\*\*\* SEQUENCING IN PROGRESS  
ACCESSION AC118794

VERSION AC118794.5 GI:21746956  
KEYWORDS HTG; HTGS; PHASE1.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 161084)  
TITLE Rattus norvegicus  
JOURNAL Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 161084)  
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 14, 2002 this sequence version replaced g1:20387310.  
COMMENT  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
Project Information  
Center project name: GVHE  
Center clone name: CH230-179C24  
Summary Statistics  
Sequencing vector: Plasmid.

Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap: version 0.990329  
 Consensus quality: 103889 bases at least Q40  
 Consensus quality: 110038 bases at least Q30  
 Consensus quality: 114035 bases at least Q20

NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 69 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 1021: contig of 1021 bp in length  
 1022 1121: gap of unknown length  
 1122 2137: contig of 1016 bp in length  
 2138 2237: gap of unknown length  
 2238 3416: contig of 1179 bp in length  
 3417 3516: gap of unknown length  
 3517 5162: contig of 1646 bp in length  
 5163 5262: gap of unknown length  
 5263 6867: contig of 1605 bp in length  
 6868 6967: gap of unknown length  
 6968 8084: gap of unknown length  
 8085 8184: gap of unknown length  
 8185 9615: contig of 1431 bp in length  
 9616 9715: gap of unknown length  
 9716 10989: contig of 1274 bp in length  
 10990 11089: gap of unknown length  
 11090 12468: contig of 1279 bp in length  
 12469 13619: gap of unknown length  
 13620 13719: gap of unknown length  
 13720 15310: contig of 1591 bp in length  
 15311 15410: gap of unknown length  
 15411 16945: contig of 1535 bp in length  
 16946 17045: gap of unknown length  
 17046 18097: contig of 1052 bp in length  
 18098 18197: gap of unknown length  
 18198 19225: contig of 1028 bp in length  
 19226 19325: gap of unknown length  
 19326 20651: contig of 1326 bp in length  
 20652 22409: gap of unknown length  
 22410 22509: gap of unknown length  
 22510 24206: contig of 1697 bp in length  
 24207 24306: gap of unknown length  
 24307 26107: contig of 1801 bp in length  
 26108 26207: gap of unknown length  
 26208 27712: contig of 1505 bp in length  
 27713 27812: gap of unknown length  
 27813 29889: contig of 2077 bp in length  
 29890 29990: gap of unknown length  
 29991 31375: contig of 1386 bp in length  
 31376 31475: gap of unknown length  
 31476 33181: contig of 1706 bp in length  
 33182 33281: gap of unknown length  
 33282 35480: contig of 2199 bp in length  
 35481 35580: gap of unknown length  
 35581 37361: contig of 1781 bp in length  
 37362 37461: gap of unknown length  
 37462 38681: contig of 1220 bp in length  
 38682 38781: gap of unknown length  
 38782 40433: contig of 1652 bp in length  
 40434 40533: gap of unknown length  
 40534 42882: contig of 2349 bp in length  
 42883 42982: gap of unknown length  
 42983 44757: contig of 1775 bp in length  
 44758 44857: gap of unknown length  
 44858 45952: contig of 1095 bp in length

45953 46052: gap of unknown length  
 46053 47292: contig of 1240 bp in length  
 47293 47392: gap of unknown length  
 47393 48941: contig of 1549 bp in length  
 48942 49041: gap of unknown length  
 49042 51345: contig of 2304 bp in length  
 51346 51445: gap of unknown length  
 51446 53727: contig of 2282 bp in length  
 53728 53827: gap of unknown length  
 53828 55744: contig of 1917 bp in length  
 55745 55844: gap of unknown length  
 55845 57208: contig of 1364 bp in length  
 57209 57308: gap of unknown length  
 57309 60348: contig of 3040 bp in length  
 60349 60448: gap of unknown length  
 60449 62848: contig of 2400 bp in length  
 62849 62948: gap of unknown length  
 62949 64537: contig of 1589 bp in length  
 64538 64637: gap of unknown length  
 64638 66922: contig of 2185 bp in length  
 66923 68918: gap of unknown length  
 68919 71460: contig of 2542 bp in length  
 71461 71560: gap of unknown length  
 71561 73738: contig of 2178 bp in length  
 73739 73838: gap of unknown length  
 73839 75223: contig of 1385 bp in length  
 75224 75323: gap of unknown length  
 75324 78256: contig of 2933 bp in length  
 78257 78357: gap of unknown length  
 78358 79698: contig of 1342 bp in length  
 79699 82434: gap of unknown length  
 82435 82535: gap of unknown length  
 82536 84744: contig of 2210 bp in length  
 84745 84844: gap of unknown length  
 84845 86510: contig of 1666 bp in length  
 86511 86610: gap of unknown length  
 86611 89257: contig of 2647 bp in length  
 89258 89357: gap of unknown length  
 89358 90516: contig of 1159 bp in length  
 90517 90616: gap of unknown length  
 90617 92954: contig of 2338 bp in length  
 92955 93054: gap of unknown length  
 93055 95333: contig of 2279 bp in length  
 95334 95433: gap of unknown length  
 95434 97200: contig of 1767 bp in length  
 97201 97300: gap of unknown length  
 97301 100826: contig of 3526 bp in length

Query Match 6.0% Score 22; DB 2; Length 161084;

Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 AGGCCCAAGAAAGCGAGATT 329

Db 156950 AGGCCCAAGAAAGCGAGATT 156971

RESULT 16

AC024061

LOCUS

DEFINITION

AC024061

AC024061

REFERENCE

157042 bp DNA linear PRI 10-JUL-2001

sequence. GI:14647263

AC024061

AC024061

AC024061

AC024061

AC024061

AC024061

AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burte, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.

TITLE Sequencing of human chromosome 15 D15S146-D15S117 region

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 157042)

AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T., and Hood, L.

TITLE Direct Submission

JOURNAL Submitted (22-FEB-2000) Multimegabase Sequencing Center, University of Washington, PO Box 357730, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 157042)

AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burte, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA

COMMENT On Jul 10, 2001 this sequence version replaced gi:13162487.

----- Genome Center

Center: Multimegabase Sequencing Center

Center code: UMWSC

Web site: [http://chroma.mbt.washington.edu/msg\\_www](http://chroma.mbt.washington.edu/msg_www)

Contact: [leerowen@systemsbiology.org](mailto:leerowen@systemsbiology.org)

----- Summary Statistics

Sequencing vector: pUC18; L08752

Chemistry: Dye-terminator Big Dye; 90% of reads

Chemistry: Dye-primer Big Dye; 10% of reads

Assembly program: Phrap; version 0.990399

Note: data AC066614 [Drafting center UMWSC] and AC066611 [Drafting center UMWSC] were added for finishing.

Location/Qualifiers

1. 157042

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="15"

/map="15q21.3"

/clone="RP11-232J12"

/clone\_lib="RPCT Human BAC library 11"

/note="This clone overlaps RP11-8068 AC066614 and RP11-348P16 AC066611. Data from overlapping BACs were combined and the consensus sequence determined from RP11-232J12 to the extent possible."

misc\_feature

1. 26818

/note="overlap with RP11-8068 AC066614"

8723

/note="low quality data."

31605. 31610

/note="low quality data."

34826

/note="low quality data."

42795. 42800

/note="low quality data."

63513. 63514

/note="low quality data."

124490. 124492

/note="low quality data."

143570. 157042

/note="low quality data."

BASE COUNT 52806 a 28493 c 28053 g 47690 t

ORIGIN

Query Match 5.4%; Score 20; DB 9; Length 157042;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 AGGGAAGTGAAGTCAAGTTT 269

|||||

DB 75943 AGGGAAGTGAAGTCAAGTTT 75962

RESULT 17

AC068808

LOCUS

DEFINITION BAC library complete sequence.

ACCESSION AC068808

VERSION AC068808.20

KEYWORDS HG. GI:11496332

SOURCE

Mus musculus

Mus musculus

ORGANISM

REFERENCE

AUTHORS

Wetzer, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwona, G., Carlack, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buha, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Fortum-Tansey, J., Gill, R., Correll, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hognes, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Worley, K. and Gibbs, R.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE

AUTHORS

Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 171146)

Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (01-DEC-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 171146)

Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (05-DEC-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

5 (bases 1 to 171146)

Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Dec 1, 2000 this sequence version replaced gi:11321701.

Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

The repeat regions shown were identified using RepeatMasker by Adrian Smit.

Sequence similarities were identified using Powerblast by Jinghui Zhang.

Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers

1. 171146

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-479J7"
58.192
repeat_region
/rpt_family="B1_MM"
401.509
repeat_region
/rpt_family="B1_MM"
510.543
repeat_region
/rpt_family="(CAA)n"
849.976
repeat_region
/rpt_family="B1_F"
complement(987.1060)
repeat_region
/rpt_family="BC1_MM"
1636.1741
repeat_region
/rpt_family="PB1D7"
complement(2737.2907)
repeat_region
/rpt_family="URR1A"
2909.3037
repeat_region
/rpt_family="B1_MM"
complement(3412.3474)
repeat_region
/rpt_family="MIR"
complement(3480.3579)
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4033.4231
repeat_region
/rpt_family="MTC"
4233.4358
repeat_region
/rpt_family="B1_MM"
4400.4558
repeat_region
/rpt_family="MTC"
4746.4989
repeat_region
/rpt_family="Trigger3(Golem)"
complement(4990.5207)
repeat_region
/rpt_family="B4A"
complement(5538.5673)
repeat_region
/rpt_family="B1_MM"
complement(5674.5684)
repeat_region
/rpt_family="B4"
5839.6000
repeat_region
/rpt_family="MER46B"
6293.6410
repeat_region
/rpt_family="(CGG)n"
complement(7811.7921)
repeat_region
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repeat_region
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15041.15152
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note="Region similar to MmS949093
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17232.17298
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/rpt_family="B2"
17736.17932
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21060.21067
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21088.21113
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21262.21337
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21623.21825
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24197.24281
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Best Local Similarity 100.0%; Pred.No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 220 CTCGCGGGGTACAGTCT 239
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Db 156695 CTCGCGGGGTACAGTCT 156714
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RESULT 18
AC099049/c AC099049 180339 bp DNA linear PRI 12-JAN-2002
LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-291P10, complete sequence.
ACCESSION AC099049 AC021722
VERSION AC099049.2 GI:18139443

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KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 180339)  
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Karen, P.K.A., Raymond, C. and Haugen, E.D.  
TITLE Direct Submission  
JOURNAL Unpublished  
2 (bases 1 to 180339)  
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.  
TITLE Direct Submission  
JOURNAL Submitted (08-NOV-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
3 (bases 1 to 180339)  
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Karen, P.K.A., Raymond, C. and Haugen, E.D.  
TITLE Direct Submission  
JOURNAL Submitted (12-JAN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  
On Jan 12, 2002 this sequence version replaced gi:16799007.

COMMENT ----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web Site: <http://www.genome.washington.edu>  
Contact: uwgchls@u.washington.edu  
Drafting Center: BCM

----- Project Information  
Center Project name: Rpl1-291p10 (bc0345)  
Center Clone name: Rpl1-291p10 (bc0345)

----- Summary Statistics  
Sequencing vector: unknown; 60% of reads  
Sequencing vector: plasmid; 40% of reads  
Chemistry: Dye-terminator Big Dye; 89% of reads  
Chemistry: Dye-terminator Big Dye; 11% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 180276 bases at least Q40  
Consensus quality: 180338 bases at least Q30  
Consensus quality: 180339 bases at least Q20  
Insert size: 180339; sum-of-contigs  
Quality coverage: 10.6x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:  
5': Rpl1-442C9 (UWGC:bc0425) AC025029  
3': Rpl1-59E22 (UWGC:bc0181) AC022071

----- Sequence Quality Assessment:  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

----- This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:  
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear

in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII		EcoRI		HindIII	
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
2267	2314	8696	8865	1626	1573
2067	2064	6	<800	6382	6296
4428	4708	7365	7655	512	<800
1965	2064	3768	3808	449	<800
4344	4422	5698	5660	4042	4009
4291	4422	1158	1226	6044	6055
9652	9511	2511	2474	123	<800
5596	5698	1375	1449	618	<800
3081	3247	4214	4275	311	<800
2672	2606	1526	1566	1409	1347
1784	1803	1618	1566	43	<800
4280	4422	135	<800	1543	1573
560	<800	1775	1770	128	<800
3554	3719	5084	5074	6374	6296
2492	2606	3600	3566	2035	2052
1858	1803	3578	3566	2420	2410
3394	3499	365	<800	6424	6515
963	963	146	<800	6075	6296
3591	3719	16	<800	1654	1573
268	<800	782	<800	109	<800
2836	2932	4634	4628	3408	3459
2447	2606	1065	1078	4620	4606
1993	2064	1272	1357	3060	3257
2593	2606	7693	7655	4720	4776
818	815	4017	3990	1752	1730
1430	1373	609	<800	2026	2052
5478	5488	7658	7655	1547	1573
7564	7629	1425	1449	10077	9960
87	<800	11265	11368	12507	12577
799	<800	1832	1770	1338	1347
1992	2064	537	<800	4829	4776
2224	2314	1456	1449	417	<800

847	843	3134	3114	1542	1573
1307	1230	1015	1078	1343	1347
845	843	3274	3263	5165	5042
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4268	4422	72	<800	4165	4154
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803	800	1636	1566	7782	7809
3139	3247	789	<800	5084	5042
4708	4986	10043	9956	1981	2052
2591	2606	3572	3566	2189	2052
3262	3499	1497	1449	3181	3257
8081	8247	2482	2319	2657	2673
4403	4708	2306	2319	2098	2052
2714	2932	5512	5457	3026	3053
2758	2932	8025	8039	2041	2052
5229	5278	1941	1916	856	878
2406	2314	11676	11368	5163	5042
975	963	179	<800	4657	4606
2859	2932	615	<800	1234	1231
794	<800	2419	2474	762	<800
71	<800	9795	9956	27	<800
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6545	6536	-----	-----	958	981

Query Match 5.4%: Score 20: DB 9: Length 180339;  
 Best Local Similarity 100.0%: Pred. No. 3.9;  
 Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 308 AGGCCCAAGAAAGGGAAG 327  
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 Db 178159 AGGCCCAAGAAAGGGAAG 178140

RESULT 19  
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 LOCUS Homo sapiens chromosome 3 clone RP11-442C9, WORKING DRAFT SEQUENCE,  
 DEFINITION 25 unordered pieces.  
 AC025029 AC025029.14 GI:22203847  
 VERSION HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 190914)

## AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
 Albrooks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T.,  
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 Weinstein, G., and Gibbs, R.

## TITLE

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 25 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

*	1	2204:	contig of 2204 bp in length
*	2205	2304:	gap of unknown length
*	2305	4408:	contig of 2104 bp in length
*	4409	4508:	gap of unknown length
*	4509	7590:	contig of 3082 bp in length
*	7591	7691:	gap of unknown length
*	7691	10151:	contig of 2461 bp in length
*	10152	10251:	gap of unknown length
*	10252	13389:	contig of 3138 bp in length
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*	16746	16845:	gap of unknown length
*	16846	20094:	contig of 3349 bp in length
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*	20195	22295:	contig of 2101 bp in length
*	22296	22395:	gap of unknown length
*	22396	27077:	contig of 4682 bp in length
*	27078	27177:	gap of unknown length
*	27178	30971:	contig of 3794 bp in length
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*	31072	35083:	contig of 4012 bp in length
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*	35184	39460:	contig of 4297 bp in length
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*	39581	44949:	contig of 5369 bp in length
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FEATURES	Location/Qualifiers
source	1. .190914

	a	c.	g	t	others
BASE COUNT	60335	33063	33135	61952	2429
ORIGIN					

Query Match	5.4%	Score 20	DB 2	Length 190914
Best Local Similarity	100.0%	Pred. No. 3.9		
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 308 AGGCCCAAGAAAAGGGGAAG 327  
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Db 75305 AGGCCCAAGAAAAGGGGAAG 75324

RESULT 20	
AL596204	
LOCUS	
DEFINITION	AL596204 205606 bp DNA linear ROD 05-APR-2002
DESCRIPTION	Mouse DNA sequence from clone RP23-180B18 on chromosome 11, complete sequence.
	at 050204

ACCESSION	AL596204	GI:20068509
VERSION	AL596204.8	
KEYWORDS	HTG.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
1  
Griffiths, C.  
Direct Submission  
Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, Sw., SNTSSPROT; Ir., TREMBL; Wp., WORMPEP; information on the WORMPEP database can be found at

For further details see <http://www.chori.org/dacpac/home.htm>  
VECTOR: pBACE3.6.

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FEATURES
source      Location/Qualifiers
1. . 205606

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/chromosome="11"
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/clone_1lb="RPC1-23"

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BASE COUNT	56071 a	47639 c	47696 g	54200 t
ORIGIN				

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Query Match          5.4%; Score 20; DB 10; Length 205606;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
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Qy	220	CTCTGCCGGGTACCAGTCT	239
Db	15409	CTCTGCCGGGTACCAGTCT	15428

RESULT	21				
LOCUS	AX392969/c				
DEFINITION	Sequence from Patent WO0214358.	DNA	linear	PAT 23-MAR-2002	
ACCESSION	AX392969				
VERSION	AX392969.1				
KEYWORDS	human,				
SOURCE	human.				



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and  
Wang, H.  
Novel secreted proteins and their uses  
Patent: WO 0214358-A 11 21-FEB-2002;  
ELI LILLY AND COMPANY (US)

TITLE  
JOURNAL  
ELI LILLY AND COMPANY (US)

FEATURES  
source  
1. .2080  
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/db\_xref="taxon:9606"  
12. .1685  
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HRSIGALRLRLHLAIALEQDNFRLPGLHLIEDNMPLEEVAGSLRGNTLSLV  
THTNITAVPAALRHQAHLICLNLSNPISTVPGSRDVLRLBELHLAALVAVP  
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LNFDRGPACATPAEVRGDALNLPDSVLEFEYFCGRPKIRERLRQVATAGEDVRF  
LCRAEGRAPATVAVMPQHRPVPTATSGRAVAFGLTEIODARODSGTYCVASNA  
GGNDYTFATITVREPANRTPGAHNETLAALAPLIDITLIVSTAMGCTIFLGVL  
FCFVLLFVMSRGQRQHNKNSVEYSFRVDSPPAAGGAGARKRMKMI"

BASE COUNT 303 a 758 c 676 g 342 t 1 others

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mat\_peptide  
96. .1682  
/product="unnamed"

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Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335  
DB 1811 AAAGGGGAAGTTCTGCCT 1793

RESULT 22  
AX392971/c 2222 bp DNA linear PAT 23-MAR-2002  
LOCUS  
DEFINITION  
Sequence 13 from Patent WO0214358.  
ACCESSION  
AX392971  
VERSION  
AX392971.1 GI:19701018  
KEYWORDS  
human.  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and  
Wang, H.  
Novel secreted proteins and their uses  
Patent: WO 0214358-A 13 21-FEB-2002;  
ELI LILLY AND COMPANY (US)

TITLE  
JOURNAL  
ELI LILLY AND COMPANY (US)

FEATURES  
source  
1. .2222  
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49. .1827  
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RRLPGLHLIEDNMPLEEVAGSLRGNTLSLVTHNITAVPAALRHQAHLICLNLSNPISTVPGSRDVLRLBELHLAALVAVP  
OAFILGROIILNLSNLTLESTLESTVLTLETRVDGNPLACDCLMLIVORRT  
LNFDRGPACATPAEVRGDALNLPDSVLEFEYFCGRPKIRERLRQVATAGEDVRF  
LCRAEGRAPATVAVMPQHRPVPTATSGRAVAFGLTEIODARODSGTYCVASNA  
GGNDYTFATITVREPANRTPGAHNETLAALAPLIDITLIVSTAMGCTIFLGVL  
FCFVLLFVMSRGQRQHNKNSVEYSFRVDSPPAAGGAGARKRMKMI"

BASE COUNT 319 a 862 c 767 g 352 t

ORIGIN  
s1g\_peptide  
127. .192

Query Match 5.1%; Score 19; DB 6; Length 2300;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335  
DB 2031 AAAGGGGAAGTTCTGCCT 2013

RESULT 24  
AF213399/c 2349 bp mRNA linear PLN 10-DEC-2000  
LOCUS

LSHNPSTVPGSRDVLRLBELHLAALVAVPQAFILGROIILNLSNLTLE  
ESTHSVNTLETLRYDGNPLACDCLMLIVORRTLNFGRPLPACATPAEVRGDALN  
LPDSVLEFEYFCGRPKIRERLRQVATAGEDVRFVLCRAEGRAPATVAVMPQHRPV  
ATSGRAVAFGLTEIODARODSGTYCVASNAGNDYTFATLTVREPANRTPG  
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BASE COUNT 317 a 827 c 733 g 345 t

ORIGIN  
mat\_peptide  
96. .1682  
/product="unnamed"

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Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335  
DB 1953 AAAGGGGAAGTTCTGCCT 1935

RESULT 23  
AX463719/c 2300 bp DNA linear PAT 15-JUL-2002  
LOCUS  
DEFINITION  
Sequence 9 from Patent WO0248361.  
ACCESSION  
AX463719  
VERSION  
AX463719.1 GI:21886478  
KEYWORDS  
human.  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Micanovic, R., Mills, B.J., Su, E.W., Varga, G., Wang, H.,  
Basinski, M.B., Sankhavarani, P.R. and Tschang, S.H.  
Novel secreted proteins and their use  
Patent: WO 0248361-A 9 20-JUN-2002;  
LILLY CO ELI (US)

TITLE  
JOURNAL  
LILLY CO ELI (US)

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1. .2300  
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127. .1905  
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/db\_xref="GI:21886479"  
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RLVRLIRGNOLKILPGVFTRLDNLILLDSENKLVLLDYTFODLSLRLEVDN  
DIVVSRAPAGLALBELTIERCMLTALSGESIGHRSIGALRLRLHLAIALEQDNF  
RRLPGLHLIEDNMPLEEVAGSLRGNTLSLVTHNITAVPAALRHQAHLICLNLSNPISTVPGSRDVLRLBELHLAALVAVPQAFILGROIILNLSNLTLE  
ESTHSVNTLETLRYDGNPLACDCLMLIVORRTLNFGRPLPACATPAEVRGDALN  
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ATSGRAVAFGLTEIODARODSGTYCVASNAGNDYTFATLTVREPANRTPG  
EAHNETLAALAPLIDITLIVSTAMGCTIFLGVLFCFVLLFVMSRGQRQHNKNSVE  
YSFRVDSPPAAGGAGARKRMKMI"

BASE COUNT 319 a 862 c 767 g 352 t

ORIGIN  
s1g\_peptide  
127. .192

Query Match 5.1%; Score 19; DB 6; Length 2300;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 AAAGGGGAAGTTCTGCCT 335  
DB 2031 AAAGGGGAAGTTCTGCCT 2013

RESULT 24  
AF213399/c 2349 bp mRNA linear PLN 10-DEC-2000  
LOCUS

DEFINITION Nicotiana tabacum SLT1 protein mRNA, complete cds.  
 ACCESSION AF213399  
 VERSION AF213399.1 GI:11611666  
 KEYWORDS  
 SOURCE  
 ORGANISM Nicotiana tabacum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.  
 REFERENCE  
 AUTHORS Matsuno, T.K., Pardo, J.M., Takeda, S., Bressan, R.A. and Hasegawa, P.M.  
 TITLE Tobacco and Arabidopsis SLT1 suppresses salt sensitivity of calcineurin-deficient yeast mutants through the regulation of ion homeostasis  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2349)  
 AUTHORS Matsuno, T.K., Pardo, J.M., Takeda, S., Bressan, R.A. and Hasegawa, P.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-DEC-1999) Horticulture and Landscape Architecture, Purdue University, 1165 Horticulture Building, West Lafayette, IN 47907-1165, USA  
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 CDS  
 /organism="Nicotiana tabacum"  
 /cultivar="W38"  
 /db\_xref="taxon:4097"  
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 /note="N-terminal truncated form at Met304 is able to complement calcineurin-deficient salt-sensitive yeast mutants"  
 /codon\_start=1  
 /product="SLT1 protein"  
 /protein\_id="FAG39002.1"  
 /db\_xref="GI:11611667"  
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 FKDRPENALGRQQLRSLYNGHSKRGSRPPFSADRFIRSHMRKHYGLSPQCVH  
 GLEVPSPNLMVLDSEERKRMKELTRGVNFTTPPADSPSSMRNLPTNELEMPAP  
 PIKCKKLNGSLNSTOPSNSNGDAMLLLPVNGRKRKDFPSNGNEECYTPVVP  
 TSYQIPDLIEHNEPYWLNFGVMDVYAGPTAAASTYEDDEGYITITSLPVDLOR  
 VVSWMNTLTHGIRKYSCTSTSRISITKQNTFKLEASSSEHCPRGEVREPIPLSTR  
 IPEDKIEYVYSGGTVETILPKVREGEEHEVAVCLRPHLVGNMLT"

BASE COUNT 656 a 407 c 532 g 754 t  
 ORIGIN  
 Query Match 5.1%; Score 19; DB 8; Length 2349;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCCAAGCCCCAGAAAG 322  
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 Db 168 GCCAAGCCCCAGAAAG 150

RESULT 25  
 LOCUS D49515 2901 bp mRNA linear INV 10-FEB-1999  
 DEFINITION American cockroach clone PL25 mRNA for lectin-related protein, complete cds.  
 ACCESSION D49515  
 VERSION D49515.1 GI:1902918  
 KEYWORDS lectin-related protein.  
 SOURCE Periplaneta americana fat body cDNA to mRNA, clone:PL25.  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattoidea; Periplaneta.  
 REFERENCE  
 AUTHORS 1 (sites)  
 Kawasaki, K., Kubo, T. and Natori, S.

TITLE Presence of the Periplaneta lectin-related protein family in the American cockroach Periplaneta americana  
 JOURNAL Insect Biochem. Mol. Biol. 26 (4), 355-364 (1996)  
 MEDLINE 96245436  
 REFERENCE  
 AUTHORS Kawasaki, K., Kubo, T. and Natori, S.  
 TITLE Presence of a lectin family in Periplaneta americana, revealed by analysis of cDNA clones of lectins related to Periplaneta lectin unpublished  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 2901)  
 AUTHORS Kawasaki, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-MAR-1995) Kiyoshi Kawasaki, University of Tokyo, Faculty of Pharmaceutical Sciences; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-1111(ex.4820), Fax:03-5684-2973)  
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 /tissue="fat body"  
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 KTCIQEGAHPLAVINSESKALKLTKMLPHRFKMDNDMDNDAHIGFHDHYEGQVTF  
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BASE COUNT 1004 a 512 c 561 g 823 t 1 others  
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 Query Match 5.1%; Score 19; DB 3; Length 2901;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 TTCACGCTGAACAGACT 89  
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 Db 2420 TTCACGCTGAACAGACT 2402

RESULT 26  
 LOCUS AB017043 3914 bp DNA linear ROD 27-AUG-1998  
 DEFINITION Rattus norvegicus gene for hepatocyte nuclear factor 3 gamma, partial cds.  
 ACCESSION AB017043  
 VERSION AB017043.1 GI:3461893  
 KEYWORDS HNF-3G; hepatocyte nuclear factor 3 gamma.  
 SOURCE Rattus norvegicus (strain:Wistar) DNA.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE  
 AUTHORS 1 (sites)  
 Saito, K., Nakamura, T., Komoda, H., Hori, N., Adachi, K., Ito, K. and Sato, K.  
 TITLE Isolation and characterization of the rat hepatocyte nuclear factor-3gamma (HNF-3G) gene  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3914)  
 AUTHORS Saito, K., Nakamura, T., Komoda, H., Hori, N., Adachi, K., Ito, K. and Sato, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-AUG-1998) Kenzo Sato, Tottori University Faculty of Medicine, Department of Molecular Biology; 86 Nishimachi, Yonago, Tottori 683-8503, Japan (E-mail:kensato@grape.med.tottori-u.ac.jp, Tel:+81-859-34-8039, Fax:+81-859-34-8274)  
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 source  
 /organism="Rattus norvegicus"  
 /strain="Wistar"



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/rpt_family="L1MB7"
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/rpt_family="L1PB3"
repeat_region complement(4912. .5079)
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repeat_region complement(5979. .6279)
/rpt_family="AluSg"
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repeat_region 8555. .8853
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/rpt_family="AluSg"
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/Note="Predicted exon, program: gra112exons_human_1.3,
frame: 2, quality: excellent, score: 76.000"
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repeat_region complement(10262. .10446)
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DNA for antizyme, complete cds"
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repeat_region 13325. .13621
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identity. -AA308557 EST179376 HCC cell line (metastasis to
liver in mouse) II Homo sapiens cDNA 5' end similar to
similar to ornithine decarboxylase antizyme (1. .200); 100%
identity. - (14748. .14942) AA307682 EST178550 Colon
carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar
to similar to ornithine decarboxylase antizyme (1. .195);
100% identity. - (14758. .14942) L49059|HMD10907F Homo
sapiens retinal fovea EST HFD010907 sequence. (221. .37);
100% identity. - Other EST matches: T53070. T47553, T27358,
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/Note="translation of first 68 residues of ODC antizyme:
Ornithine decarboxylase antizyme is likely expressed
through translational frameshifting which results in the
products of ORF1 and ORF2 being synthesized as a single
polypeptide. In rat (D10706) the mRNA sequence at the
junction of the two ORFs, UCC UGA U (253. .259, shown as
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AA317001 EST188650 HCC cell line (metastasis to liver in
mouse) II Homo sapiens cDNA 5' end similar to similar to
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identity. -AA308557 EST179376 HCC cell line (metastasis to
liver in mouse) II Homo sapiens cDNA 5' end similar to
similar to ornithine decarboxylase antizyme (201. .346);
100% identity. -AA307682 EST178550 Colon carcinoma (HCC)
cell line Homo sapiens cDNA 5' end similar to similar to

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Best Local Similarity 5.1%; Score 19; DB 9; Length 37635;  
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QY 317 AAAAGGGAAGTTCTGCCT 335  
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DB 35070 AAAAGGGAAGTTCTGCCT 35088



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* 53775 56960: contig of 3186 bp in length
* 56961 57060: gap of unknown length
* 57061 61630: contig of 4570 bp in length
* 61631 61730: gap of unknown length
* 61731 64986: contig of 3256 bp in length
* 64987 65086: gap of unknown length
* 65087 69206: contig of 4120 bp in length
* 69207 69306: gap of unknown length
* 72414: contig of 3108 bp in length
* 72415 72514: gap of unknown length
* 72515 74919: gap of 2405 bp in length
* 74920 75019: gap of unknown length
* 75020 78723: contig of 3703 bp in length
* 78723 78822: gap of unknown length
* 78823 82956: contig of 4134 bp in length
* 82957 83056: gap of unknown length
* 83057 88408: contig of 5352 bp in length
* 88409 88509: gap of unknown length
* 88509 93944: contig of 5436 bp in length
* 93945 94044: gap of unknown length
* 94045 99586: contig of 5542 bp in length
* 99587 99686: gap of unknown length
* 99687 106051: contig of 6365 bp in length
* 106052 106151: gap of unknown length
* 106152 112417: contig of 6265 bp in length
* 112417 112516: gap of unknown length
* 112517 123175: contig of 10659 bp in length
* 123176 123275: gap of unknown length
* 123276 132799: contig of 9524 bp in length
* 132800 132899: gap of unknown length
* 132900 142329: contig of 9430 bp in length.

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BASE COUNT 38184 a 29231 c 28990 g 36898 t 9026 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 244 CTCGCCAGGGAAGTGAAC 262
DB 65792 CTCGCCAGGGAAGTGAAC 65774

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RESULT 30
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AC105316
AC105316 GI:20522215
VERSION AC105316.5
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 148571)
REFERENCE 1 (bases 1 to 148571)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
2 (bases 1 to 148571)
REFERENCE Buatsi, D., Haakenson, W., Boyer, E. and Spalding, L.
AUTHORS The sequence of Homo sapiens BAC clone RP11-524B5
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 148571)
AUTHORS Waterston, R.H.
TITLE Direct Submission

```

```

JOURNAL Submitted (29-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 148571)
REFERENCE Waterston, R.H.
AUTHORS Direct Submission
TITLE Submitted (30-APR-2002) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 148571)
REFERENCE Waterston, R.H.
AUTHORS Direct Submission
TITLE Submitted (10-MAY-2002) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 148571)
REFERENCE Submitted (29-MAY-2002) Department of Genetics, Washington
AUTHORS University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
TITLE On May 10, 2002 this sequence version replaced g1:20340527.
JOURNAL ----- Genome Center
COMMENT Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0524B05

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pletter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-620C21, 2000 bp overlap; the clone sequenced to the right is RP11-138A23, 2000 bp overlap. Actual start of this clone is at base position 70882 of RP11-620C21; actual end is at base position 47389 of RP11-138A23.

```

FEATURES
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    1. 148571
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="4"
      /map="4"
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      /clone_1lb="RPCI-11"
      repeat_region 138..322

```

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843. .1111
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1229. .1290
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3298. .3474
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4629. .4818
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5769. .6077
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6450. .6756
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6769. .6798
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7072. .7174
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8053. .8105
repeat_region /rpt_family="L2"
8355. .8649
repeat_region /rpt_family="Alu"
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9774. .9823
repeat_region /rpt_family="(TA)n"
9965. .10238
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10385. .10669
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11986. .12070
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13662. .14678
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14679. .14980
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14982. .15391
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19632. .19652
repeat_region /rpt_family="AT_rich"
21836. .21935
repeat_region /rpt_family="MIR"
22898. .23204
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25683. .25707
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25922. .26184
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27224. .28092
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31620. .31712
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35246. .35804
repeat_region /rpt_family="L2"
35805. .36110
repeat_region /rpt_family="Alu"
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repeat_region /rpt_family="L2"
36931. .36981
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38498. .38635
repeat_region /rpt_family="L2"
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repeat_region /rpt_family="L1"
39770. .40000
repeat_region /rpt_family="MIR"
40222. .40250
repeat_region /rpt_family="(T)n"
40893. .41036
repeat_region /rpt_family="MIR"
42561. .42741
repeat_region /rpt_family="(TTTC)n"
42742. .42779
repeat_region /rpt_family="(TTC)n"

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Query Match 5.1%; Score 19; DB 9; Length 148571;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 315 AGAAAGGGAAGTCTGC 333
Db 22080 AGAAAGGGAAGTCTGC 22062

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RESULT 31
AC084750 154693 bp DNA linear PRI 09-JAN-2002
LOCUS AC084750
DEFINITION Homo sapiens BAC clone RP11-215J17 from 4, complete sequence.
ACCESSION AC084750
VERSION AC084750.3 GI:17155079
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 154693)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 154693)
AUTHORS Isak, A. and Kozlowski, A.
TITLE The sequence of Homo sapiens BAC clone RP11-215J17
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 154693)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 154693)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2001) Genome Sequencing Center, Washington

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
5 (bases 1 to 154693)  
Waterston, R. H.  
Direct Submission  
Submitted (03-JAN-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
6 (bases 1 to 154693)  
Waterston, R.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Direct Submission  
Submitted (09-JUN-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Nov 30, 2001 this sequence version replaced g1:16799050.  
----- Genome Center

## COMMENT

Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
----- Summary Statistics  
Center project name: H\_NH0215J17  
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NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping  
clone sections once, or longer because we provide a small overlap  
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D.  
McPherson, Department of Genetics, Washington University, St. Louis  
MO. For additional information about the map position of this  
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RPCI-11 human BAC library was made from the blood of one male  
donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E.,  
Tateno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong  
and coworkers at the Roswell Park Cancer Institute  
(<http://daccpac.med.buffalo.edu>)  
VECTOR: pBACE3.6  
NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-362M19, 2000 bp overlap;  
the clone sequenced to the right is RP11-509I10. Actual start of  
this clone is at base position 151949 of RP11-362M19; actual end is  
at base position 154693 of RP11-215J17.

## FEATURES

## SOURCE

Data from AC091490 was used to finish this clone, AC084750.

## Location/Qualifiers

1. 154693  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="4"  
/map="4"  
/clone="RP11-215J17"  
/clone\_lib="RPCI-11"  
145. .272  
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4574. .4607  
repeat\_region  
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6208. .6327  
repeat\_region  
/rpt\_family="MaLR"

repeat\_region 6322. .6349  
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repeat\_region 6496. .6526  
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repeat\_region 7110. .7251  
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repeat\_region 8487. .8763  
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repeat\_region 9234. .10888  
/rpt\_family="L1"  
repeat\_region 10870. .10920  
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repeat\_region 10969. .12204  
/rpt\_family="L1"  
repeat\_region 11857. .11907  
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repeat\_region 13609. .13629  
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repeat\_region 18134. .18177  
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repeat\_region 20262. .20282  
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repeat\_region 20678. .20764  
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repeat\_region 21089. .21139  
/rpt\_family="AT\_rich"  
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repeat\_region 21358. .21757  
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repeat\_region 21764. .22238  
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repeat\_region 31892. .31917  
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* 11953 12052: gap of unknown length
* 12053 13451: contig of 1399 bp in length
* 13452 13551: gap of unknown length
* 13552 14859: contig of 1308 bp in length
* 14860 14959: gap of unknown length
* 14960 15983: contig of 1024 bp in length
* 15984 16083: gap of unknown length
* 16084 17353: contig of 1269 bp in length
* 17353 17453: gap of unknown length
* 17453 18905: contig of 1453 bp in length
* 18906 19005: gap of unknown length
* 19006 20634: contig of 1629 bp in length
* 20635 21951: contig of 1217 bp in length
* 21952 22051: gap of unknown length
* 22052 23512: contig of 1461 bp in length
* 23513 23612: gap of unknown length
* 23613 25111: contig of 1499 bp in length
* 25112 25211: gap of unknown length
* 25212 26295: contig of 1084 bp in length
* 26296 26396: gap of unknown length
* 26396 28255: contig of 1860 bp in length
* 28256 28356: gap of unknown length
* 28356 29759: contig of 1404 bp in length
* 29760 29859: gap of unknown length
* 29860 30998: contig of 1139 bp in length
* 30999 31098: gap of unknown length
* 31099 32270: contig of 1172 bp in length
* 32271 32370: gap of unknown length
* 32371 34072: contig of 1702 bp in length
* 34073 34172: gap of unknown length
* 34173 35716: contig of 1544 bp in length
* 35717 35816: gap of unknown length
* 35817 37261: contig of 1445 bp in length
* 37262 37361: gap of unknown length
* 37362 38480: contig of 1119 bp in length
* 38481 38580: gap of unknown length
* 38581 39609: contig of 1029 bp in length
* 39610 39709: gap of unknown length
* 39710 41831: contig of 2122 bp in length
* 41832 41931: gap of unknown length
* 41932 43536: contig of 1605 bp in length
* 43537 43636: gap of unknown length
* 43637 45470: contig of 1834 bp in length
* 45471 45570: gap of unknown length
* 45571 46972: contig of 1402 bp in length
* 46973 47072: gap of unknown length
* 47073 48378: contig of 1306 bp in length
* 48379 48478: gap of unknown length
* 48479 49869: contig of 1391 bp in length
* 49870 49969: gap of unknown length
* 49970 52101: contig of 2132 bp in length
* 52102 52201: gap of unknown length
* 52202 53702: contig of 1501 bp in length
* 53703 53802: gap of unknown length
* 53803 55595: contig of 1793 bp in length
* 55596 55695: gap of unknown length
* 55696 58025: contig of 2330 bp in length
* 58026 58125: gap of unknown length
* 58126 60175: contig of 2050 bp in length
* 60176 60275: gap of unknown length
* 60276 61611: contig of 1336 bp in length
* 61612 61711: gap of unknown length
* 61712 63647: contig of 1936 bp in length
* 63648 63747: gap of unknown length
* 63748 65445: contig of 1698 bp in length
* 65446 65545: gap of unknown length
* 65546 67327: contig of 1782 bp in length
* 67328 67427: gap of unknown length
* 67428 69058: contig of 1631 bp in length
* 69059 69158: gap of unknown length
* 69159 70888: contig of 1730 bp in length

```

```

* 70889 70988: gap of unknown length
* 70989 72471: contig of 1483 bp in length
* 72472 72571: gap of unknown length
* 72572 74285: contig of 1714 bp in length
* 74286 74385: gap of unknown length
* 74386 76948: contig of 2563 bp in length
* 76949 77048: gap of unknown length
* 77049 79348: contig of 2300 bp in length
* 79349 79448: gap of unknown length
* 79449 81596: contig of 2148 bp in length
* 81597 81696: gap of unknown length
* 81697 83376: contig of 1680 bp in length
* 83377 83476: gap of unknown length
* 83477 85248: contig of 1772 bp in length
* 85249 85348: gap of unknown length
* 85349 87542: contig of 2194 bp in length
* 87543 87642: gap of unknown length
* 87643 89581: contig of 1939 bp in length

Query Match      5.1%: Score 19; DB 2; Length 154772;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CCCCCGAGTTCATTGTGAA 114
Db 59719 CCCCCGAGTTCATTGTGAA 59737

RESULT 33
AC113265/c
LOCUS
DEFINITION
MUS musculus chromosome 17 clone rp23-46k8 strain C57BL/6J, WORKING
DRAFT SEQUENCE, 6 ordered pieces.
AC113265
AC113265.18 GI:22038589
VERSION
HTG; HTGS-PHASE2; HTGS-DRAFT.
KEYWORDS
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 156128)
REFERENCE
Mullam,J. and Roe,B.A.
MUS musculus BAC clone rp23-46k8
Unpublished
2 (bases 1 to 156128)
REFERENCE
Mullam,J. and Roe,B.A.
Direct Submission
Submitted (28-FEB-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 156128)
REFERENCE
Mullam,J. and Roe,B.A.
Direct Submission
Submitted (16-AUG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Aug 1, 2002 this sequence version replaced gi:22002191.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 2249: contig of 2249 bp in length
* 2250 2349: gap of unknown length

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\* 2350 6830: contig of 4481 bp in length  
 \* 6831 6930: gap of unknown length  
 \* 16530 16530: contig of 9600 bp in length  
 \* 16531 16530: gap of unknown length  
 \* 16531 16530: gap of unknown length  
 \* 43301 43300: contig of 26670 bp in length  
 \* 43401 43400: gap of unknown length  
 \* 91379 91379: contig of 47979 bp in length  
 \* 91380 91379: gap of unknown length  
 \* 91480 156128: contig of 64649 bp in length.

FEATURES  
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 /db\_xref="taxon:10090"  
 /chromosome="17"  
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 /clone\_1lb="RPC1 - 23 Female (C57BL/6J) Mouse BAC Library"  
 /clone\_1lb="RPC1 - 23 Female (C57BL/6J) Mouse BAC Library"

BASE COUNT 45867 a 33372 c 32918 g 43471 t 500 others  
 ORIGIN

Query Match 5.1% Score 19; DB 2; Length 156128;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 CTCGCCAGGAACTGAC 262  
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 Db 12667 CTCGCCAGGAACTGAC 12649

RESULT 34  
 AL354709 157533 bp DNA linear PRI 26-JUN-2001  
 LOCUS Human DNA sequence from clone RP11-14555 on chromosome 9, complete  
 DEFINITION sequence.  
 ACCESSION AL354709  
 VERSION AL354709.15 GI:14572562  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 157533)

REFERENCE  
 AUTHORS Laird, G.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 requests: clonequests@sanger.ac.uk

## COMMENT

On Jun 27, 2001 this sequence version replaced gi:14272267.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP  
 database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr9  
 RP11-14555 is from the library RPC1-11.1 constructed by the group  
 of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP11-14555. It may be shorter because we sequence overlapping  
 sections only one, except for a 100 base overlap.  
 The true left end of clone RP11-14555 is at 1 in this sequence. The  
 true left end of clone RP11-408N14 is at 157434 in this sequence.  
 The true right end of clone RP11-14912 is at 48466 in this  
 sequence.

FEATURES  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP11-14555"  
 /clone\_1lb="RPC1-11.1"  
 58294  
 /note="Single clone region. Assembly confirmed by  
 restriction digest data."

BASE COUNT 45649 a 29239 c 31401 g 51244 t  
 ORIGIN

Query Match 5.1% Score 19; DB 9; Length 157533;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 265 AGTTTCATCAGCTGCTGC 283  
 ||||||||||||||||  
 Db 43472 AGTTTCATCAGCTGCTGC 43490

RESULT 35  
 AC116273 163041 bp DNA linear HTG 18-JUN-2002  
 LOCUS Rattus norvegicus clone CH230-354C23, \*\*\* SEQUENCING IN PROGRESS  
 DEFINITION \*\*\* 59 unordered pieces.  
 ACCESSION AC116273  
 VERSION AC116273.5 GI:21746202  
 KEYWORDS HTG; HTGS\_PHASE1.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 163041)

REFERENCE  
 AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-oshman, F.R., Allen, C.,  
 Alshrooks, S.L., Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T.,  
 Barbieri, J., Benton, J., Bimaye, K., Blankenburg, K., Bonnin, D.,  
 Bouck, J., Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,  
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 Li, J., Li, Z., Lichtenarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,  
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 Maheshwari, M., Mapua, P., Martin, R., Matindale, A., Martinez, E.,  
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 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, N.,  
 Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogun, K., Okunolu, G.,  
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REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 163041)  
 Worley, K. C.  
 Direct Submission  
 Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Jul 14, 2002 this sequence version replaced gi:20467689.

Center: Baylor College of Medicine  
 Genome Center  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc.help@bcm.tmc.edu](mailto:hgsc.help@bcm.tmc.edu)  
 Project Information  
 Center project name: GTXN  
 Center clone name: CH230-354C23  
 Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap, version 0.990329  
 Consensus quality: 116366 bases at least Q40  
 Consensus quality: 120870 bases at least Q30  
 Consensus quality: 124554 bases at least Q20

NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
 NOTE: This is a "working draft" sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1  
 1097 1096: contig of 1096 bp in length  
 1197 1196: gap of unknown length  
 2601 2600: contig of 1404 bp in length  
 2701 2700: gap of unknown length  
 4000 3999: contig of 1299 bp in length  
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 5207 5207: contig of 1108 bp in length  
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 7025 7024: contig of 1717 bp in length  
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 8266 8265: gap of unknown length  
 9510 9509: contig of 1244 bp in length  
 9610 9609: gap of unknown length  
 10765 10764: contig of 1155 bp in length  
 10865 10864: gap of unknown length  
 12047 12046: contig of 1182 bp in length  
 12147 12146: gap of unknown length  
 13187 13186: contig of 1040 bp in length  
 13286: gap of unknown length  
 14687 14687: contig of 1401 bp in length

\* 104540 109623: contig of 5084 bp in length  
 \* 109624 109723: gap of unknown length  
 \* 109724 113402: contig of 3679 bp in length  
 \* 113403 113502: gap of unknown length  
 \* 113503 117935: contig of 4433 bp in length  
 \* 117936 118035: gap of unknown length  
 \* 118036 122534: contig of 4499 bp in length  
 \* 122535 122634: gap of unknown length  
 \* 122635 127202: contig of 4568 bp in length  
 \* 127203 127302: gap of unknown length  
 \* 127303 132412: contig of 5110 bp in length  
 \* 132413 132512: gap of unknown length  
 \* 132513 135347: contig of 2835 bp in length

Query Match 5.18; Score 19; DB 2; Length 163041;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 CCCCCGAGTCATTGTGAA 114  
 Db 39872 CCCCCGAGTCATTGTGAA 39890

RESULT 36 165873 bp DNA linear PRI 05-APR-2002  
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 LOCUS AC066593  
 DEFINITION sequence.  
 AC066593.4 GI:10799383  
 VERSION AC066593.4  
 KEYWORDS HTG: HTGS.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 165873)  
 AUTHORS Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,  
 Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,  
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 Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, L.,  
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 Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M.,  
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 Yu, J. and Yang, H.  
 TITLE Chromosome 3p genomic sequence  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 165873)  
 AUTHORS Kang, N., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B.,  
 Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y.,  
 Qi, X., Li, Y., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y.,  
 Li, G., Li, C., Bao, Q., Bao, J., Song, L., Zhang, L., Guo, D.,  
 Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J.,  
 and Yang, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Human Genomic Center, Institute of  
 Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing  
 100101, P.R.China  
 100101, P.R.China  
 3 (bases 1 to 165873)  
 Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,  
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 TITLE Direct Submission  
 JOURNAL Submitted (12-Oct-2000) Human Genomic Center, Institute of

REFERENCE 4 (bases 1 to 165873)  
 AUTHORS Niu, Y., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,  
 Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,  
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 Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,  
 Yu, J. and Yang, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2002) Human Genomic Center, Institute of  
 Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing  
 100101, P.R.China  
 On Oct 12, 2000 this sequence version replaced gi:10719643.  
 COMMENT -----Genome Center  
 Center: Beijing Center  
 Center code: Beijing  
 Website: <http://hgci.gtp.ac.cn>  
<http://www.genomics.org.cn>  
 Contact: [hgci@gtp.ac.cn](mailto:hgci@gtp.ac.cn)  
 Project Information  
 Center project name: 1# project  
 Center clone name: RP11-34405  
 -----Summary Statistics  
 Sequencing vector: pUC18; 100% of reads  
 Chemistry: Dye-terminator; ET 5% of reads  
 Chemistry: Dye-terminator Big Dye; 45% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 167281 bases at least Q40  
 Consensus quality: 169056 bases at least Q30  
 Consensus quality: 169188 bases at least Q20  
 Insert size: 165873; sum-of-contigs  
 Quality coverage: 6.54x in Q20 bases; sum-of-contigs

FEATURES  
 source  
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 /organism="Homo sapiens"  
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 /chromosome="3"  
 /map="3p"  
 /clone="RP11-34405"  
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 Query Match 5.18; Score 19; DB 9; Length 165873;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 142 TCAGAAAGAGTGTGAG 160  
 Db 65260 TCAGAAAGAGTGTGAG 65278

RESULT 37 177070 bp DNA linear HTG 18-FEB-2001  
 AC018875/c Homo sapiens chromosome UNK clone RP11-28956, WORKING DRAFT  
 LOCUS AC018875  
 DEFINITION sequence, 31 unordered pieces.  
 AC018875  
 AC018875.7 GI:12963043  
 VERSION HTG: HTGS\_PHASE1, HTGS\_DRAFT; HTGS\_FULLTOP.  
 KEYWORDS HTG: HTGS\_PHASE1, HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 177070)  
 AUTHORS Waterston, R.H.  
 TITLE The sequence of Homo sapiens clone

JOURNAL  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

Unpublished  
2 (bases 1 to 177070)  
Waterston, R.H.  
Direct Submission  
Submitted (21-DEC-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Feb 18, 2001 this sequence version replaced gi:11192196.

Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Project Information  
Center project name: H.NH0289E06

## Summary Statistics

Sequencing vector: M13, 86%  
Chemistry: Dye-terminator, 14%  
Chemistry: Dye-terminator Big Dye, 14% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 163528 bases at least Q40  
Consensus quality: 169714 bases at least Q30  
Consensus quality: 173054 bases at least Q20  
Insert size: 178000; agarose-fp  
Insert size: 176607; sum-of-contigs  
Quality coverage: 5.28 in Q20 bases; agarose-fp  
Quality coverage: 5.08 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 31 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 1368 1467: gap of unknown length  
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\* 2666 2765: gap of unknown length  
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\* 3874 3973: gap of unknown length  
\* 3974 5142: contig of 1169 bp in length  
\* 5143 5242: gap of unknown length  
\* 5243 6835: contig of 1593 bp in length  
\* 6836 6935: gap of unknown length  
\* 6936 8704: contig of 1769 bp in length  
\* 8705 8804: gap of unknown length  
\* 8805 10231: contig of 1427 bp in length  
\* 10232 10331: gap of unknown length  
\* 10332 12457: contig of 2126 bp in length  
\* 12458 12557: gap of unknown length  
\* 12558 14011: contig of 1454 bp in length  
\* 14012 14111: gap of unknown length  
\* 14112 15897: contig of 1786 bp in length  
\* 15898 15997: gap of unknown length  
\* 15998 17916: contig of 1919 bp in length  
\* 17917 18016: gap of unknown length  
\* 18017 19872: contig of 1856 bp in length  
\* 19873 19972: gap of unknown length  
\* 19973 22611: contig of 2639 bp in length  
\* 22612 22711: gap of unknown length  
\* 22712 25838: contig of 3127 bp in length  
\* 25839 25938: gap of unknown length  
\* 25939 27145: contig of 1207 bp in length  
\* 27146 27245: gap of unknown length  
\* 27246 29836: contig of 2591 bp in length  
\* 29837 29937: gap of unknown length  
\* 29938 31395: contig of 1459 bp in length  
\* 31396 31495: gap of unknown length  
\* 31496 35219: contig of 3724 bp in length  
\* 35220 35319: gap of unknown length

## FEATURES

## Source

\* 35320 36695: contig of 1376 bp in length  
\* 36696 36795: gap of unknown length  
\* 36796 39548: contig of 2753 bp in length  
\* 39549 39648: gap of unknown length  
\* 39649 41067: contig of 1419 bp in length  
\* 41068 41167: gap of unknown length  
\* 41168 44600: contig of 3433 bp in length  
\* 44601 44700: gap of unknown length  
\* 44701 47437: contig of 2736 bp in length  
\* 47437 47537: gap of unknown length  
\* 47537 51070: contig of 3533 bp in length  
\* 51070 51170: gap of unknown length  
\* 51170 56387: contig of 5217 bp in length  
\* 56387 56486: gap of unknown length  
\* 56486 61787: contig of 5301 bp in length  
\* 61787 61888: gap of unknown length  
\* 61888 65440: contig of 3553 bp in length  
\* 65440 65541: gap of unknown length  
\* 65541 70097: contig of 4556 bp in length  
\* 70097 70197: gap of unknown length  
\* 70197 79053: contig of 8857 bp in length  
\* 79054 79154: gap of unknown length  
\* 79154 109291: contig of 30138 bp in length  
\* 109292 109391: gap of unknown length  
\* 109392 177070: contig of 67679 bp in length.  
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2766. 3873  
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3974. 5142  
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6936. 8704  
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misc-feature      56487..61787
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misc-feature      61888..65440
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misc-feature      65541..70096
                   /note="assembly_name:Contig48"
misc-feature      70197..79053
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misc-feature      79154..109291
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ORIGIN

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Best Local Similarity 100.0%: Pred. No. 16:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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Db 20274 AAATCAGTCTACCACTG 20256

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RESULT 38
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LOCUS             Homo sapiens chromosome 11 clone RP11-567M21, WORKING DRAFT
DEFINITION        AC021222.4 GI:7770692
ACCESSION          AC021222.4
VERSION            HTG: HTGS-PHASE1; HTGS-DRAFT.
KEYWORDS           Homo sapiens.
SOURCE             Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 177426)
AUTHORS            Waterston,R.H.
TITLE              The sequence of Homo sapiens clone
JOURNAL            Unpublished
AUTHORS            2 (bases 1 to 177426)
TITLE              Waterston,R.H.
JOURNAL            Direct Submission
REFERENCE          Submitted (15-JAN-2000) Genome Sequencing Center, Washington
AUTHORS            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
TITLE              MO 63108, USA
JOURNAL            On May 12, 2000 this sequence version replaced gi:7233676.
COMMENT

```

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0567M21
----- Summary Statistics -----
Sequencing vector: MJ3, 100%
Sequencing vector: plasmid, 0%
Chemistry: Dye-terminator Big Dye, 0% of reads
Chemistry: Dye-terminator Big Dye, 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154559 bases at least Q40
Consensus quality: 161804 bases at least Q30
Consensus quality: 166430 bases at least Q20

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## FEATURES

```

Insert size: 189000; agarose-fp
Insert size: 174526; sum-of-contigs
Quality coverage: 2.77 in Q20 bases; agarose-fp
Quality coverage: 3.06 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1045 1044: contig of 1044 bp in length
1145 1144: gap of unknown length
2530 2529: contig of 1385 bp in length
2630 2629: gap of unknown length
3740 3739: contig of 1110 bp in length
3839 3838: gap of unknown length
5188 5187: contig of 1349 bp in length
5288 5287: gap of unknown length
6861 6860: contig of 1573 bp in length
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8387 8386: contig of 1426 bp in length
8488 8487: gap of unknown length
9957 9956: contig of 1470 bp in length
10058 10057: gap of unknown length
11934 11933: contig of 1877 bp in length
12034 12033: gap of unknown length
15639 15638: contig of 3605 bp in length
15739 15738: gap of unknown length
18805 18804: contig of 3066 bp in length
18905 18904: gap of unknown length
21750 21749: contig of 2845 bp in length
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24673 24672: contig of 2823 bp in length
24773 24772: gap of unknown length
27874 27873: contig of 3101 bp in length
27974 27973: gap of unknown length
32401 32400: contig of 4427 bp in length
32501 32500: gap of unknown length
33585 33584: contig of 3358 bp in length
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38608 38607: contig of 2649 bp in length
38708 38707: gap of unknown length
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50370 50369: contig of 6287 bp in length
50470 50469: gap of unknown length
55419 55418: contig of 4949 bp in length
55519 55518: gap of unknown length
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65990 65989: contig of 5744 bp in length
66090 66089: gap of unknown length
72519 72518: contig of 6429 bp in length
72619 72618: gap of unknown length
79368 79367: contig of 6749 bp in length
79468 79467: gap of unknown length
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98271 98270: gap of unknown length
10874 10873: contig of 10603 bp in length
108974 108973: gap of unknown length
120956 120955: contig of 11882 bp in length
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133932 133931: gap of unknown length
151337 151336: contig of 17405 bp in length
151437 151436: gap of unknown length
17426 17425: contig of 25989 bp in length.
Location/Qualifiers

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133933. 151337
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151438. 177426
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ORIGIN
Query Match 5.1%; Score 19; DB 2; Length 177426;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 304 GCCAAGCCCCAGAAAAGG 322
Db 50699 GCCAAGGCCCAAGAAAAGG 50717

RESULT 39
AC112477
LOCUS
DEFINITION
Rattus norvegicus clone CH230-191H11, *** SEQUENCING IN PROGRESS
***, 63 unordered pieces.
AC112477
VERSION
AC112477.3 GI:21745567
KEYWORDS
HTG; HTGS; PHASE1.
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 185551)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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Harris,C., Harris,K., Hart,M., Haylak,P., Hayes,A., Hernandez,J.,
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Homsli,F., Howard,S., Huber,J., Huik,S., Hume,J., Jackson,L.E.,
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Miner,G., Miner,Z., Mitchell,T., Mohabadi,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
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Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshark,N., Sisson,I.,
Sodergren,E., Sonalike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
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Usmani,K., Vasquez,L., Vera,V., Vialation,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 185551)
Worley,K.C.
Direct Submission
Submitted (21-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 185551)
Worley,K.C.
Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

```



## COMMENT

Baylor Plaza, Houston, TX 77030, USA  
On Jul 14, 2002 this sequence version replaced gi:20303368.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GSSY  
Center clone name: CH230-191H11  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap version 0.990329  
Consensus quality: 138102 bases at least Q40  
Consensus quality: 143613 bases at least Q30  
Consensus quality: 148883 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length.  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 63 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
1003 1102: contig of 1002 bp in length  
1103 2102: contig of 1000 bp in length  
2103 2202: gap of unknown length  
2203 3426: contig of 1224 bp in length  
3427 3526: gap of unknown length  
3527 4701: contig of 1175 bp in length  
4702 4801: gap of unknown length  
4802 6301: contig of 1500 bp in length  
6302 6401: gap of unknown length  
6402 7861: contig of 1460 bp in length  
7862 7961: gap of unknown length  
7962 8994: contig of 1033 bp in length  
8995 9094: gap of unknown length  
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10210 10309: gap of unknown length  
10310 11813: contig of 1504 bp in length  
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11914 13306: contig of 1393 bp in length  
13307 13406: gap of unknown length  
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14855 14954: gap of unknown length  
14955 15969: contig of 1015 bp in length  
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16070 17610: contig of 1541 bp in length  
17611 17710: gap of unknown length  
17711 19243: contig of 1533 bp in length  
19244 19343: gap of unknown length  
19344 21972: contig of 2629 bp in length  
21973 22072: gap of unknown length  
22073 23420: contig of 1348 bp in length  
23421 23520: gap of unknown length  
23521 25976: contig of 2456 bp in length  
25977 26076: gap of unknown length  
26077 27910: contig of 1834 bp in length  
27911 28010: gap of unknown length  
28011 29116: contig of 1106 bp in length  
29117 29216: gap of unknown length  
29217 30272: contig of 1056 bp in length  
30273 30372: gap of unknown length  
30373 31532: contig of 1160 bp in length  
31533 31632: gap of unknown length  
31633 33259: contig of 1627 bp in length  
33260 33359: gap of unknown length  
33360 34755: contig of 1396 bp in length

34756 34855: gap of unknown length  
34856 35954: contig of 1099 bp in length  
35955 36054: gap of unknown length  
36055 37883: contig of 1829 bp in length  
37884 37983: gap of unknown length  
37984 40017: contig of 2034 bp in length  
40018 40117: gap of unknown length  
40118 42375: contig of 2258 bp in length  
42376 42475: gap of unknown length  
42476 44342: contig of 1867 bp in length  
44343 44442: gap of unknown length  
44443 46003: contig of 1561 bp in length  
46004 46103: gap of unknown length  
46104 47435: contig of 1332 bp in length  
47436 47535: gap of unknown length  
47536 50415: contig of 2880 bp in length  
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50516 54064: contig of 3349 bp in length  
54064 54164: gap of unknown length  
54165 57106: contig of 2942 bp in length  
57107 57206: gap of unknown length  
57207 59706: contig of 2500 bp in length  
59707 59806: gap of unknown length  
59806 62887: contig of 2481 bp in length  
62887 62387: gap of unknown length  
62388 65758: contig of 3371 bp in length  
65759 65858: gap of unknown length  
65859 68739: contig of 2881 bp in length  
68740 68839: gap of unknown length  
68840 70238: contig of 1399 bp in length  
70239 70338: gap of unknown length  
70339 73742: contig of 3404 bp in length  
73743 73842: gap of unknown length  
73843 76328: contig of 2486 bp in length  
76329 76429: gap of unknown length  
76429 79753: contig of 3325 bp in length  
79753 79853: gap of unknown length  
79853 82522: contig of 2659 bp in length  
82523 82622: gap of unknown length  
82623 84875: contig of 2253 bp in length  
84876 84975: gap of unknown length  
84976 88118: contig of 3143 bp in length  
88119 88218: gap of unknown length  
88219 90713: contig of 2495 bp in length  
90714 90813: gap of unknown length  
90814 94914: contig of 4101 bp in length  
94915 95014: gap of unknown length  
95015 99367: contig of 4353 bp in length  
99368 99468: gap of unknown length  
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107722 113653: contig of 5932 bp in length  
113654 113753: gap of unknown length  
113754 117798: contig of 4045 bp in length  
117799 117898: gap of unknown length  
117899 121628: contig of 3730 bp in length  
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Query Match 5.1%; Score 19; DB 2; Length 185551;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 GAAGTGAAGGAGCAAGTC 167

Db 42662 GAAGTGAAGGAGCAAGTC 42680

RESULT 40

AP003041/c  
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 DEFINITION Homo sapiens genomic DNA, chromosome 11 clone:RP11-567M21, complete sequence.  
 ACCESSION AP003041  
 VERSION AP003041.3 GI:22202826  
 KEYWORDS HTG.  
 SOURCE Homo sapiens DNA, clone:RP11-567M21.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1  
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Matsubae, H. and Sakaki, Y.  
 TITLE Homo sapiens genomic DNA  
 JOURNAL Published Only in Database (2000)  
 REFERENCE 2 (bases 1 to 188172)  
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Matsubae, H. and Sakaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-DEC-2000) Masahiro Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)  
 COMMENT On Aug 9, 2002 this sequence version replaced gi:20334333.  
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 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 42556 GCCAAGGCCCAAGAAAG 42538  
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 LOCUS Mus musculus clone RP23-358A18, WORKING DRAFT SEQUENCE, 9 ordered pieces.  
 DEFINITION AC113489  
 ACCESSION AC113489  
 VERSION AC113489.2 GI:21313864  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULFILLTOP.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 194769)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Mus musculus, clone RP23-358A18  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 194769)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Batta, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,

McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfay, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 194769)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Batta, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Mlenga, V., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfay, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 COMMENT Direct Submission  
 TITLE JOURNAL  
 JOURNAL Submitted (02-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L23802  
 Center clone name: 358\_A\_18  
 ----- Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960721  
 Consensus quality: 191646 bases at least Q40  
 Consensus quality: 193107 bases at least Q40  
 Consensus quality: 193517 bases at least Q20  
 Insert size: 194000; agarose-ff  
 Insert size: 193969; sum-of-contigs  
 Quality coverage: 6.0 in Q20 bases; sum-of-contigs  
 Quality coverage: 6.0 in Q20 bases; sum-of-contigs  
 ----- NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 9 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.



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Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 CTCGCCAGGGAAGTGAAC 262
Db 159434 CTCGCCAGGGAAGTGAAC 159452

RESULT 43
AC010290/c      AC010290      238472 bp      DNA      linear      PRI 23-OCT-2001
LOCUS      Homo sapiens chromosome 5 clone CTB-125B20, complete sequence.
DEFINITION      AC010290
ACCESSION      AC010290.7 GI:16328257
VERSION      HTG.
KEYWORDS      Homo sapiens.
SOURCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 238472)
AUTHORS      DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE      Direct Submission
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 238472)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 238472)
REFERENCE      DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS      Direct Submission
TITLE      Submitted (23-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
JOURNAL      On Oct 23, 2001 this sequence version replaced gi:7711412.
COMMENT      Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.hgsc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.5.
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BASE COUNT      73389 a 52011 c 48279 g 64793 t
ORIGIN
Query Match      5.1%; Score 19; DB 9; Length 238472;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 304 GCCAAGGCCCAAGAAAG 322
Db 134911 GCCAAGGCCCAAGAAAG 134893

RESULT 44

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AC096319
LOCUS      AC096319      239904 bp      DNA      linear      HTG 11-JUL-2002
DEFINITION      Rattus norvegicus clone CH230-162p21, *** SEQUENCING IN PROGRESS
ACCESSION      AC096319
VERSION      AC096319.6 GI:21723476
KEYWORDS      HTG, HTGS_PHASE1.
SOURCE      Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 239904)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Aisbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbiera,J., Benton,J., Benton,K., Blakenburg,K., Bonnin,D.,
Bouch,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carion,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulik,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudad,S.,
Karlisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kresh,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Licharge,O., Lien,C., Liu,J., Liu,W., Lousaged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawliny,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokwenko,S., Ogun,M., Okwomah,G.,
Oragunye,N., Oyiedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Severy,G.,
Scherer,S., Scott,G., Shen,H., Shoshari,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 239904)
AUTHORS      Worley,K.C.
TITLE      Direct Submission
JOURNAL      Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 239904)
REFERENCE      Worley,K.C.
AUTHORS      Direct Submission
TITLE      Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT      On Jul 10, 2002 this sequence version replaced gi:18846093.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

```

```

----- Project Information
Center project name: GEXO
Center clone name: CH230-162P21
----- Summary Statistics
Sequencing vector: plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 191179 bases at least Q40
Consensus quality: 196736 bases at least Q30
Consensus quality: 201345 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1019: contig of 1018 bp in length
1118: gap of unknown length
1119: contig of 1222 bp in length
2340: gap of unknown length
2440: gap of unknown length
3466: contig of 1026 bp in length
3566: gap of unknown length
5122: contig of 1556 bp in length
5223: gap of unknown length
6324: contig of 1102 bp in length
6325: gap of unknown length
6425: gap of unknown length
7551: contig of 1126 bp in length
7650: gap of unknown length
8832: contig of 1182 bp in length
8932: gap of unknown length
10049: contig of 1117 bp in length
10149: gap of unknown length
10150: contig of 1681 bp in length
11830: gap of unknown length
11930: gap of unknown length
13098: contig of 1168 bp in length
13099: gap of unknown length
13199: contig of 1956 bp in length
15154: gap of unknown length
15155: contig of 1854 bp in length
15255: gap of unknown length
17108: contig of 1854 bp in length
17209: gap of unknown length
18984: contig of 1776 bp in length
19085: gap of unknown length
19085: contig of 2153 bp in length
21237: gap of unknown length
21238: gap of unknown length
21338: contig of 2435 bp in length
23772: gap of unknown length
23773: gap of unknown length
27420: contig of 3548 bp in length
27421: gap of unknown length
31622: contig of 4102 bp in length
31623: gap of unknown length
36778: contig of 5056 bp in length
36779: gap of unknown length
36878: gap of unknown length
40626: contig of 3748 bp in length
40627: gap of unknown length
42823: gap of unknown length
42824: contig of 2097 bp in length
42924: gap of unknown length
47021: contig of 4098 bp in length
47121: gap of unknown length
53664: contig of 6543 bp in length
53665: gap of unknown length
53764: gap of unknown length
57594: contig of 3830 bp in length
57595: gap of unknown length
62772: contig of 5078 bp in length
62773: gap of unknown length
62872: gap of unknown length
67852: contig of 4980 bp in length
67853: gap of unknown length
72957: contig of 5005 bp in length
72958: gap of unknown length
73057: gap of unknown length

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* 73058 81506: contig of 8449 bp in length
* 81507 81506: gap of unknown length
* 81607 87909: contig of 6303 bp in length
* 87910 88009: gap of unknown length
* 88010 88009: gap of unknown length
* 94461 94561: contig of 6452 bp in length
* 94562 94561: gap of unknown length
* 101193 101192: contig of 6631 bp in length
* 101292 101192: gap of unknown length
* 101293 107536: contig of 6244 bp in length
* 107537 107536: gap of unknown length
* 107637 112983: contig of 5347 bp in length
* 112984 113083: gap of unknown length
* 113084 120878: contig of 7795 bp in length
* 120879 120978: gap of unknown length
* 120979 127185: contig of 6206 bp in length
* 127185 127284: gap of unknown length
* 127285 133119: contig of 5835 bp in length
* 133120 133220: gap of unknown length
* 133220 143648: contig of 10429 bp in length
* 143649 143748: gap of unknown length
* 143749 154717: contig of 10969 bp in length
* 154718 154817: gap of unknown length
* 154818 164405: contig of 9588 bp in length
* 164406 164505: gap of unknown length
* 164506 170277: contig of 5772 bp in length
* 170278 170377: gap of unknown length
* 170378 179323: contig of 8946 bp in length
* 179324 179423: gap of unknown length
* 179424 193498: contig of 14075 bp in length
* 193499 193598: gap of unknown length
* 193599 208152: contig of 14554 bp in length
* 208153 208252: gap of unknown length
* 208253 223131: contig of 14679 bp in length
* 223132 223231: gap of unknown length
* 223232 239904: contig of 16673 bp in length.

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FEATURES
source 1..239904
            Location/Qualifiers

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BASE COUNT 68735 a 49743 c 49983 g 64401 t 7042 others
ORIGIN

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Query Match 5.1% Score 19; DB 2; Length 239904;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 62 TGTGAAGATTCCAGCTGA 80
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DB 87434 TGTGAAGATTCCAGCTGA 87452

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RESULT 45
AC0971172/c 247865 bp DNA linear HTG 24-AUG-2002
LOCUS
DEFINITION Rattus norvegicus clone CH230-2G16, *** SEQUENCING IN PROGRESS ***
40 unordered pieces.
AC0971172.3 GI:21953449
VERSION
KEYWORDS HTGS_PHASE1.
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 247865)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,
Alabrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbacia,J., Benton,J., Blimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carion,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Dellane, K.R., Delgado, O., Denn, A.L., Ding, Y., Dihn, H.H., Douthett, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Huliy, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, J., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Koryah, J., Kovar, C., Kratoch, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichner, O., Lieu, C., Liu, J., Liu, W., Lousaged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkwo, S., Ogun, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shoochari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umanal, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 247865)  
Worley, K.C.

Direct Submission  
Submitted (11-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 247865)  
Worley, K.C.

Direct Submission  
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 24, 2002 this sequence version replaced gi:17063105.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: TUVI  
Center clone name: CH230-2G16  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye: 100% of reads  
Assembly program: Phrap: version 0.990329  
Consensus quality: 211853 bases at least Q40  
Consensus quality: 215254 bases at least Q30  
Consensus quality: 217501 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length  
\* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank/draft.data.html>).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 40 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will

\* be preserved.  
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1097 1096: contig of 1096 bp in length  
1197 1196: gap of unknown length  
1197 2530: contig of 1334 bp in length  
2531 2530: gap of unknown length  
2631 3702: contig of 1072 bp in length  
3703 3802: gap of unknown length  
3803 4896: contig of 1094 bp in length  
4897 4996: gap of unknown length  
4997 6170: contig of 1174 bp in length  
6171 6270: gap of unknown length  
6271 7322: contig of 1052 bp in length  
7323 7422: gap of unknown length  
7423 8427: contig of 1005 bp in length  
8428 8527: gap of unknown length  
8528 9547: contig of 1019 bp in length  
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9647 11320: contig of 1674 bp in length  
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11421 13074: contig of 1654 bp in length  
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13175 14255: contig of 1081 bp in length  
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16720 16820: contig of 1052 bp in length  
16821 18498: gap of unknown length  
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21960 22601: contig of 3362 bp in length  
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23501 23501: contig of 1441 bp in length  
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37822 42562: contig of 4841 bp in length  
42562 42762: gap of unknown length  
42763 48044: gap of 5282 bp in length  
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59505 59605: gap of unknown length  
59606 67767: contig of 8162 bp in length  
67768 75525: gap of unknown length  
75525 75625: gap of 7658 bp in length  
75626 83842: gap of unknown length  
83843 83942: gap of 8217 bp in length  
83943 91792: gap of unknown length  
91793 91892: contig of 7850 bp in length  
91893 99982: gap of unknown length  
99982 100082: contig of 8090 bp in length  
100082 100887: gap of unknown length  
100887 108887: gap of 8805 bp in length  
108888 116779: gap of unknown length  
116779 116779: contig of 7792 bp in length  
116780 126915: gap of unknown length  
126915 127015: gap of 10036 bp in length  
127016 127015: gap of unknown length  
127016 138752: contig of 11737 bp in length  
138753 138852: gap of unknown length  
138853 149877: gap of 11025 bp in length  
149878 149977: gap of unknown length  
149978 161922: contig of 11945 bp in length  
161923 162022: gap of unknown length  
162023 174262: contig of 12240 bp in length  
174263 174362: gap of unknown length

\* 174363 188460: contig of 14098 bp in length  
 \* 188461 188560: gap of unknown length  
 \* 188561 203563: contig of 15003 bp in length  
 \* 203564 203663: gap of unknown length  
 \* 203664 221346: contig of 17683 bp in length  
 \* 221347 221446: gap of unknown length  
 \* 221447 247865: contig of 26419 bp in length.

FEATURES  
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 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone="CH230-2G16"

BASE COUNT 67196 a 54622 c 53919 g 67619 t 4509 others  
 ORIGIN

Query Match 5.1%; Score 19; DB 2; Length 247865;  
 Best Local Similarity 100.0%; Pred. NO. 16;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GAAGTGATGGAGCAAGTG 167  
 ||||||||||||||||  
 Db 44325 GAAGTGATGGAGCAAGTG 44307

Search completed: November 7, 2002, 21:51:28  
 Job time : 2444.62 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 : Search time 72.6545 Seconds  
(without alignments)  
11437.514 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggcacatttgcgattgt.....tgcctccgacacacatcct 369

Scoring table: OLIGO.MNC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 458492

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	22	AAF95007
2	369	100.0	369	24	ABT03274
3	369	100.0	369	24	ABL48956
4	315	85.4	1524	24	ABK33543
5	315	85.4	1619	24	ABT03277
6	315	85.4	1619	24	ABT03281
7	315	85.4	1619	24	ABL40345
8	315	85.4	1619	24	ABL40349
9	315	85.4	1890	22	AAF93845

10	315	85.4	1897	24	ABT03284
11	315	85.4	1897	24	ABL40352
12	314	85.1	2528	22	ABL18690
13	283	76.7	1953	21	AAF22400
14	283	76.7	1956	22	AAF64188
15	281	76.2	396	22	AAF94818
16	281	76.2	396	24	ABT03085
17	281	76.2	396	24	ABL48768
18	271	73.4	1010	24	ABT03282
19	271	73.4	1010	24	ABL40350
20	221	59.9	591	22	AAF94044
21	142	38.5	1608	24	ABQ54231
22	117	31.7	480	24	ABT03283
23	117	31.7	480	24	ABL40351
24	55	14.9	430	24	ABL81273
25	19	5.1	1226	22	AAI07456
26	19	5.1	2080	24	ABK62080
27	19	5.1	2222	24	ABK62081
28	18	4.9	237	24	ABL75913
29	18	4.9	256	24	ABL76335
30	18	4.9	286	24	ABL75647
31	18	4.9	484	22	AAK66339
32	18	4.9	484	22	AAK66340
33	18	4.9	1152	22	AAH52496
34	18	4.9	1542	23	AAK583729
35	18	4.9	1587	24	ABN91962
36	18	4.9	1596	24	ABN92620
37	18	4.9	1633	21	AACT74983
38	18	4.9	1791	21	AAK55958
39	18	4.9	2253	23	AAK591414
40	18	4.9	3281	22	AAH54960
41	18	4.9	3556	22	AAH54963
42	18	4.9	3633	22	AAH54943
43	18	4.9	4106	22	AAH54174
44	18	4.9	6399	23	ABL13144
45	18	4.9	8268	23	ABL15972

## ALIGNMENTS

RESULT 1	
AAF95007	AAF95007 standard; DNA; 369 BP.
XX	XX
AC	AAF95007:
XX	XX
DT	23-MAY-2001 (first entry)
XX	XX
DE	Human ovarian cancer associated coding sequence SEQ ID NO: 199.
XX	XX
KW	Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO200118046-A2.
XX	XX
PD	15-MAR-2001.
XX	XX
PF	08-SEP-2000; 2000WO-US24827.
XX	XX
PR	10-SEP-1999; 99US-0394374.
XX	XX
PR	01-MAY-2000; 2000US-0561778.
XX	XX
PR	15-AUG-2000; 2000US-0640173.
XX	XX
PR	07-SEP-2000; 2000US-0656668.
XX	XX
PA	(CORI-) CORIXA CORP.
XX	XX
PI	Xu J, Stolck JA;
XX	XX
DR	WPI, 2001-211395/21.
XX	XX
PT	Isolated polypeptides associated with ovarian carcinomas, and the

Human ovarian carc  
Ovarian carcinoma  
Human g protein co  
Human secreted pro  
Human secreted pro  
Human ovarian carc  
Human ovarian carc  
Ovarian carcinoma  
Human ovarian carc  
Ovarian carcinoma  
Primer specific fo  
Human ovarian ant  
Human ovarian carc  
Ovarian carcinoma  
Human ovarian carc  
Human reproductive  
Human CDNA encodin  
Human CDNA encodin  
Corn tassal-derive  
Corn tassal-derive  
Human immune/haema  
Human immune/haema  
S. epidermidis ope  
DNA encoding novel  
staphylococcus epi  
Human ORFX ORF538  
Murine G713 encodi  
DNA encoding novel  
S. epidermidis gen  
Human polypucleoti  
S. epidermidis gen  
S. epidermidis gen  
Drosophila melanog  
Drosophila melanog

PT nucleic acids that encode them, useful for the prevention diagnosis and  
 PT treatment of ovarian cancers -

PS Claim 18; Page 189; 189pp; English.

CC The present invention provides a number of coding sequences and proteins,  
 CC the over-expression of which is associated with ovarian carcinoma/cancer.  
 CC These can be used in the diagnosis, treatment and prevention of ovarian  
 CC cancer, optionally by gene therapy or in the form of a vaccine. The  
 CC present sequence is an example of one of these sequences.

SO Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match

Best Local Similarity 100.0%; Score 369; DB 22; Length 369;  
 Pred. No. 5,5e-187;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGCGATTGTTCTTCTTNCAGGCTTTGCGCTGCAATTCAGTCTACCA 60
   |||||||
DB 1 GGCACCTTTTGGCGATTGTTCTTCTTNCAGGCTTTGCGCTGCAATTCAGTCTACCA 60
QY 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGGAGTCATTGTGAATTGCAC 120
   |||||||
DB 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGGAGTCATTGTGAATTGCAC 120
QY 121 GGTGAACCTTCAAGACATGTCTCAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
   |||||||
DB 121 GGTGAACCTTCAAGACATGTCTCAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
QY 181 CCGCAAGCTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGTACCAAGTCTT 240
   |||||||
DB 181 CCGCAAGCTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGTACCAAGTCTT 240
QY 241 CTGCTCCCGCAGGAACTGAATCAGTTTGATCAGCTGTGCAACACCCCTTTTGTAA 300
   |||||||
DB 241 CTGCTCCCGCAGGAACTGAATCAGTTTGATCAGCTGTGCAACACCCCTTTTGTAA 300
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
   |||||||
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
QY 361 CACCATCCT 369
   |||||||
DB 361 CACCATCCT 369

```

RESULT 2

ABT03274

ID ABT03274 standard; cDNA; 369 BP.

XX ABT03274;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytostatic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX WPI; 2002-500186/53.

DR

PT Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Example 1; Page 187; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins

CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence

CC of the invention.

SO Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match

Best Local Similarity 100.0%; Score 369; DB 24; Length 369;  
 Pred. No. 5,5e-187;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGCGATTGTTCTTCTTNCAGGCTTTGCGCTGCAATTCAGTCTACCA 60
   |||||||
DB 1 GGCACCTTTTGGCGATTGTTCTTCTTNCAGGCTTTGCGCTGCAATTCAGTCTACCA 60
QY 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGGAGTCATTGTGAATTGCAC 120
   |||||||
DB 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGGAGTCATTGTGAATTGCAC 120
QY 121 GGTGAACCTTCAAGACATGTCTCAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
   |||||||
DB 121 GGTGAACCTTCAAGACATGTCTCAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
QY 181 CCGCAAGCTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGTACCAAGTCTT 240
   |||||||
DB 181 CCGCAAGCTCTGTGCATCATCAGGCGCTGTCTCATGCTCTGCGGGTACCAAGTCTT 240
QY 241 CTGCTCCCGCAGGAACTGAATCAGTTTGATCAGCTGTGCAACACCCCTTTTGTAA 300
   |||||||
DB 241 CTGCTCCCGCAGGAACTGAATCAGTTTGATCAGCTGTGCAACACCCCTTTTGTAA 300
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
   |||||||
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTTCTGCTCGGCCCTCANGCCATGGCTCCGAC 360
QY 361 CACCATCCT 369
   |||||||
DB 361 CACCATCCT 369

```

RESULT 3

ABL48956

ID ABL48956 standard; cDNA; 369 BP.

XX ABL48956;

DT 18-JUN-2002 (first entry)

DE Ovarian carcinoma sequence isolate 57887.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

OS Homo sapiens.

PN US2002004491-A1.

PD 10-JAN-2002.

PR 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

```

PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP.
PI WPI: 2002-171027/22.
XX
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX
PS Claim 1a; Page 116; 131pp; English.
XX
CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilized in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The sequences
CC given in records ABL48760-ABL48956 represent polynucleotides encoding
CC ovarian carcinoma proteins.
XX
SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other:
Query Match 100.0%; Score 369; DB 24; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.5e-187;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGCACCTTTTGGCGATTGTTGCTTTCAGCGCTTTCGCTGCAATCCAGTCTACCA 60
DB 1 GGCACCTTTTGGCGATTGTTGCTTTCAGCGCTTTCGCTGCAATCCAGTCTACCA 60
OY 61 GGTGAAGATTCCAGCTGACACAGACAGCTGCTCCCGAGTTCATTGTGAATTGCAC 120
DB 61 GGTGAAGATTCCAGCTGACACAGACAGCTGCTCCCGAGTTCATTGTGAATTGCAC 120
OY 121 GGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
OY 181 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTCCGCGGATACAGTCTCT 240
DB 181 CGGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTTCCGCGGATACAGTCTCT 240
OY 241 CCGTCTCCCGAGGAAATCACTGATTCATCAGTCTGTGATGACACCCCTCTTTTAA 300
DB 241 CCGTCTCCCGAGGAAATCACTGATTCATCAGTCTGTGATGACACCCCTCTTTTAA 300
OY 301 CGGGCCAAAGGCCCAAGAAAGGGGAGATTCTGCTCGGCTCANGCCATGAGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAGATTCTGCTCGGCTCANGCCATGAGCTCCGAC 360
OY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

```

ABK33543
ID ABK33543 standard; cDNA; 1524 BP.
XX
AC ABK33543;
XX
XX 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 15.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 23-AUG-2000; 2000WO-US23322.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001WO-US54280.
XX 25-MAY-2001; 2001WO-US17092.
XX
XX (GENE ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2002-172001/22.
XX P-PSDB: AAU83599.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour.
XX
XX Claim 2; Figure 15; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,

```

CC and in chromosome and gene mapping. ABK3356-ABK33657 represent human  
CC PRO protein coding sequences of the invention.

XX Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 85.4%; Score 315; DB 24; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 4.1e-158;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTGTACCAAGTGTGAAGATTCACCTGAAACAACGACT 89  
DB 170 CAGGCTTGGCGCTGCAATCCAGTGTACCAAGTGTGAAGATTCACCTGAAACAACGACT 229  
QY 90 GCTCTCTCCCGAGTTCATTTGTAATGACAGGTGAACGTTCAAGACATGTGTGAGAAG 149  
DB 230 GCTCTCTCCCGAGTTCATTTGTAATGACAGGTGAACGTTCAAGACATGTGTGAGAAG 289  
QY 150 AAGTATGAGACAAAGTCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 290 AAGTATGAGACAAAGTCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 349  
QY 210 GTCATATGCGCTTGTCCGGGTACAGTCTCTGCTCCCGAGGAAACTGAACAGTTT 269  
DB 350 GTCATATGCGCTTGTCCGGGTACAGTCTCTGCTCCCGAGGAAACTGAACAGTTT 409  
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTT 329  
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTT 469  
QY 330 CTGCTCGGCGCTCA 344  
DB 470 CTGCTCGGCGCTCA 484

## RESULT 5

ABT03277  
ID ABR03277 standard; cDNA; 1619 BP.

XX ABR03277;

DT 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.

DE Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX Cytostatic; gene; ss.

OS Homo sapiens.

XX WO200239885-A2.

PN 23-MAY-2002.

PD 13-NOV-2001; 2001WO-US45395.

PF 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Moles DA;

XX WPI: 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for

XX detecting the presence of ovarian cancer in a patient, and in

XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX Claim 2; Page 189-190; 197pp; English.

CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 85.4%; Score 315; DB 24; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 4.1e-158;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTGTACCAAGTGTGAAGATTCACCTGAAACAACGACT 89  
DB 30 CAGGCTTGGCGCTGCAATCCAGTGTACCAAGTGTGAAGATTCACCTGAAACAACGACT 89  
QY 90 GCTCTCTCCCGAGTTCATTTGTAATGACAGGTGAACGTTCAAGACATGTGTGAGAAG 149  
DB 90 GCTCTCTCCCGAGTTCATTTGTAATGACAGGTGAACGTTCAAGACATGTGTGAGAAG 149  
QY 150 AAGTATGAGACAAAGTCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 150 AAGTATGAGACAAAGTCCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
QY 210 GTCATATGCGCTTGTCCGGGTACAGTCTCTGCTCCCGAGGAAACTGAACAGTTT 269  
DB 210 GTCATATGCGCTTGTCCGGGTACAGTCTCTGCTCCCGAGGAAACTGAACAGTTT 269  
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTT 329  
DB 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTT 329  
QY 330 CTGCTCGGCGCTCA 344  
DB 330 CTGCTCGGCGCTCA 344

## RESULT 6

ABT03281  
ID ABR03281 standard; cDNA; 1619 BP.

XX ABR03281;

DT 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.

DE Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

XX Cytostatic; gene; ss.

OS Homo sapiens.

XX WO200239885-A2.

PN 23-MAY-2002.

PD 13-NOV-2001; 2001WO-US45395.

PF 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Moles DA;

XX WPI: 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for

XX detecting the presence of ovarian cancer in a patient, and in

XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

XX Claim 2; Page 195; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins  
CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 85.4%; Score 315; DB 24; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 4.1e-158;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89  
DB 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89  
QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGATGTGTCAAGAAG 149  
DB 90 GCTCTCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGATGTGTCAAGAAG 149  
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209  
DB 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209  
QY 210 GTCTCATCGCTCTGCGGGATCAGTCTGTGCTCCCGAGGAATGAACTCAGTTT 269  
DB 210 GTCTCATCGCTCTGCGGGATCAGTCTGTGCTCCCGAGGAATGAACTCAGTTT 269  
QY 270 GCATCAGCTGTGTGCAACACCCCTCTTTGTAAAGGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
DB 270 GCATCAGCTGTGTGCAACACCCCTCTTTGTAAAGGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
QY 330 CTGCTCTGGGCTCTCA 344  
DB 330 CTGCTCTGGGCTCTCA 344

RESULT 7  
ABL40345  
ID ABL40345 standard; CDNA; 1619 BP.  
XX ABL40345;  
XX 28-JUN-2002 (first entry)  
XX Ovarian carcinoma sequence isolate 57887 extended CDNA.  
DE Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
KW ss.  
XX Homo sapiens.  
XX US2002004491-A1.  
PN 10-JAN-2002.  
XX 03-APR-2001; 2001US-0825294.  
XX 10-SEP-1999; 99US-0394374.  
PR 01-MAY-2000; 2000US-0561778.  
PR 15-AUG-2000; 2000US-0640173.  
PR 07-SEP-2000; 2000US-065668.  
PR 14-NOV-2000; 2000US-0713550.  
XX (XUJJ/) XU J.  
PA (STOLJ/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
XX Xu J, Stolk JA, Algate PA, Fling SP;  
PI Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
XX WPI: 2002-171027/22.  
XX PF Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

PT prevention and/or treatment of cancer, especially ovarian cancer  
XX Claim 1a; Page 119-120; 131pp; English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides  
CC that may be utilized in cancer therapy, for example in a vaccine or  
CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the  
CC development of a cancer in a patient. They are also useful for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient and for determining the presence of a cancer in a patient.  
CC The isolated polynucleotides of the invention are useful for their  
CC ability to selectively form duplex molecules with complementary stretches  
CC of the entire desired gene or gene fragments, and for designing and  
CC preparing ribozyme molecules for inhibiting expression of tumour  
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
CC invention are also useful in recombinant DNA molecules to direct  
CC expression of a polypeptide in appropriate host cells. The current  
CC sequence represents the extended CDNA sequence of ovarian carcinoma  
CC isolate 57887 given in record ABL48956.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 85.4%; Score 315; DB 24; Length 1619;  
Best Local Similarity 100.0%; Pred. No. 4.1e-158;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89  
DB 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAACAAGACT 89  
QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGATGTGTCAAGAAG 149  
DB 90 GCTCTCTCCCGAGTTCATTGTGAATTGACGGTGAACGTTCAAGATGTGTCAAGAAG 149  
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209  
DB 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209  
QY 210 GTCTCATCGCTCTGCGGGATCAGTCTGTGCTCCCGAGGAATGAACTCAGTTT 269  
DB 210 GTCTCATCGCTCTGCGGGATCAGTCTGTGCTCCCGAGGAATGAACTCAGTTT 269  
QY 270 GCATCAGCTGTGTGCAACACCCCTCTTTGTAAAGGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
DB 270 GCATCAGCTGTGTGCAACACCCCTCTTTGTAAAGGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
QY 330 CTGCTCTGGGCTCTCA 344  
DB 330 CTGCTCTGGGCTCTCA 344

RESULT 8  
ABL40349  
ID ABL40349 standard; CDNA; 1619 BP.  
XX ABL40349;  
XX 28-JUN-2002 (first entry)  
XX Ovarian carcinoma O5915 nucleotide sequence.  
DE Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
KW ss.  
XX Homo sapiens.  
XX US2002004491-A1.  
PN 10-JAN-2002.  
XX 03-APR-2001; 2001US-0825294.  
XX PF

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XX 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
FI Xu J, Stolck JA, Algate PA, Fling SP;
XX WPI; 2002-171027/22.
XX
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
PT prevention and/or treatment of cancer, especially ovarian cancer -
XX
PS Claim 1a; Page 125-126; 131pp; English.
XX
CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The current
CC sequence represents the ovarian carcinoma O5915 nucleotide sequence.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other:

```

```

Query Match      85.4%; Score 315; DB 24; Length 1619;
Best Local Similarity 100.0%; Pred. No. 4.1e-158;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTGGCGCTCAATCCAGGCTACAGTGTGAAGATTCCAGCTGAACAACGACT 89
DB 30 CAGGCTTGGCGCTCAATCCAGGCTACAGTGTGAAGATTCCAGCTGAACAACGACT 89
QY 90 GCTCCTCCCGAGTTCATTGTGAATGCAACGGTGAACGTTCAAGACATGTGTGAGAAG 149
DB 90 GCTCCTCCCGAGTTCATTGTGAATGCAACGGTGAACGTTCAAGACATGTGTGAGAAG 149
QY 150 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 150 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
QY 210 GTTCATCAGGCTGCGGGGATACCAAGTCTTCTCCCAAGGGAACCTGAACCAATTT 269
DB 210 GTTCATCAGGCTGCGGGGATACCAAGTCTTCTCCCAAGGGAACCTGAACCAATTT 269
QY 270 GCATCAGCTCTGTGCAACACCCCTTTTGAAGGGGCCAAGGCCCAAGAAAGGGAGGTT 329
DB 270 GCATCAGCTCTGTGCAACACCCCTTTTGAAGGGGCCAAGGCCCAAGAAAGGGAGGTT 329
QY 330 CTGCTCTGGCCCTCA 344
DB 330 CTGCTCTGGCCCTCA 344

```

```

RESULT 9
AAF93845
ID AAF93845 standard; cDNA; 1890 BP.
XX

```

```

AC AAF93845;
XX
XX 23-MAY-2001 (first entry)
XX
XX Human cDNA encoding a membrane or secretory protein clone PSBC0181.
DE
XX Human: secretory protein; membrane protein; vaccine; gene therapy;
XX rheumatoid arthritis; diabetes; ss.
XX
XX Homo sapiens.
XX
XX EPI067182-A2.
XX
XX 10-JAN-2001.
XX
XX 07-JUL-2000; 2000EP-0114090.
XX
XX 08-JUL-1999; 99JP-0194179.
XX 11-JAN-2000; 2000JP-0118775.
XX 02-MAY-2000; 2000JP-0183766.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
XX P-PSDB: AAB88418.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by
XX AAB88317 - AAB88419. Included in the invention are primers
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX cDNA sequences of the invention. The invention also includes methods for
XX the production of antibodies directed against the proteins, and cDNA
XX sequences, which can be used in vaccines. The polynucleotide sequences
XX can be used in gene therapy. The polynucleotide sequences and the
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with inappropriate secretory
XX protein/membrane protein expression. The nucleic acids and complementary
XX sequences may also be used as DNA probes in diagnostic assays
XX (e.g. polymerase chain reactions (PCR)) to detect and quantify the
XX presence of similar nucleic acid sequences in samples. They may also be
XX used to study the expression and function of secretory proteins/membrane
XX polypeptides and their role in metabolism. The polypeptides may be used
XX as antigens in the production of antibodies against them and in assays to
XX identify modulators (agonists and antagonists) of expression and
XX activity. The antibodies and antagonists may also be used as therapeutic
XX agents to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of the
XX polypeptides in samples (e.g. by enzyme linked immunosorbent assay
XX (ELISA)). Examples of diseases which may be treated include rheumatoid
XX arthritis and diabetes.
XX
XX Sequence 1890 BP; 419 A; 528 C; 533 G; 410 T; 0 other:

```

```

Query Match      85.4%; Score 315; DB 22; Length 1890;
Best Local Similarity 100.0%; Pred. No. 4.2e-158;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTGGCGCTCAATCCAGGCTACAGTGTGAAGATTCCAGCTGAACAACGACT 89
DB 323 CAGGCTTGGCGCTCAATCCAGGCTACAGTGTGAAGATTCCAGCTGAACAACGACT 382
QY 90 GCTCCTCCCGAGTTCATTGTGAATGCAACGGTGAACGTTCAAGACATGTGTGAGAAG 149
DB 383 GCTCCTCCCGAGTTCATTGTGAATGCAACGGTGAACGTTCAAGACATGTGTGAGAAG 442
QY 150 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209

```

```

Db      443  AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTT 502
        |||
Oy      210  GTCTCATGCGCTCTGCCGGGTACAGTCTTGTGCTCCCGAGGAACTGAATCAGTTT 269
        |||
Db      503  GTCTCATGCGCTCTGCCGGGTACAGTCTTGTGCTCCCGAGGAACTGAATCAGTTT 562
        |||
Oy      270  GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329
        |||
Db      563  GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 622
        |||
Oy      330  CTGCTCGGCGCTCA 344
        |||
Db      623  CTGCTCGGCGCTCA 637

```

## RESULT 10

ABT03284  
ID ABT03284 standard; cDNA; 1897 BP.

AC ABT03284;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI: 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for

PT detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Claim 2; Page 196; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins

CC and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence

CC of the invention.

CC Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;

CC Query Match 85.4%; Score 315; DB 24; Length 1897;

CC Best Local Similarity 100.0%; Pred. NO. 4.2e-158;

CC Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy      150  AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTT 209
        |||
Db      429  AAGTATGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCTT 488
        |||
Oy      210  GTCTCATGCGCTCTGCCGGGTACAGTCTTGTGCTCCCGAGGAACTGAATCAGTTT 269
        |||
Db      489  GTCTCATGCGCTCTGCCGGGTACAGTCTTGTGCTCCCGAGGAACTGAATCAGTTT 548
        |||
Oy      270  GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329
        |||
Db      549  GCATCAGCTGCTGCAACACCCCTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 608
        |||
Oy      330  CTGCTCGGCGCTCA 344
        |||
Db      609  CTGCTCGGCGCTCA 623

```

## RESULT 11

ABL40352  
ID ABL40352 standard; cDNA; 1897 BP.

AC ABL40352;

DT 28-JUN-2002 (first entry)

DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

OS Homo sapiens.

PN US2002004491-A1.

PD 10-JAN-2002.

PF 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.

PA (STOLK/) STOLK J A.

PA (ALGATE/) ALGATE P A.

PA (FLIN/) FLIN S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;

DR WPI: 2002-171027/22.

DR P-PSDB: ABB09417.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

PT prevention and/or treatment of cancer, especially ovarian cancer

PS Claim 1a; Page 127-128; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides

CC that may be utilized in cancer therapy, for example in a vaccine or

CC gene therapy. Polypeptides and polynucleotides of the invention are

CC useful for detecting a cancer in a patient, for stimulating and/or

CC expanding T-cells specific for a tumour protein, and for inhibiting the

CC development of a cancer in a patient. They are also useful for

CC stimulating an immune response in a patient, and for treating a cancer in

CC a patient and for determining the presence of a cancer in a patient.

CC The isolated polynucleotides of the invention are useful for their

CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma O1034C/0591S consensus  
 CC nucleotide sequence.

Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other:

Query Match 85.4%; Score 315; DB 24; Length 1897;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-158;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTCAATCCAGTCTACCTGTCGTAAGAAATTCAGTGAACACGACT 89  
 Db 309 CAGGCTTGGCGCTCAATCCAGTCTACCTGTCGTAAGAAATTCAGTGAACACGACT 368  
 QY 90 GCTTCCTCCCGAGTTCATTGTGAATTGCAAGGTCGTAAGACATGTGTGAGAAAG 149  
 Db 369 GCTTCCTCCCGAGTTCATTGTGAATTGCAAGGTCGTAAGACATGTGTGAGAAAG 428  
 QY 150 AAGTATGAGAACAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCT 209  
 Db 429 AAGTATGAGAACAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCT 488  
 QY 210 GTTCATCGGCTGCGCGGATACGATCTTGTCTCCCAAGGAAATTCAGTCAATTT 269  
 Db 489 GTTCATCGGCTGCGCGGATACGATCTTGTCTCCCAAGGAAATTCAGTCAATTT 548  
 QY 270 GCATCAGCTCTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGGGAAGTT 329  
 Db 549 GCATCAGCTCTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGGGAAGTT 608  
 QY 330 CTGCTCGGCGCTCA 344  
 Db 609 CTGCTCGGCGCTCA 623

RESULT 12  
 AAD18690/c  
 ID AAD18690 standard; cDNA; 2528 BP.

XX AAD18690;

DT 18-DEC-2001 (first entry)

DE Human G protein coupled receptor (GPCR) 4941 cDNA.

KW Human: cardiovascular; tumourigenic disorder; aberrant angiogenesis;  
 KW gene therapy; aberrant vascularisation; arteriosclerosis; ovarian cancer;  
 KW ischaemia/reperfusion injury; hypertension; arterial inflammation;  
 KW psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;  
 KW myocardial infarction; Grave's disease; G protein coupled receptor;  
 KW GPCR 4941; vasotropic; hypotensive; antiinflammatory; cytostatic;  
 KW antidiabetic; antipsoriatic; leukaemia; ss.

XX Homo sapiens.

OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 42..1403

FT /product= "Human GPCR 4941"  
 FT /note= "The CDS is specifically claimed in claim 1 of  
 FT the specification"

XX WO200181634-A2.

XX 01-NOV-2001.

XX 25-APR-2001; 2001WO-US13788.

PR 26-APR-2000; 2000US-199908P.  
 PR 09-AUG-2000; 2000US-0635521.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Galvin KA, Rudolph-owen LA;  
 PI WPI: 2001-611743/70.  
 XX P-PSDB: AAE11751.

PT Identifying nucleic acids for the diagnosis and treatment of  
 PT cardiovascular and tumorigenic disorders, comprises identifying G  
 PT protein coupled receptor (GPCR)-4941

PS Example 1; Fig 1; 118pp: English.

CC The present invention relates to a method for identifying a nucleic acid  
 CC molecule (G protein coupled receptor gene, GPCR 4941) associated with a  
 CC cardiovascular or tumorigenic disorder. The method comprising contacting  
 CC a sample containing a nucleic acid molecule with a hybridisation probe or  
 CC amplification primers and detecting the presence. The invention is used  
 CC in gene therapy. The method of the invention is used for identifying  
 CC nucleic acids or polypeptides associated with a cardiovascular or  
 CC tumorigenic disorder such as aberrant angiogenesis, aberrant  
 CC vascularisation, arteriosclerosis, or ovarian cancer, ischaemia/  
 CC reperfusion injury, hypertension, restenosis, arterial inflammation,  
 CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial  
 CC infarction, Grave's disease and leukaemia. The methods can also detect  
 CC mRNA or genomic DNA in a sample. The present sequence is G protein  
 CC coupled receptor (GPCR) 4941 cDNA.

Sequence 2528 BP; 516 A; 766 C; 677 G; 567 T; 2 other:

Query Match 85.1%; Score 314; DB 22; Length 2528;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-157;  
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTGGCGCTCAATCCAGTCTACCTGTCGTAAGAAATTCAGTGAACACGACTG 90  
 Db 2217 AGGCTTGGCGCTCAATCCAGTCTACCTGTCGTAAGAAATTCAGTGAACACGACTG 2158  
 QY 91 CTCCTCCCGAGTTCATTGTGAATTGCAAGGTCGTAAGACATGTGTGAGAAAG 150  
 Db 2157 CTCCTCCCGAGTTCATTGTGAATTGCAAGGTCGTAAGACATGTGTGAGAAAG 2098  
 QY 151 AGTATGAGAACAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCT 210  
 Db 2097 AGTATGAGAACAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCT 2038  
 QY 211 TCTCATCGCTTGGCGGATACGATCTTGTCTCCCAAGGAAATTCAGTGAATTTG 270  
 Db 2037 TCTCATCGCTTGGCGGATACGATCTTGTCTCCCAAGGAAATTCAGTGAATTTG 1978  
 QY 271 CATCAGCTGTGTAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGGGAAGTTG 330  
 Db 1977 CATCAGCTGTGTAACACCCCTCTTTGTAAAGGGCCCAAGGCAAGGGAAGTTG 1918  
 QY 331 TGCCTCGGCGCTCA 344  
 Db 1917 TGCCTCGGCGCTCA 1904

RESULT 13  
 AAF22400/c  
 ID AAF22400 standard; cDNA; 1953 BP.

XX AAF22400;

DT 26-MAR-2001 (first entry)

DE Human secreted protein gene 28 SEQ ID NO:38.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;



KM antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KM cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
KM fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;  
KM rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
KM cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
KM ocular disorder; corneal infection; wound healing; skin aging;  
KM food additive; preservative; ss.  
XX  
OS Homo sapiens.  
XX  
PM WO200061629-A1.  
XX  
PD 19-OCT-2000.  
XX  
PF 06-APR-2000; 2000WO-US09071.  
XX  
PR 09-APR-1999; 99US-0128694.  
PR 20-JAN-2000; 2000US-0176931.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
PI Ruben SM, Komatsoulis G;  
XX  
DR WPI; 2000-647420/62.  
DR P-PSDB; AAB63161.  
XX  
PT Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX  
XX Claim 1; Page 440; 533pp; English.  
XX  
XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134  
XX to AAB63187. AAB63183 to AAB63231 represent more human secreted proteins  
XX and polypeptides homologous to them. Human secreted proteins have  
XX activities based on the tissues and cells the genes are expressed in.  
XX Examples of activities include: immunosuppressive; antiarthritic;  
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
XX cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
XX fungicide; and ophthalmological. The polynucleotides and proteins can be  
XX used to prevent, treat or ameliorate a medical condition in e.g. humans,  
XX mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are  
XX also used in diagnosing a pathological condition or susceptibility to a  
XX pathological condition. Disorders which are diagnosed or treated include  
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
XX disorders e.g. neoplasms of the breast or liver, cardiovascular  
XX disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral  
XX ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's  
XX disease, infections caused by bacteria, viruses and fungi and ocular  
XX disorders e.g. corneal infection. The polypeptides can also be used to  
XX aid wound healing and epithelial cell proliferation, to prevent skin  
XX aging due to sunburn, to maintain organs before transplantation, for  
XX supporting cell culture of primary tissues, to regenerate tissues and in  
XX chemotaxis. The polypeptides can also be used as a food additive or  
XX preservative to increase or decrease storage capabilities. AAF22374 to  
XX AAF22372 and AAB63133 represent sequences used in the exemplification of  
XX the present invention.  
XX  
XX Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;  
XX  
XX Query Match 76.7%; Score 283; DB 21; Length 1953;  
XX Best Local Similarity 100.0%; Pred. No. 5,3e-141;  
XX Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 30 CAGCGTTTCCGCTGCAATTCAGTGCACAGTGTGAAGATTCCAGCTGACAAACGACT 89  
DB 1645 CAGGCTTTCCGCTGCAATTCAGTGCACAGTGTGAAGATTCCAGCTGACAAACGACT 1586  
OY 90 GCCTCTCCCGCAGTTCATGTGATGATGACGAGGTTCAAGACATGTGTGAGAAG 149  
DB 1585 GCCTCTCCCGCAGTTCATGTGATGATGACGAGGTTCAAGACATGTGTGAGAAG 1526

OY 150 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGCCT 209  
DB 1525 AAGTATGAGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCATCAGCGCCT 1466  
OY 210 GTCCTATGCGCCCTCTCCGGGTACAGTCTTCTGCTGCCAGGGAACATCACTCACTT 269  
DB 1465 GTCCTATGCGCCCTCTCCGGGTACAGTCTTCTGCTGCCAGGGAACATCACTCACTT 1406  
OY 270 GCATCAGCTGCTGCAACACCCCTCTTGTACGGGCAAGGCC 312  
DB 1405 GCATCAGCTGCTGCAACACCCCTCTTGTACGGGCAAGGCC 1363  
RESULT 14  
AAF64188/c  
ID AAF64188 standard; cDNA; 1956 BP.  
XX  
AC AAF64188;  
XX  
DT 06-APR-2001 (first entry)  
XX  
XX Human secreted protein gene 13 SEQ ID NO:23.  
XX  
XX Human, secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
XX antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
XX nootropic; neuroprotective; antibacterial; virucide; fungicide;  
XX ophthalmological; vulnerability; autoimmune disease; cardiovascular disorder;  
XX hyperproliferative disorders; cerebrovascular disorder; wound healing;  
XX nervous system disorder; ocular disorder; skin aging; chemotaxis;  
XX food additive; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200077026-A1.  
XX  
XX 21-DEC-2000.  
XX  
XX 01-JUN-2000; 2000WO-US14973.  
XX  
XX 11-JUN-1999; 99US-0138630.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX  
XX Rosen CA, Ruben SM, Komatsoulis GA;  
XX  
XX WPI; 2001-071258/08.  
XX P-PSDB; AAB75318.  
XX  
XX Nucleic acid molecules encoding human secreted proteins, used in  
XX preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
XX Parkinson's diseases and cancers -  
XX  
XX Claim 1; Page 443-444; 542pp; English.  
XX  
XX Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide  
XX sequences AAF64176 - AAF64224. The specification includes amino acid  
XX sequences AAB75555 - AAB75606 which represent fragments of the human  
XX secreted proteins, and protein sequences with which they share homology.  
XX The proteins and polynucleotides, their agonists and antagonists have  
XX activities dependent on the tissues and cells in which they are  
XX expressed, examples of these activities include; immunosuppressive;  
XX antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;  
XX vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;  
XX virucide; fungicide; ophthalmological; and veterinary. The proteins  
XX polynucleotides, agonists and antagonists can be used to treat or detect  
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders  
XX e.g. neoplasms of the breast or liver, cardiovascular disorders  
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
XX infections caused by bacteria, viruses and fungi and ocular disorders  
XX e.g. corneal infection. The polypeptides can also be used to aid wound

CC healing and epithelial cell proliferation, to prevent skin ageing due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. Included in the invention are  
CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which  
CC are used in the isolation, identification and characterisation of the  
CC proteins of the invention.

XX Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;

Query Match 76.7%; Score 283; DB 22; Length 1956;

Best Local Similarity 100.0%; Pred. No. 5,3e-141;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAATCCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 89  
DB 1645 CAGGCTTTCGCTGCAATCCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 1586  
QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTGAACGTTCAAGCATGTGTCAAGAAG 149  
DB 1585 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTGAACGTTCAAGCATGTGTCAAGAAG 1526  
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209  
DB 1525 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 1466  
QY 210 GTCTCATCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAAGTCAAGTT 269  
DB 1465 GTCTCATCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAAGTCAAGTT 1406  
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCC 312  
DB 1405 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCAAGGCC 1363

RESULT 15

AAF94818

ID AAF94818 standard; cDNA; 396 BP.

XX AAF94818;

DT 23-MAY-2001 (first entry)

DE Human ovarian cancer associated coding sequence SEQ ID NO: 9.

XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

OS Homo sapiens.

PN WO200118046-A2.

PD 15-MAR-2001.

PF 08-SEP-2000; 2000WO-US24827.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA;

DR WPI; 2001-211395/21.

XX Isolated polypeptides associated with ovarian carcinomas, and the  
XX nucleic acids that encode them, useful for the prevention diagnosis and  
XX treatment of ovarian cancers -  
PS Claim 5; Page 119; 189pp; English.

CC The present invention provides a number of coding sequences and proteins,  
CC the over-expression of which is associated with ovarian carcinoma/cancer.  
CC These can be used in the diagnosis, treatment and prevention of ovarian  
CC cancer, optionally by gene therapy or in the form of a vaccine. The  
CC present sequence is an example of one of these sequences.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match 76.2%; Score 281; DB 22; Length 396;

Best Local Similarity 100.0%; Pred. No. 6e-140;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTCGCTGCAATCCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 89  
DB 40 CAGGCTTTCGCTGCAATCCAGTGTACCAAGTGAAGATTCACGCTGACACAGACT 99  
QY 90 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTGAACGTTCAAGCATGTGTCAAGAAG 149  
DB 100 GCTCTCTCCCGAGTTCATTGTGAATTGACAGGTGAACGTTCAAGCATGTGTCAAGAAG 159  
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209  
DB 160 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 219  
QY 210 GTCTCATCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAAGTCAAGTT 269  
DB 220 GTCTCATCGCTCTGCGGGGTACCACTCTTCTGCTCCCGAGGAAACTGAAGTCAAGTT 279  
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCAAGG 310  
DB 280 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGCGCAAGG 320

RESULT 16

ABT03085

ID ABT03085 standard; cDNA; 396 BP.

XX ABT03085;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 9.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytostatic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
XX detecting the presence of ovarian cancer in a patient, and in  
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
XX -  
PS Example 1; Page 116; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins  
XX and coding sequences. The sequences can be used in the diagnosis and

CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other:

Query Match 76.2%; Score 281; DB 24; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6e-140;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGAATTCAGTGTACAGTGTGAAGTAATTCAGCTGAACAGACT 89  
DB 40 CAGGCTTGGCGTGAATTCAGTGTACAGTGTGAAGTAATTCAGCTGAACAGACT 99  
QY 90 GCTCTCCCGCGAGTTCATGTGAATTCAGGGAAGTTCAGACATGTGTGAGAAAG 149  
DB 100 GCTCTCCCGCGAGTTCATGTGAATTCAGGGAAGTTCAGACATGTGTGAGAAAG 159  
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 160 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 219  
QY 210 GTCTCATCCGCTTGGCGGATCATGTACAGTGTCTCTCTCCCGGGAAGTGAACAGCTT 269  
DB 220 GTCTCATCCGCTTGGCGGATCATGTACAGTGTCTCTCTCCCGGGAAGTGAACAGCTT 279  
QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAG 310  
DB 280 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAG 320

RESULT 17  
ABL48768  
ID ABL48768 standard; cDNA; 396 BP.

XX ABL48768:

XX 18-JUN-2002 (first entry)

XX Ovarian carcinoma sequence isolate 21920.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
XX ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOL/) STOLK J A.

XX (ALGA/) ALGATE P A.

XX (FLIN/) FLING S P.

XX Xu J, Stolk JA, Algate PA, Fling SP;

XX WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
XX prevention and/or treatment of cancer, especially ovarian cancer,  
XX Claim 1a; Page 41-42; 131pp; English.  
XX The invention relates to ovarian tumour polynucleotides and polypeptides  
XX that may be utilised in cancer therapy, for example in a vaccine or

CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the

CC development of a cancer in a patient. They are also useful for

CC stimulating an immune response in a patient, and for treating a cancer in

CC a patient and for determining the presence of a cancer in a patient.

CC The isolated polynucleotides of the invention are useful for their

CC ability to selectively form duplex molecules with complementary stretches

CC of the entire desired gene or gene fragments, and for designing and

CC preparing ribozyme molecules for inhibiting expression of tumour

CC polypeptides in tumour cells. Polypeptides and polynucleotides of the

CC invention are also useful in recombinant DNA molecules to direct

CC expression of a polypeptide in appropriate host cells. The sequences

CC given in records ABL48760-ABL48956 represent polynucleotides encoding

CC ovarian carcinoma proteins.

XX Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other:

QY 30 CAGGCTTGGCGTGAATTCAGTGTACAGTGTGAAGTAATTCAGCTGAACAGACT 89  
DB 40 CAGGCTTGGCGTGAATTCAGTGTACAGTGTGAAGTAATTCAGCTGAACAGACT 99  
QY 90 GCTCTCCCGCGAGTTCATGTGAATTCAGGGAAGTTCAGACATGTGTGAGAAAG 149  
DB 100 GCTCTCCCGCGAGTTCATGTGAATTCAGGGAAGTTCAGACATGTGTGAGAAAG 159  
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 160 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 219  
QY 210 GTCTCATCCGCTTGGCGGATCATGTACAGTGTCTCTCTCCCGGGAAGTGAACAGCTT 269  
DB 220 GTCTCATCCGCTTGGCGGATCATGTACAGTGTCTCTCTCCCGGGAAGTGAACAGCTT 279  
QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAG 310  
DB 280 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCAAAG 320

RESULT 18  
ABF03282  
ID ABF03282 standard; cDNA; 1010 BP.

XX ABF03282:

XX 05-SEP-2002 (first entry)

XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 212.

XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
XX cytoskeletal; gene; ss.

XX Homo sapiens.

XX MO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX WPI; 2002-500186/53.

XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
PT detecting the presence of ovarian cancer in a patient, and in  
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
XX  
XX  
PS Claim 2; Page 195; 197pp; English.  
XX  
CC The present invention provides human ovarian cancer associated proteins  
CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.  
XX  
SQ Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;  
Query Match 73.4%; Score 271; DB 24; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 1.4e-134; Indels 0; Gaps 0;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 31 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCAGCTGAAACGACTG 90  
DB 258 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCAGCTGAAACGACTG 317  
OY 91 CTCCTCCCCAGTTCATGTGATGATGACGCGTGAACGTTCAAGACATGTGACAGAA 150  
DB 318 CTCCTCCCCAGTTCATGTGATGATGACGCGTGAACGTTCAAGACATGTGACAGAA 377  
OY 151 AGTGATGAGCAAGATGCGCGGATCATGTACCGCAAGTCTGTGATCATGACGGCCCTG 210  
DB 378 AGTGATGAGCAAGATGCGCGGATCATGTACCGCAAGTCTGTGATCATGACGGCCCTG 437  
OY 211 TCTCATGCGCTTCCCGGATGACAGTCTTCTGCTCCCGAGGAAATGAACTCAGTTTG 270  
DB 438 TCTCATGCGCTTCCCGGATGACAGTCTTCTGCTCCCGAGGAAATGAACTCAGTTTG 497  
OY 271 CATCAGCTGCTGCAACACCCCTCTTTGTAAAC 301  
DB 498 CATCAGCTGCTGCAACACCCCTCTTTGTAAAC 528  
RESULT 19  
ABL40350  
ID ABL40350 standard; cDNA; 1010 BP.  
XX  
AC ABL40350;  
XX  
DT 28-JUN-2002 (first entry)  
XX  
DE Ovarian carcinoma BF345141 nucleotide sequence.  
XX  
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
XX ss.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN US2002004491-A1.  
XX  
PD 10-JAN-2002.  
XX  
PE 03-APR-2001; 2001US-0825294.  
XX  
PR 10-SEP-1999; 99US-0394374.  
XX  
PR 01-MAY-2000; 2000US-0561778.  
XX  
PR 15-AUG-2000; 2000US-0640173.  
XX  
PR 07-SEP-2000; 2000US-065668.  
XX  
PR 14-NOV-2000; 2000US-0713550.  
XX  
PA (XUJ/) XU J.  
PA (STOLK/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PI XU J, Stolk JA, Algate PA, Fling SP;

XX  
DR WPI; 2002-171027/22.  
XX  
XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
PT prevention and/or treatment of cancer, especially ovarian cancer  
XX  
XX  
PS Claim 1a; Page 126-127; 131pp; English.  
XX  
CC The invention relates to ovarian tumour polynucleotides and polypeptides  
CC that may be utilised in cancer therapy, for example in a vaccine or  
CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the  
CC development of a cancer in a patient. They are also useful for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient and for determining the presence of a cancer in a patient.  
CC The isolated polynucleotides of the invention are useful for their  
CC ability to selectively form duplex molecules with complementary stretches  
CC of the entire desired gene or gene fragments, and for designing and  
CC preparing ribozyme molecules for inhibiting expression of tumour and  
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
CC invention are also useful in recombinant DNA molecules to direct  
CC expression of a polypeptide in appropriate host cells. The current  
CC sequence represents the ovarian carcinoma BF345141 nucleotide  
CC sequence.  
XX  
SQ Sequence 1010 BP; 266 A; 344 C; 254 G; 146 T; 0 other;  
Query Match 73.4%; Score 271; DB 24; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 1.4e-134;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 31 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCAGCTGAAACGACTG 90  
DB 258 AGGCTTGGCGCTGCAAAATCCAGTGTACAGTGTGAAGATTCAGCTGAAACGACTG 317  
OY 91 CTCCTCCCCAGTTCATGTGATGATGACGCGTGAACGTTCAAGACATGTGACAGAA 150  
DB 318 CTCCTCCCCAGTTCATGTGATGATGACGCGTGAACGTTCAAGACATGTGACAGAA 377  
OY 151 AGTGATGAGCAAGATGCGCGGATCATGTACCGCAAGTCTGTGATCATGACGGCCCTG 210  
DB 378 AGTGATGAGCAAGATGCGCGGATCATGTACCGCAAGTCTGTGATCATGACGGCCCTG 437  
OY 211 TCTCATGCGCTTCCCGGATGACAGTCTTCTGCTCCCGAGGAAATGAACTCAGTTTG 270  
DB 438 TCTCATGCGCTTCCCGGATGACAGTCTTCTGCTCCCGAGGAAATGAACTCAGTTTG 497  
OY 271 CATCAGCTGCTGCAACACCCCTCTTTGTAAAC 301  
DB 498 CATCAGCTGCTGCAACACCCCTCTTTGTAAAC 528  
RESULT 20  
AAF94044  
ID AAF94044 standard; DNA; 591 BP.  
XX  
AC AAF94044;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 478.  
XX  
XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
KW rheumatoid arthritis; diabetes; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
XX EP1067182-A2.  
XX  
PN 10-JAN-2001.  
XX  
PD 07-JUL-2000; 2000EP-0114090.  
PE

XX 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-018775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX  
 XX (HELI-) HELIX RES INST.  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 DR WPI; 2001-093989/11.  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 XX gene therapy or as candidate target molecules in drug development -  
 XX  
 PS Claim 4: SEQ ID 478; 609pp + CD ROM; English.  
 XX  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by  
 CC AAB88317 - AAB88419. Included in the invention are primers  
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
 CC cDNA sequences of the invention. The invention also includes methods for  
 CC the production of antibodies directed against the proteins, and cDNA  
 CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretory and  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g., polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies and antagonists may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g., by enzyme linked immunosorbent assay  
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.  
 CC  
 XX Sequence 591 BP; 108 A; 198 C; 173 G; 109 T; 3 other;  
 SQ  
 Query Match 59.9%; Score 221; DB 22; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-108;  
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTCAATTCAGTGTGAGAGATTCAGCTGAACAACGACT 89  
 DB 323 CAGGCTTGGCGCTCAATTCAGTGTGAGAGATTCAGCTGAACAACGACT 382  
 QY 90 GCTTCCTCCCGAGTTCATGTAATTCAGGTAAGGTTCAACATGTTGCAAGAAG 149  
 DB 383 GCTTCCTCCCGAGTTCATGTAATTCAGGTAAGGTTCAACATGTTGCAAGAAG 442  
 QY 150 AAGTATGAGAGCAAGTCCGGGATCATGACCGCAAGTCTGTGCATCATCAGCGGCT 209  
 DB 443 AAGTATGAGAGCAAGTCCGGGATCATGACCGCAAGTCTGTGCATCATCAGCGGCT 502  
 QY 210 GTCTCATGCGCTGTGCGGGTACCAAGTCTTGTCTCCCA 250  
 DB 503 GTCTCATGCGCTGTGCGGGTACCAAGTCTTGTCTCCCA 543

RESULT 21  
 AB054231  
 ID AB054231 standard; cDNA; 1608 BP.  
 XX  
 XX AB054231;  
 AC  
 XX 22-AUG-2002 (first entry)  
 DT  
 XX Human ovarian antigen HVCAG04 cDNA, SEQ ID NO:111.  
 DE

XX Human: ovarian antigen: ovary: ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive; chromosome 2q21-22;  
 KW gene; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO200200677-A1.  
 XX  
 XX 03-JAN-2002.  
 XX  
 XX 07-JUN-2001; 2001WO-US18569.  
 XX  
 XX 07-JUN-2000; 2000US-209467P.  
 XX  
 XX (HDMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Birse CE, Rosen CA;  
 XX WPI; 2002-147878/19.  
 XX P-PSDB; ABP41154.  
 XX  
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 XX useful in the prevention, treatment and diagnosis of cancer (e.g.,  
 XX ovarian cancer), immune disorders, cardiovascular disorders and  
 XX neurological diseases -  
 XX  
 XX Claim 1: SEQ ID NO 111; 2922pp; English.  
 XX  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 XX ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also  
 XX encompasses polypeptides 90% identical and polynucleotides 95% identical  
 XX to the sequences of the invention. The invention additionally relates to  
 XX recombinant vectors and host cells comprising human ovarian antigen  
 XX polynucleotides, antibodies against human ovarian antigens, and the use  
 XX of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 XX treating, prognosing or preventing various ovarian and/or breast-related  
 XX disorders. Such conditions include ovarian cancer and breast cancer, and  
 XX metastatic tumours of ovarian or breast origin, reproductive system  
 XX disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 XX vaginitis), immune disorders (e.g., congenital and acquired  
 XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 XX blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 XX respiratory disorders, neurological disorders, gastrointestinal disorders  
 XX and urinary system disorders. Ovarian antigen polypeptides and  
 XX polynucleotides may also be used in screening for compounds which  
 XX modulate ovarian antigen expression or activity. The polynucleotides may  
 XX further be used for gene therapy, chromosome mapping, in the  
 XX identification of individuals and in forensic analysis, and the  
 XX polypeptides may be used as food additives or to prepare antibodies  
 XX useful in disease diagnosis, drug targeting and phenotyping. The present  
 XX sequence represents cDNA encoding a human ovarian antigen of the  
 XX invention.  
 XX Note: The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format directly from WIPO  
 XX at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 1608 BP; 402 A; 402 C; 417 G; 381 T; 6 other;  
 Query Match 38.5%; Score 142; DB 24; Length 1608;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-65;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGATCATGTACCGCAAGTCTGTGATCATCAGCGCCGTCTCATGCGCTTGCAGGCT 230  
 |||||||  
 Db 106 GGATCATGTACCGCAAGTCTGTGATCATCAGCGCCGTCTCATGCGCTTGCAGGCT 165  
 |||||||  
 QY 231 ACCAGTCTTCTGCTCCCGCAGGAACTGAACTGAGTTTGCATCAGCTGCTGCACACC 290  
 |||||||  
 Db 166 ACCAGTCTTCTGCTCCCGCAGGAACTGAACTGAGTTTGCATCAGCTGCTGCACACC 225  
 |||||||  
 QY 291 CTCTTTGTAAAGGCGGCAAGGCC 312  
 |||||||  
 Db 226 CTCTTTGTAAAGGCGGCAAGGCC 247  
 |||||||  
 RESULT 22  
 ABR03283  
 ID ABR03283 standard; cDNA; 480 BP.  
 XX  
 AC ABR03283;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 213.  
 XX  
 KM Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
 KW cytosolic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200239885-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 13-NOV-2001; 2001WO-US45395.  
 XX  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PR 03-APR-2001; 2001US-0825294.  
 PR 02-OCT-2001; 2001US-0970966.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;  
 XX  
 DR WPI; 2002-500186/53.  
 XX  
 PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PT  
 PS Claim 2; Page 196; 197pp; English.  
 XX  
 XX The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.  
 CC  
 CC Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;  
 SO  
 Query Match 31.7%; Score 117; DB 24; Length 480;  
 Best Local Similarity 99.4%; Pred. No. 2.8e-52;  
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 30 CAGGCTTTCGCTGCATAATCCAGTGTGAGAAATTCAGCTGAACAACGACT 89  
 |||||||  
 Db 309 CAGGCTTTCGCTGCATAATCCAGTGTGAGAAATTCAGCTGAACAACGACT 368  
 |||||||  
 QY 90 GGTCTCCCGCCGAGTTTCATGTGAATGACGCTGAACCTTAAAGCATGTGTGAGAAG 149  
 |||||||  
 Db 369 GGTCTCCCGCCGAGTTTCATGTGAATGACGCTGAACCTTAAAGCATGTGTGAGAAG 428  
 |||||||  
 QY 150 AAGTATGAGCAAGTGCAGGATCATGTACCGCAAGTCTGTGCAT 197  
 |||||||

Db 429 AAGTATGAGCAAGTGCAGGATCATGTACCGCAAGTCTGTGCAT 476  
 |||||||  
 RESULT 23  
 ABL40351  
 ID ABL40351 standard; cDNA; 480 BP.  
 XX  
 AC ABL40351;  
 XX  
 DT 28-JUN-2002 (first entry)  
 XX  
 DE Ovarian carcinoma BE336607 nucleotide sequence.  
 XX  
 KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002004491-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 XX  
 DR WPI; 2002-171027/22.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer.  
 XX  
 XX Claim 1a; Page 127; 131pp; English.  
 XX  
 XX The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma BE336607 nucleotide sequence.  
 CC  
 CC Sequence 480 BP; 86 A; 154 C; 153 G; 87 T; 0 other;  
 SO  
 Query Match 31.7%; Score 117; DB 24; Length 480;  
 Best Local Similarity 99.4%; Pred. No. 2.8e-52;  
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 30 CAGGCTTTCGCTGCATAATCCAGTGTGAGAAATTCAGCTGAACAACGACT 89  
 |||||||  
 Db 309 CAGGCTTTCGCTGCATAATCCAGTGTGAGAAATTCAGCTGAACAACGACT 368  
 |||||||  
 QY 90 GGTCTCCCGCCGAGTTTCATGTGAATGACGCTGAACCTTAAAGCATGTGTGAGAAG 149  
 |||||||

DB 369 GCCTCTCCCCGAGTTCATGTGATTCGACGGTGAAGCTTCAAGACATCTGTGGAAG 428  
OY 150 AAGTATGAGCAAGTCCCGGATCATGTACCGCAAGTCTGTGCAT 197  
DB 429 AAGTATGAGCAAGTCCCGGATCATGTACCGCAAGTCTGTGCAT 476

RESULT 24  
ABL81273  
ID ABL81273 standard; cDNA; 430 BP.  
XX  
AC ABL81273;  
XX  
XX 17-MAY-2002 (first entry)  
DE Human ovarian cancer related cDNA clone SEQ ID NO:4251.  
XX  
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192581-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 29-MAY-2001; 2001WO-US17756.  
XX  
XX 26-MAY-2000; 2000US-207484P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Algate PA, Harlocker SL, Jones R;  
XX  
XX WPI; 2002-122075/16.  
XX  
XX Composition for therapy and diagnosis of ovarian cancer comprising  
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
PT polypeptide, antibody specific to polypeptide or T cell expressing  
PT polypeptide -

Claim 1; SEQ ID 4251; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers  
XX and immunostimulants; and a polypeptide (II) of a ovarian tumour  
XX polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
XX (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
XX ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
XX population of (II), or antigen presenting cells that express (II).  
XX (S1) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
XX (S1) can be used for detecting ovarian cancer in a patient's biological  
XX sample preferably serum or ovarian tissue. The method comprises  
XX contacting a biological sample from a patient with (IV), detecting the  
XX amount of polynucleotide hybridising to (IV) and comparing the amount to  
XX a predetermined cutoff value and thereby detecting ovarian cancer in the  
XX patient, where the amount of polynucleotide hybridising to (IV) is  
XX detected preferably by polymerase chain reaction (PCR). (I) comprising  
XX (III) and/or (II) is useful for stimulating and/or expanding T cells  
XX specific for an ovarian tumour protein comprising contacting T cells  
XX with (III) or (II). (III) is useful in design and preparation of  
XX ribozyme molecules for inhibiting expression of the tumour polypeptides  
XX and proteins in tumour cells; and to isolate a full length gene from a  
XX suitable library e.g., a tumour cDNA library using well known  
XX techniques.

XX Sequence 430 BP; 92 A; 121 C; 108 G; 109 T; 0 other:

XX  
XX Query Match 14.9%; Score 55; DB 24; Length 430;  
XX Best Local Similarity 100.0%; Pred. No. 3.8e-19;  
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 TCCCGAGGAACGACACAGTTCGATCAGCTGCTGCAACACCCCTCTTGA 299  
DB 1 TCCCGAGGAACGACACAGTTCGATCAGCTGCTGCAACACCCCTCTTGA 55

RESULT 25  
AAL07456/C  
ID AAL07456 standard; DNA; 1226 BP.  
XX  
XX AAL07456;  
AC  
XX 21-NOV-2001 (first entry)  
XX  
XX Human reproductive system related antigen DNA SEQ ID NO: 10144.  
DE Human; reproductive system related antigen; reproductive system disorder;  
XX cancer; gene therapy; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200155320-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01339.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX  
XX 04-FEB-2000; 2000US-0180628.  
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XX 24-FEB-2000; 2000US-0184664.  
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XX 02-MAR-2000; 2000US-0186350.  
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XX 16-MAR-2000; 2000US-0189874.  
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XX 17-MAR-2000; 2000US-0190076.  
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XX 18-APR-2000; 2000US-0198123.  
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XX 19-MAY-2000; 2000US-0205515.  
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XX 07-JUN-2000; 2000US-0209467.  
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XX 28-JUN-2000; 2000US-0214886.  
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XX 30-JUN-2000; 2000US-0215135.  
XX  
XX 07-JUL-2000; 2000US-0216647.  
XX  
XX 07-JUL-2000; 2000US-0216880.  
XX  
XX 11-JUL-2000; 2000US-0217487.  
XX  
XX 11-JUL-2000; 2000US-0217496.  
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XX 14-JUL-2000; 2000US-0218290.  
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XX 26-JUL-2000; 2000US-0220963.  
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XX 26-JUL-2000; 2000US-0220964.  
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XX 14-AUG-2000; 2000US-0224518.  
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XX 14-AUG-2000; 2000US-0224519.  
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XX 14-AUG-2000; 2000US-0225213.  
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XX 14-AUG-2000; 2000US-0225214.  
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XX 14-AUG-2000; 2000US-0225266.  
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XX 14-AUG-2000; 2000US-0225267.  
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XX 14-AUG-2000; 2000US-0225268.  
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XX 14-AUG-2000; 2000US-0225270.  
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XX 14-AUG-2000; 2000US-0225447.  
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XX 14-AUG-2000; 2000US-0225757.  
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XX 14-AUG-2000; 2000US-0225758.  
XX  
XX 14-AUG-2000; 2000US-0225759.  
XX  
XX 14-AUG-2000; 2000US-0225759.  
XX  
XX 18-AUG-2000; 2000US-0226279.  
XX  
XX 22-AUG-2000; 2000US-0226681.  
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XX 22-AUG-2000; 2000US-0226868.  
XX  
XX 22-AUG-2000; 2000US-0227182.  
XX  
XX 23-AUG-2000; 2000US-0227009.  
XX  
XX 30-AUG-2000; 2000US-0228924.  
XX  
XX 01-SEP-2000; 2000US-0229287.  
XX  
XX 01-SEP-2000; 2000US-0229343.  
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XX 01-SEP-2000; 2000US-0229343.  
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XX 01-SEP-2000; 2000US-0229344.  
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XX 01-SEP-2000; 2000US-0229345.  
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XX 05-SEP-2000; 2000US-0229509.  
XX  
XX 05-SEP-2000; 2000US-0229513.  
XX  
XX 06-SEP-2000; 2000US-0230437.  
XX  
XX 06-SEP-2000; 2000US-0230438.  
XX  
XX 08-SEP-2000; 2000US-0231242.  
XX  
XX 08-SEP-2000; 2000US-0231243.  
XX  
XX 08-SEP-2000; 2000US-0231244.  
XX  
XX 08-SEP-2000; 2000US-0231413.  
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XX 08-SEP-2000; 2000US-0231414.  
XX  
XX 08-SEP-2000; 2000US-0232080.





PA (ELIL ) LILLY & CO ELL.  
 XX  
 PI Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;  
 XX  
 DR WPI: 2002-304057/34.  
 DR P-PSDB: AAU91328.  
 XX  
 PT Novel polypeptides and polynucleotides of secreted proteins useful for  
 PT treating various diseases such as multiple sclerosis, cancer,  
 PT autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's  
 PT disease -  
 XX  
 PS Claim 1: Page 154-157; 235pp: English.  
 XX  
 CC The invention relates to a novel human secreted polypeptide having  
 CC sequence 90% identical to the polypeptide sequences of LP105, LP061,  
 CC LP224, LP240, LP239(a), LP243(a), LP243(b), LP253, LP218, LP251(a),  
 CC LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b),  
 CC or LP223(b). Also included are the nucleic acids encoding the LP  
 CC proteins (including complement, fragments encoding mature forms of the  
 CC polypeptide or variant), a vector comprising the nucleic acid, a  
 CC host cell comprising the vector, the preparation of the protein,  
 CC an anti-LP antibody, anti/agonists of LP and anti-LP-encoding mRNA  
 CC ribozymes. The secreted protein or its agonist is useful in the  
 CC manufacture of a medicament for treating a mammal suffering from a  
 CC disease (and in diagnosis), condition or disorder associated with a  
 CC aberrant levels of the secreted protein e.g. cancer, autoimmune diseases,  
 CC arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease,  
 CC meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction,  
 CC mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid  
 CC arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple  
 CC sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive  
 CC disorder, autism, panic disorder, learning disabilities, ALS  
 CC (amyotrophic lateral sclerosis) psychoses, disorders in feeding,  
 CC sleep patterns, balance, and perception. The secreted protein is further  
 CC useful for identifying compounds that bind to the secreted protein. The  
 CC present sequence encodes a novel secreted protein of the invention.  
 CC  
 SQ Sequence 2080 BP; 303 A; 758 C; 676 G; 342 T; 1 other;  
 XX  
 Query Match 5.1%; Score 19; DB 24; Length 2080;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 317 AAAAGGGGAAGTTCTGCTT 335  
 Db 1811 AAAAGGGGAAGTTCTGCTT 1793  
 RESULT 27  
 ABLK62081/c  
 ID ABLK62081 standard; cDNA: 2222 BP.  
 XX  
 AC ABLK62081;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human cDNA encoding novel secreted protein LP243(b).  
 XX  
 KW Human; ss: gene: secreted protein; cancer; autoimmune disease;  
 KW arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease;  
 KW meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction;  
 KW mania; stroke; cardiovascular disease; atherosclerosis; sepsis; anaemia;  
 KW rheumatoid arthritis; hypothyroidism; allergic response; liver failure;  
 KW multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder;  
 KW autism; panic disorder; learning disability; feeding disorder;  
 KW sleep pattern disorder; balance; perception; Th1-dependent insulinitis;  
 KW adult respiratory distress syndrome; ARDS.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200214358-A2.  
 PN

XX  
 PD 21-FEB-2002.  
 XX  
 PE 30-JUL-2001; 2001WO-US21124.  
 XX  
 PR 11-AUG-2000; 2000US-224642P.  
 XX  
 PR 19-OCT-2000; 2000US-241779P.  
 XX  
 PA (ELIL ) LILLY & CO ELL.  
 XX  
 PI Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;  
 XX  
 DR WPI: 2002-304057/34.  
 DR P-PSDB: AAU91329.  
 XX  
 PT Novel polypeptides and polynucleotides of secreted proteins useful for  
 PT treating various diseases such as multiple sclerosis, cancer,  
 PT autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's  
 PT disease -  
 XX  
 PS Claim 1: Page 160-163; 235pp: English.  
 XX  
 CC The invention relates to a novel human secreted polypeptide having  
 CC sequence 90% identical to the polypeptide sequences of LP105, LP061,  
 CC LP224, LP240, LP239(a), LP243(a), LP243(b), LP253, LP218, LP251(a),  
 CC LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b),  
 CC or LP223(b). Also included are the nucleic acids encoding the LP  
 CC proteins (including complement, fragments encoding mature forms of the  
 CC polypeptide or variant), a vector comprising the nucleic acid, a  
 CC host cell comprising the vector, the preparation of the protein,  
 CC an anti-LP antibody, anti/agonists of LP and anti-LP-encoding mRNA  
 CC ribozymes. The secreted protein or its agonist is useful in the  
 CC manufacture of a medicament for treating a mammal suffering from a  
 CC disease (and in diagnosis), condition or disorder associated with a  
 CC aberrant levels of the secreted protein e.g. cancer, autoimmune diseases,  
 CC arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease,  
 CC meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction,  
 CC mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid  
 CC arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple  
 CC sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive  
 CC disorder, autism, panic disorder, learning disabilities, ALS  
 CC (amyotrophic lateral sclerosis) psychoses, disorders in feeding,  
 CC sleep patterns, balance, and perception. The secreted protein is further  
 CC useful for identifying compounds that bind to the secreted protein. The  
 CC present sequence encodes a novel secreted protein of the invention.  
 CC  
 SQ Sequence 2222 BP; 317 A; 827 C; 733 G; 345 T; 0 other;  
 XX  
 Query Match 5.1%; Score 19; DB 24; Length 2222;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 317 AAAAGGGGAAGTTCTGCTT 335  
 Db 1953 AAAAGGGGAAGTTCTGCTT 1935  
 RESULT 28  
 ABL75913  
 ID ABL75913 standard; cDNA: 237 BP.  
 XX  
 AC ABL75913;  
 XX  
 DT 14-MAY-2002 (first entry)  
 XX  
 DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO: 5287.  
 XX  
 KW Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPS;  
 KW inheritance; characteristic; growth; development; disease resistance;  
 KW environmental adaptability; quality; yield; molecular marker;  
 KW multigene trait; plant breeding; corn tassel; gene; ss.  
 XX



PM US2001051335-A1.  
XX  
PD 13-DEC-2001.  
XX  
PF 16-APR-1999; 99US-0294093.  
XX  
PR 21-APR-1998; 98US-082567P.  
XX  
PA (LALG/) LALGUDI R V.  
PA (ITOL/) ITO L Y.  
PA (SHER/) SHERMAN B K.  
PI Laljudi RV, Ito LY, Sherman BK;  
DR WPI: 2002-163647/21.  
XX  
PT Novel purified corn tassel-derived polynucleotide useful for  
PT determining altered gene expression, to recover regulatory elements and  
PT to follow inheritance of desirable characteristics through hybrid  
PT breeding programs -  
XX  
PS Claim 1; SEQ ID 5021; 201pp; English.  
XX  
CC The present sequence describes a purified corn tassel-derived  
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence  
CC selected from those given in ABL70627 to ABL76833. The cdps sequences  
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences (1)  
CC can be used for determining altered gene expression, to recover  
CC regulatory elements and to follow inheritance of desirable  
CC characteristics through hybrid breeding programs. (1) are also useful  
CC in the evaluation, and alteration of desired characteristics associated  
CC with growth and development, disease resistance, environmental  
CC adaptability, quality and yield, and as molecular markers for studying  
CC inheritance of multigene traits in a plant breeding program. (1) can be  
CC used to produce a tassel-specific profile of gene transcription, a  
CC transcript image, to clone regulatory elements for use in transformation  
CC vectors, to express a polypeptide, to identify, isolate or extend  
CC identical or related corn tassel nucleic acid sequences from DNA  
CC libraries, in nucleic acid hybridisation or amplification technologies,  
CC as query sequences to determine homology of known sequences, as probe  
CC for use in Southern or Northern hybridisation, and to identify the  
CC presence of and/or to determine the degree of similarity between two  
CC (or more) nucleic acid sequences.  
XX  
SQ Sequence 286 BP; 69 A; 74 C; 83 G; 52 T; 8 other:  
Query Match 4.9%; Score 18; DB 24; Length 286;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 192 GTGCATCATCAGCGCCT 209  
DB 58 GTGCATCATCAGCGCCT 75  
RESULT 31  
AAK66339/C  
ID AAK66339 standard; DNA; 484 BP.  
XX  
AC AAK66339;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21151.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
OS Homo sapiens.  
XX  
XX MO200157182-A2.  
PN  
PD 09-AUG-2001.

XX  
PF 17-JAN-2001; 2001WO-0501354.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0225759.  
PR 22-AUG-2000; 2000US-0225759.  
PR 22-AUG-2000; 2000US-0226881.  
PR 22-AUG-2000; 2000US-0226881.  
PR 22-AUG-2000; 2000US-0226881.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0228287.  
PR 01-SEP-2000; 2000US-0228287.  
PR 01-SEP-2000; 2000US-0228343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0233397.  
PR 14-SEP-2000; 2000US-0233398.  
PR 14-SEP-2000; 2000US-0233399.  
PR 14-SEP-2000; 2000US-0233400.  
PR 14-SEP-2000; 2000US-0234001.  
PR 14-SEP-2000; 2000US-0234011.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.

PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251899.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0255978.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 PR Rosen CA, Barash SC, Ruben SM;  
 PR WPI; 2001-483426/52.  
 PR XX

PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metastasis -  
 PS Disclosure: SEQ ID NO 21151; 3071bp + Sequence Listing; English.  
 XX  
 XX AAK64951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
 CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patient's own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/haematopoietic-related diseases, especially  
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
 CC to AAK67694 represent human immune/haematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169  
 CC represent sequences used in the exemplification of the present invention.  
 CC  
 SQ Sequence 484 BP; 124 A; 110 C; 69 G; 181 T; 0 other;  
 Query Match 4.9%; Score 18; DB 22; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 143 CAGAAAGAAGTGTGAG 160  
 Db 457 CAGAAAGAAGTGTGAG 440  
 ID AAK66340 standard; DNA; 484 BP.  
 AC AAK66340;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DT  
 XX  
 XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21152.  
 DE  
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytostatic; gene therapy; vaccine; metastasis; ds.  
 OS Homo sapiens.  
 XX  
 PN WO200157182-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 XX 17-JAN-2001; 2001WO-US01354.  
 PF  
 XX  
 XX 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 11-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR

PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226686.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241121.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251899.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-JAN-2001; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-483426/52.  
XX  
XX  
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and  
PT metastasis -  
PT  
XX  
XX  
PS Disclosure; SEQ ID NO 21152; 3071pp + Sequence Listing; English.  
XX  
XX  
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX

SO Sequence 484 BP; 124 A; 110 C; 69 G; 181 T; 0 other;

Query Match 4.9%; Score 18; DB 22; Length 484;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 CAGAAAGAGTGTGAG 160  
|||||  
DB 457 CAGAAAGAGTGTGAG 440

## RESULT 33

AAH52496/c  
ID AAH52496 standard; DNA; 1152 BP.

AC AAH52496;

DT 03-SEP-2001 (first entry)

DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:385.

KW Staphylococcus epidermidis sri strain; infection; diagnosis;  
KM vaccination; endocarditis; ds.

OS Staphylococcus epidermidis.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000WO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAX) GLAXO GROUP LTD.

PI Kimerly WJ;

DR WPI: 2001-316495/33.

DR P-PSDB; AAG81646.

PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 144; 2188pp; English.

CC AAH5304 to AAH5370 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG8120, from Staphylococcus epidermidis.  
CC (I) and (II) can have antibacterial activity and therefore can be used  
CC in vaccination. The nucleic acids (I) may be used to produce the  
CC S. epidermidis polypeptides (II) via the production of vectors  
CC containing them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to  
CC AAH5509 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5501 to  
CC AAH5508 represent oligonucleotide sequences and primers which are used  
CC in the exemplification of the present invention.  
CC N.B. The present invention specifically claims all the polynucleotide  
CC sequences given in the sequence listing of the present specification,  
CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
CC no sequences are present for SEQ ID NO:4455 to 4464.

SO Sequence 1152 BP; 429 A; 169 C; 241 G; 313 T; 0 other;

Query Match 4.9%; Score 18; DB 22; Length 1152;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGCTGCAAC 286  
|||||  
DB 864 TGCATCAGCTGCTGCAAC 847

## RESULT 34

AAH83729/c  
ID AAH83729 standard; cDNA; 1542 BP.

AC AAH83729;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19533.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB; ABG19542.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -

PS Claim 1; SEQ ID NO 19533; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 1542 BP; 416 A; 434 C; 433 G; 259 T; 0 other;

Query Match 4.9%; Score 18; DB 23; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 23;



KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KM thrombosis; contraceptive; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200058473-A2.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 31-MAR-2000; 2000MO-US08621.  
 XX  
 PR 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach M;  
 PI  
 DR WPI: 2000-602362/57.  
 DR P-PSDB; AAB40774.  
 XX  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX  
 PS Claim 5; Page 1013-1014; 5507pp; English.  
 XX  
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;  
 CC antiparasitic; antiparkinsonian; neurotropic; neuroprotective;  
 CC osteoplastic; anticoagulant; antithrombotic; immunosuppressive;  
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotrophic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antineoplastic; antibacterial; antiviral; antifungal; antineumatic;  
 CC antihypertensive; antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease, to enhance  
 CC coagulation, to inhibit thrombosis, and as a contraceptive.  
 XX  
 SO Sequence 1633 BP; 335 A; 515 C; 480 G; 303 T; 0 other;  
 XX  
 Query Match 4.9%; Score 18; DB 21; Length 1633;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 ACCAGTCTTCTGCTCC 248  
 DB 315 ACCAGTCTTCTGCTCC 332  
 XX  
 RESULT 38  
 AAS55968/c  
 ID AAS55968 standard; cDNA; 1791 BP.  
 XX  
 AC AAS55968;  
 XX  
 DT 05-SEP-2000 (first entry)  
 XX  
 DE Murine G713 encoding cDNA SEQ ID NO:6.  
 XX

KM Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia;  
 KM diallelic marker; polymorphism; central nervous disease; detection;  
 KM neuroleptic; G713 gene expression inhibitor; genotyping;  
 KM brain disorder; psychiatric disorder; bipolar disorder; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200022122-A2.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 12-OCT-1999; 99WO-IB01730.  
 XX  
 PR 13-OCT-1998; 98US-0103955.  
 PR 30-OCT-1998; 98US-0106457.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D, Essiloux L;  
 PI  
 DR WPI: 2000-317979/27.  
 DR P-PSDB; AAY90963.  
 XX  
 XX Novel polynucleotide of human G713 gene useful for diagnosis and  
 PT prophylactic treatment of brain, psychiatric disorders like  
 PT schizophrenia and bipolar disorders -  
 XX  
 PS Claim 1; Page 234-236; 271pp; English.  
 XX  
 CC The present invention describes an isolated, purified or recombinant  
 CC polynucleotide (PN) (I) comprising a contiguous span of 8 to 50  
 CC nucleotides, where the span includes a G713 or chromosome 13q31-q33  
 CC related diallelic marker. (I) has neuroleptic activity and can be used  
 CC as a G713 gene expression inhibitor. (I) can be used genotyping to  
 CC estimate the frequency of an allele of a G713 or chromosome 13q31-q33  
 CC related diallelic marker in a population, and of a haplotype for a set  
 CC of diallelic markers in a population. (I) is also useful in detecting  
 CC an association between a haplotype and a trait. The frequency is used  
 CC for detecting an association between a genotype and a trait being  
 CC schizophrenia. The genotype is used to determine whether an individual  
 CC is at risk of developing schizophrenia. (I) can also be used as a  
 CC medication against several disorders preferably brain, psychiatric  
 CC disorders such as schizophrenia and bipolar disorder. Early  
 CC identification of risk of developing schizophrenia is possible, which  
 CC would enable early and/or prophylactic treatment. AAS55964 to AAS55966  
 CC represent human G713 genomic DNA sequences; AAS55967 encodes the human  
 CC G713 protein AAY90962; AAS55968 encodes the murine G713 protein  
 CC AAY90963; AAS55992 to AAS56030 represent human chromosome 13q31-q33 locus  
 CC diallelic markers A12 to A49; AAS55969 to AAS55991, and AAS56031 and  
 CC AAS56032 represent PCR primers used in the exemplification of the present  
 CC invention.  
 XX  
 SO Sequence 1791 BP; 389 A; 531 C; 508 G; 363 T; 0 other;  
 XX  
 Query Match 4.9%; Score 18; DB 21; Length 1791;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 84 ACGACTGCTCTCCGCCG 101  
 DB 695 ACGACTGCTCTCCGCCG 678  
 XX  
 RESULT 39  
 AAS91414/c  
 ID AAS91414 standard; cDNA; 2253 BP.  
 XX  
 AC AAS91414;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #27218.  
 XX



KN	Human; chromosome mapping; gene mapping; gene therapy; forensics;
KV	Food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX	
OS	Homo sapiens.
PN	WO200175067-A2.
PD	11-OCT-2001.
XX	
PE	30-MAR-2001; 2001WO-US08631.
PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	
PA	(HYSE-) HYSEQ INC.
PI	Drmamac RT, Liu C, Tang YT;
XX	
DR	WPI: 2001-639362/73.
XX	
PT	P-PSDB; ABG27227.
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
XX	biodiversity
XX	
PS	Claim 1: SEQ ID No 27218; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations in
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_ptc_sequences.
XX	
SO	Sequence 2253 BP; 541 A; 612 C; 527 G; 573 T; 0 other;
	Query Match 4.9%; Score 18; DB 23; Length 2253;
	Best Local Similarity 100.0%; Pred. No. 23;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	91 CTCCTCCCCGAGTTCAT 108
DB	739 CTCCTCCCCGAGTTCAT 722
RESULT 40	
AAH54960/c	
ID	AAH54960 standard; DNA: 3281 BP.
XX	
XX	AAH54960;
DT	03-SEP-2001 (first entry)
DE	S. epidermidis genomic polynucleotide sequence SEQ ID NO:4324.
XX	Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX	vacillation; endocarditis; ds.
XX	

XX	Staphylococcus epidermidis.
OS	
XX	WO200134809-A2.
PN	
XX	17-May-2001.
PD	
XX	
PJ	09-Nov-2000; 2000WO-US30782.
XX	
PR	09-Nov-1999; 99US-0164258.
XX	
PA	(GLAXO ) GLAXO GROUP LTD.
XX	
PI	Kimmerly WJ;
XX	
DR	WPI; 2001-316495/33.
XX	
PT	Nucleic acids encoding polypeptides from staphylococcus epidermidis,
XX	useful for vaccinating against infections, e.g. endocarditis -
PS	Claim 8; Page 2062-2063; 2188bp; English.
CC	AH52304 to AH5970 represent nucleic acids (I) encoding polypeptides
CC	(II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC	(I) and (II) can have antibacterial activity and therefore can be used
CC	in vaccination. The nucleic acids (I) may be used to produce the
CC	S. epidermidis polypeptides (II) via the production of vectors
CC	containing them which are used to produce hosts cells which express the
CC	polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC	used to vaccinate subjects and to raise antibodies against the bacteria.
CC	The polypeptides may also be used to assay for other inhibitors of their
CC	activity and therefore identify compounds that may be used for the
CC	treatment of S. epidermidis infections, e.g. endocarditis. AAH5971 to
CC	AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC	polynucleotide sequences from the present invention. AAH5091 to
CC	AAH5098 represent oligonucleotide sequences and primers which are used
CC	in the exemplification of the present invention.
CC	N.B. The present invention specifically claims all the polynucleotide
CC	sequences given in the sequence listing of the present specification,
CC	however the sequence listing only goes up to SEQ ID NO:4454 so even
CC	though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC	no sequences are present for SEQ ID NO:4455 to 4464.
XX	
SO	Sequence 3281 BP; 1226 A; 464 C; 636 G; 955 T; 0 other;
Query Match	4.9%; Score 18; DB 22; Length 3281;
Best Local Similarity	100.0%; Pred. No. 23;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	269 TGCAACGACTGCTGCAC 286 
Db	1118 TGCAACGACTGCTGCAC 1101
RESULT 41	
AA159883	
ID	AA159883 standard; cDNA; 3556 BP.
XX	
AC	AA159883;
XX	
D7	22-OCT-2001 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 3872.
XX	
KW	Human; neotropic; immunosuppressant; cytosolic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW	leukaemia; ss.
XX	
SS	Homo sapiens.
XX	

PN WO200153312-A1.  
XX  
XX 26-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US34263.  
XX  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI: 2001-442253/47.  
DR P-PSDB; AAM40727.  
XX  
XX Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
XX Claim 1; SEQ ID NO 3872; 10078bp; English.  
XX  
XX The invention relates to human nucleic acids (AA15798-AA161369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilization of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
XX Sequence 3556 BP; 776 A; 1071 C; 1057 G; 652 T; 0 other;  
SQ  
Query Match 4.9%; Score 18; DB 22; Length 3556;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 231 ACCAGTCTCTGCTGCC 248  
DB 629 ACCAGTCTCTGCTGCC 646  
|||||  
RESULT 42  
AAH54943/c  
ID AAH54943 standard; DNA; 3633 BP.  
XX  
XX AAH54943;  
XX  
XX 03-SEP-2001 (first entry)  
XX  
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:4307.  
DE  
XX  
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;  
KW vaccination; endocarditis; ds.  
XX  
XX Staphylococcus epidermidis.  
OS  
XX  
XX WO200134809-A2.  
PN

XX  
XX 17-MAY-2001.  
PD  
XX  
XX 09-NOV-2000; 2000WO-US30782.  
FE  
XX  
XX 09-NOV-1999; 99US-0164258.  
PR  
XX  
XX (GLAXO) GLAXO GROUP LTD.  
PA  
XX  
XX Kimmery WJ;  
PI  
XX  
XX WPI: 2001-316495/33.  
DR  
XX  
XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
PT useful for vaccinating against infections, e.g. endocarditis -  
XX  
XX Claim 8; Page 2042-2043; 2188bp; English.  
XX  
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.  
CC (I) and (II) can have antibacterial activity and therefore can be used  
CC in vaccination. The nucleic acids (I) may be used to produce the  
CC S. epidermidis polypeptides (II) via the production of vectors  
CC containing them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH55091 to  
CC AAH55098 represent oligonucleotide sequences and primers which are used  
CC in the exemplification of the present invention.  
CC N.B. The present invention specifically claims all the polynucleotide  
CC sequences given in the sequence listing of the present specification,  
CC however the sequence listing only goes up to SEQ ID NO:4454, so even  
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
CC no sequences are present for SEQ ID NO:4455 to 4464.  
XX  
XX Sequence 3633 BP; 1340 A; 498 C; 707 G; 1088 T; 0 other;  
SQ  
Query Match 4.9%; Score 18; DB 22; Length 3633;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 269 TGCATCAGCTGCTGCAAC 286  
DB 1763 TGCATCAGCTGCTGCAAC 1746  
|||||  
RESULT 43  
AAH54174/c  
ID AAH54174 standard; DNA; 4106 BP.  
XX  
XX AAH54174;  
XX  
XX 03-SEP-2001 (first entry)  
XX  
XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3538.  
DE  
XX  
XX Staphylococcus epidermidis SRI strain; infection; diagnosis;  
KW vaccination; endocarditis; ds.  
XX  
XX Staphylococcus epidermidis.  
OS  
XX  
XX WO200134809-A2.  
PN  
XX  
XX 17-MAY-2001.  
PD  
XX  
XX 09-NOV-2000; 2000WO-US30782.  
PF  
XX  
XX 09-NOV-1999; 99US-0164258.  
PR  
XX  
XX

PA (GLAXO) GLAXO GROUP LTD.  
XX  
PI Kimerly MJ;  
XX  
DR WPI; 2001-316495/33.  
XX  
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
XX useful for vaccinating against infections, e.g. endocarditis -  
PS  
XX Claim 8; Page 1118-1119; 2188pp; English.  
CC  
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
CC (II), given in AA681454 to AA683120, from Staphylococcus epidermidis.  
CC (I) and (II) can have antibacterial activity and therefore can be used  
CC in vaccination. The nucleic acids (I) may be used to produce the  
CC S. epidermidis polypeptides (II) via the production of vectors  
CC containing them which are used to produce hosts cells which express the  
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
CC used to vaccinate subjects and to raise antibodies against the bacteria.  
CC The polypeptides may also be used to assay for other inhibitors of their  
CC activity and therefore identify compounds that may be used for the  
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA  
CC polynucleotide sequences from the present invention. AAH5091 to  
CC AAH5098 represent oligonucleotide sequences and primers which are used  
CC in the exemplification of the present invention.  
CC N.B. The present invention specifically claims all the polynucleotide  
CC sequences given in the sequence listing of the present specification,  
CC however the sequence listing only goes up to SEQ ID NO:454 so even  
CC though sequences are given in the disclosure for SEQ ID NO:445 to 4472,  
CC no sequences are present for SEQ ID NO:4455 to 4464.  
XX  
SQ Sequence 4106 BP; 1436 A; 659 C; 643 G; 1368 T; 0 other;  
XX  
Query Match 4.9%; Score 18; DB 22; Length 4106;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 269 TGCATCAGCTGCTGCAC 286  
DB 2916 TGCATCAGCTGCTGCAC 2899  
XX  
RESULT 44  
ABLI3144/c  
ID ABLI3144 standard; cDNA; 6399 BP.  
XX  
AC ABLI3144;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33914.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KM pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
XX  
XX 23-MAR-2000; 2000US-191637P.  
XX  
XX 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
XX  
XX P-PSDB; ABB69041.

XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Claim 1; SEQ ID NO 33914; 21pp + Sequence Listing; English.  
PS  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA  
CC sequences (ABLI01840-ABLI6175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 6399 BP; 1706 A; 1543 C; 1399 G; 1751 T; 0 other;  
XX  
Query Match 4.9%; Score 18; DB 23; Length 6399;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 GTGAATTGCAGCTGCAC 127  
DB 5810 GTGAATTGCAGCTGCAC 5793  
XX  
RESULT 45  
ABLI5972/c  
ID ABLI5972 standard; cDNA; 8268 BP.  
XX  
AC ABLI5972;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42398.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KM pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
XX  
XX 23-MAR-2000; 2000US-191637P.  
XX  
XX 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
XX  
XX P-PSDB; ABB71869.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Claim 1; SEQ ID NO 42398; 21pp + Sequence Listing; English.  
PS  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA

476

CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

SO Sequence 8268 BP: 2539 A; 1758 C; 1674 G; 2297 T; 0 other;

Query Match 4.9%; Score 18; DB 23; Length 8268;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GTGAATGCACGGTGAC 127

Db 837 GTGAATGCACGGTGAC 820

Search completed: November 7, 2002, 18:15:15  
 Job time : 90.6545 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 13.8273 Seconds  
(without alignments)  
8184.096 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369  
Sequence: 1 ggcacatttcgagatgcttgcgcgcacacacatcct 369

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 10

Total number of hits satisfying chosen parameters: 61274

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A-COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS-COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	4.9	1587	4 US-09-134-001C-1425	Sequence 1425, App
2	18	4.9	1586	4 US-09-134-001C-2083	Sequence 2083, App
3	17	4.6	383	4 US-09-134-001C-263	Sequence 263, App
4	17	4.6	603	4 US-09-221-017B-627	Sequence 627, App
5	17	4.6	1263	1 US-08-532-828B-11	Sequence 11, Appl
6	17	4.6	1263	1 US-08-532-828B-12	Sequence 12, Appl
7	17	4.6	1643	1 US-08-532-828B-1	Sequence 1, Appl
8	17	4.6	1643	1 US-08-532-828B-2	Sequence 2, Appl
9	17	4.6	1643	1 US-08-532-828B-7	Sequence 7, Appl
10	17	4.6	1643	1 US-08-532-828B-8	Sequence 8, Appl
11	17	4.6	1643	1 US-08-532-828B-9	Sequence 9, Appl
12	17	4.6	1643	1 US-08-532-828B-10	Sequence 10, Appl
13	17	4.6	1643	1 US-08-700-359-7	Sequence 7, Appl
14	17	4.6	1643	1 US-08-700-359-8	Sequence 8, Appl
15	17	4.6	1643	1 US-08-700-359-10	Sequence 10, Appl
16	17	4.6	1643	1 US-08-674-168-21	Sequence 21, Appl
17	17	4.6	1643	2 US-08-596-366-5	Sequence 5, Appl
18	17	4.6	1643	2 US-08-596-366-7	Sequence 7, Appl
19	17	4.6	1643	2 US-08-967-104-5	Sequence 5, Appl
20	17	4.6	1643	2 US-08-967-104-7	Sequence 7, Appl
21	17	4.6	1643	2 US-08-985-908-3	Sequence 3, Appl
22	17	4.6	1643	3 US-08-985-908-4	Sequence 4, Appl
23	17	4.6	1643	3 US-08-985-908-6	Sequence 6, Appl
24	17	4.6	1643	3 US-08-852-730-12	Sequence 12, Appl
25	17	4.6	1643	3 US-08-852-730-13	Sequence 13, Appl
26	17	4.6	1643	3 US-08-852-730-15	Sequence 15, Appl
27	17	4.6	1643	4 US-08-985-916-3	Sequence 3, Appl

28	17	4.6	1643	4 US-08-985-916-4	Sequence 4, Appl
29	17	4.6	1643	4 US-08-985-916-6	Sequence 6, Appl
30	17	4.6	19307	3 US-08-836-022A-10	Sequence 10, Appl
31	17	4.6	19307	4 US-09-427-048A-10	Sequence 10, Appl
32	16	4.3	535	3 US-09-094-287-8	Sequence 8, Appl
33	16	4.3	908	3 US-09-094-287-1	Sequence 1, Appl
34	16	4.3	932	3 US-09-094-287-3	Sequence 3, Appl
35	16	4.3	1572	4 US-09-612-964-1	Sequence 1, Appl
36	16	4.3	2502	1 US-08-062-472B-2	Sequence 2, Appl
37	16	4.3	2702	4 US-09-453-702B-258	Sequence 258, App
38	16	4.3	8729	4 US-09-338-907-183	Sequence 183, App
39	16	4.3	37950	4 US-09-218-207-183	Sequence 183, App
40	16	4.3	48974	4 US-08-920-422-17	Sequence 17, Appl
41	16	4.3	72928	3 US-09-009-913-1	Sequence 1, Appl
42	16	4.3	87563	4 US-09-453-702B-57	Sequence 57, Appl
43	15	4.1	36	1 US-08-368-803-21	Sequence 21, Appl
44	15	4.1	36	2 US-08-578-096A-22	Sequence 22, Appl
45	15	4.1	36	2 US-08-578-096A-22	Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-09-134-001C-1425  
Sequence 1425, Application US/09134001C  
Patent No. 6380370

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 1425  
LENGTH: 1587  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-1425

Query Match 4.9% Score 18: DB 4: Length 1587:  
Best Local Similarity 100.0% Pred No. 4.6:  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 AATTCACGCTGACACAG 86  
DB 567 AATTCACGCTGACACAG 584

RESULT 2  
US-09-134-001C-2083/C  
Sequence 2083, Application US/09134001C  
Patent No. 6380370

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 2083  
LENGTH: 1596  
TYPE: DNA

ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-2083

Query Match  
Best Local Similarity 100.0%; Score 18; DB 4; Length 1596;  
Pred. No. 4.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 269 TGCATCAGCTGCTGCAC 286  
Db 1308 TGCATCAGCTGCTGCAC 1291

RESULT 3  
US-09-134-001C-263/C  
Sequence 263, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 263  
LENGTH: 393  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-263

Query Match  
Best Local Similarity 100.0%; Score 17; DB 4; Length 393;  
Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TCATTTGTGATTCGACG 121  
Db 389 TCATTTGTGATTCGACG 373

RESULT 4  
US-09-221-017B-627  
Sequence 627, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: ROSS, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P11182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P11546  
FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 627:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1...603  
US-09-221-017B-627

Query Match  
Best Local Similarity 100.0%; Score 17; DB 4; Length 603;  
Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 AAGTCCTGTGCATCATC 201  
Db 104 AAGTCCTGTGCATCATC 120

RESULT 5  
US-08-532-828B-11/C  
Sequence 11, Application US/08532828B  
Patent No. 5688671  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: OGAWA, Yuri  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: TANAKA, Akiko  
APPLICANT: MATSUI, Hiroshi  
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS TEXT EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,828B  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-101450  
FILING DATE: 27-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-764-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC13869  
US-08-532-828B-11

Query Match 4.6%; Score 17; DB 1; Length 1263;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 720 CAAAGTCCGGGATCAT 704

RESULT 6  
US-08-532-828B-12/c  
Sequence 12, Application US/08532828B  
Patent No. 568671  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: OGAWA, Yuri  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: TANAKA, Akiko  
APPLICANT: MATSUI, Hiroshi  
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS TEXT EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,828B  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-101450  
FILING DATE: 27-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-764-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
TOPOLOGY: linear  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: AJ3463  
US-08-532-828B-12

Query Match 4.6%; Score 17; DB 1; Length 1263;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 720 CAAAGTCCGGGATCAT 704

RESULT 7  
US-08-532-828B-1/c  
Sequence 1, Application US/08532828B  
Patent No. 568671  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: OGAWA, Yuri  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: TANAKA, Akiko  
APPLICANT: MATSUI, Hiroshi  
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS TEXT EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,828B  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-101450  
FILING DATE: 27-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-764-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC 13869  
US-08-532-828B-1

Query Match 4.6%; Score 17; DB 1; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||

Db 936 CAAAGTCCGGGATCAT 920

## RESULT 8

US-08-532-828B-2/C

Sequence 2, Application US/08532828B  
Patent No. 5688671

## GENERAL INFORMATION:

APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: OGAWA, Yuri  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: TANAKA, Akiko  
APPLICANT: MATSUI, Hiroshi  
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS TEXT EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,828B  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-101450  
FILING DATE: 27-APR-1993

## ATTORNEY/AGENT INFORMATION:

NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-764-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Corynebacterium glutamicum  
STRAIN: AJ3463

US-08-532-828B-2

## Query Match

Best Local Similarity 4.6%; Score 17; DB 1; Length 1643;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177

Db 936 CAAAGTCCGGGATCAT 920

## RESULT 9

US-08-532-828B-7/C

Sequence 7, Application US/08532828B  
Patent No. 5688671

## GENERAL INFORMATION:

APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: OGAWA, Yuri  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: TANAKA, Akiko

APPLICANT: MATSUI, Hiroshi

TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS-DOS TEXT EDITOR

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/532,828B

FILING DATE: 27-OCT-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-101450

FILING DATE: 27-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: NORMAN F. OBLON

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-764-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1643 nucleotides

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Corynebacterium glutamicum

STRAIN: ATCC13869

FEATURE:

NAME/KEY: mat peptide

LOCATION: 217..1482

US-08-532-828B-7

## Query Match

Best Local Similarity 4.6%; Score 17; DB 1; Length 1643;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 161 CAAAGTCCGGGATCAT 177

Db 936 CAAAGTCCGGGATCAT 920

## RESULT 10

US-08-532-828B-8/C

Sequence 8, Application US/08532828B  
Patent No. 5688671

## GENERAL INFORMATION:

APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: OGAWA, Yuri  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: TANAKA, Akiko  
APPLICANT: MATSUI, Hiroshi  
TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA



```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-101450
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-764-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Corynebacterium glutamicum
STRAIN: ATCC13869
FEATURE:
NAME/KEY: mat peptide
LOCATION: 964..1482
US-08-532-828B-9

Query Match 4.6%; Score 17; DB 1; Length 1643;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 161 CAAAGTCCGGGATCAT 177
|||||
Db 936 CAAAGTCCGGGATCAT 920

RESULT 12
US-08-532-828B-10/C
; Sequence 10, Application US/08532828B
; Patent No. 5688671
; GENERAL INFORMATION:
; APPLICANT: SUGIMOTO, Masakazu
; APPLICANT: OGAWA, Yuri
; APPLICANT: SUZUKI, Tomoko
; APPLICANT: TANAKA, Akiko
; APPLICANT: MATSUI, Hiroshi
; TITLE OF INVENTION: MUTANT ASPARTOKINASE GENE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS TEXT EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,828B
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-101450
; FILING DATE: 27-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-764-0 PCT
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: AJ3463  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: 964..1482  
US-08-532-828B-10

Query Match 4.6%; Score 17; DB 1; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 936 CAAAGTCCGGGATCAT 920

RESULT 13  
US-08-700-359-7/c  
Sequence 7, Application US/08700359  
Patent No. 5766925  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, MASAKAZU  
APPLICANT: USUDA, YOSHIHIRO  
APPLICANT: SUZUKI, TOMOKO  
APPLICANT: TANAKA, AKIKO  
APPLICANT: MATSUI, HIROSHI  
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS TEXT EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,359  
FILING DATE: 08-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-35019  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-819-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC 13869  
US-08-700-359-7

Query Match 4.6%; Score 17; DB 1; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 936 CAAAGTCCGGGATCAT 920

RESULT 14  
US-08-700-359-8/c  
Sequence 8, Application US/08700359  
Patent No. 5766925  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, MASAKAZU  
APPLICANT: USUDA, YOSHIHIRO  
APPLICANT: SUZUKI, TOMOKO  
APPLICANT: TANAKA, AKIKO  
APPLICANT: MATSUI, HIROSHI  
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS TEXT EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,359  
FILING DATE: 08-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP-35019  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-819-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC13869  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: 217..1479  
IDENTIFICATION METHOD: S  
US-08-700-359-8

Query Match 4.6%; Score 17; DB 1; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177

DB 936 CAAAGTCCGGGATCAT 920

## RESULT 15

US-08-700-359-10/C

; Sequence 10, Application US/08700359  
; Patent No. 5766925

## GENERAL INFORMATION:

APPLICANT: SUGIMOTO, MASAKAZU

APPLICANT: USUDA, YOSHIHIRO

APPLICANT: SUZUKI, TOMOKO

APPLICANT: TANAKA, AKIKO

APPLICANT: MATSUI, HIROSHI

TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS-DOS TEXT EDITOR

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/700,359

FILING DATE: 08-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP-35019

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: NORMAN F. OBLON

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-819-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1643

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE:

ORGANISM: Corynebacterium glutamicum

STRAIN: ATCC13869

FEATURE:

NAME/KEY: mat peptide

LOCATION: 964..1479

LOCATION: S

US-08-700-359-10

Query Match 4.6%; Score 17; DB 1; Length 1643;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177

DB 936 CAAAGTCCGGGATCAT 920

## RESULT 16

US-08-674-168-21/C

; Sequence 21, Application US/08674168  
; Patent No. 5804414

## GENERAL INFORMATION:

APPLICANT: MORIYA, MIKA

APPLICANT: MATSUI, HIROSHI

APPLICANT: YOKOZEKI, Kenzo

APPLICANT: HIRANO, Seiko

APPLICANT: HAYAKAWA, Atsushi

APPLICANT: IZUI, Masako

APPLICANT: SUGIMOTO, Masakazu

TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING

ARTIFICIAL TRANSPONSON

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/674,168

FILING DATE: 01-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-166541

FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-810-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 1643 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Brevibacterium lactofermentum

STRAIN: ATCC 13869

US-08-674-168-21

Query Match 4.6%; Score 17; DB 1; Length 1643;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177

DB 936 CAAAGTCCGGGATCAT 920

## RESULT 17

US-08-596-366-5/C

; Sequence 5, Application US/08596366  
; Patent No. 5876983

## GENERAL INFORMATION:

APPLICANT: SUGIMOTO, Masakazu

APPLICANT: SUZUKI, Tomoko

APPLICANT: MATSUI, Hiroshi

APPLICANT: IZUI, Katsura

TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,

ITS GENE, AND PRODUCTION METHOD OF AMINO ACID

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,

ADDRESSEE: P.C.  
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,366  
FILING DATE: 29-APR-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 5-209775  
FILING DATE: 24-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 5-209776  
FILING DATE: 24-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-153876  
FILING DATE: 05-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-784-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC13869  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 217..1482  
US-08-596-366-5

Query Match 4.6%; Score 17; DB 2; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
Db 936 CAAAGTCCGGGATCAT 920

RESULT 18  
US-08-596-366-7/C  
Sequence 7, Application US/08596366  
Patent No. 5876983  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: MATSUI, Hiroshi  
APPLICANT: IZUI, Katsura  
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,  
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER, & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400  
CITY: ARLINGTON

STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,366  
FILING DATE: 29-APR-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 5-209775  
FILING DATE: 24-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 5-209776  
FILING DATE: 24-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-153876  
FILING DATE: 05-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-784-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC13869  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 964..1482  
US-08-596-366-7

Query Match 4.6%; Score 17; DB 2; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
Db 936 CAAAGTCCGGGATCAT 920

RESULT 19  
US-08-967-104-5/C  
Sequence 5, Application US/08967104  
Patent No. 5919694  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: MATSUI, Hiroshi  
APPLICANT: IZUI, Katsura  
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,  
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER, & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,104  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/596,366  
FILING DATE: 29-APR-1996  
APPLICATION NUMBER: JP 5-209775  
FILING DATE: 24-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-209776  
FILING DATE: 24-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-153876  
FILING DATE: 05-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-784-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC13869  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 217..1482  
US-08-967-104-5

Query Match  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 936 CAAAGTCCGGGATCAT 920

RESULT 20  
US-08-967-104-7/c  
Sequence 7, Application US/08967104  
Patent No. 5919694  
GENERAL INFORMATION:  
APPLICANT: SUGIMOTO, Masakazu  
APPLICANT: SUZUKI, Tomoko  
APPLICANT: MATSUI, Hiroshi  
APPLICANT: IZUI, Katsura  
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,  
TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACID  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT, P.C.  
ADDRESS: P.C.  
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,104  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/596,366  
FILING DATE: 29-APR-1996  
APPLICATION NUMBER: JP 5-209775  
FILING DATE: 24-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-209776  
FILING DATE: 24-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-153876  
FILING DATE: 05-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-784-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Corynebacterium glutamicum  
STRAIN: ATCC13869  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 964..1482  
US-08-967-104-7

Query Match  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 936 CAAAGTCCGGGATCAT 920

RESULT 21  
US-08-985-908-3/c  
Sequence 3, Application US/08985908  
Patent No. 6004773  
GENERAL INFORMATION:  
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,908  
FILING DATE: 05-DEC-1997

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325659  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869  
US-08-985-908-3

Query Match  
Best Local Similarity 100.0%; Score 17; DB 3; Length 1643;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
Db 936 CAAAGTCCGGGATCAT 920

RESULT 22  
US-08-985-908-4/c  
Sequence 4, Application US/08985908  
Patent No. 6004773  
GENERAL INFORMATION:  
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI NA  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,908  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325659  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869

FEATURE:  
NAME/KEY: CDS  
LOCATION: 217..1482  
US-08-985-908-4

Query Match  
Best Local Similarity 100.0%; Score 17; DB 3; Length 1643;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
Db 936 CAAAGTCCGGGATCAT 920

RESULT 23  
US-08-985-908-6/c  
Sequence 6, Application US/08985908  
Patent No. 6004773  
GENERAL INFORMATION:  
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,908  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325659  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 964..1482  
US-08-985-908-6

Query Match  
Best Local Similarity 100.0%; Score 17; DB 3; Length 1643;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
Db 936 CAAAGTCCGGGATCAT 920

RESULT 24  
US-08-852-730-12/c  
Sequence 12, Application US/08852730

Patent No. 6090597  
GENERAL INFORMATION:  
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,  
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI  
APPLICANT: NAKAMATSU  
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
ZIP: 22026  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,730  
FILING DATE: 05-07-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-142812  
FILING DATE: 05-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE: Brevibacterium lactofermentum  
ORGANISM: ATCC 13869  
STRAIN: ATCC 13869  
US-08-852-730-12

Query Match 4.6%; Score 17; DB 3; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 936 CAAAGTCCGGGATCAT 920

RESULT 25  
US-08-852-730-13/c  
Sequence 13, Application US/08852730  
Patent No. 6090597  
GENERAL INFORMATION:  
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,  
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI  
APPLICANT: NAKAMATSU  
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
ZIP: 22026  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,730  
FILING DATE: 05-07-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-142812  
FILING DATE: 05-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE: Brevibacterium lactofermentum  
ORGANISM: ATCC 13869  
STRAIN: ATCC 13869  
US-08-852-730-13

Query Match 4.6%; Score 17; DB 3; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGATCAT 177  
|||||  
DB 936 CAAAGTCCGGGATCAT 920

RESULT 26  
US-08-852-730-15/c  
Sequence 15, Application US/08852730  
Patent No. 6090597  
GENERAL INFORMATION:  
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,  
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI  
APPLICANT: NAKAMATSU  
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
ZIP: 22026  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,730  
FILING DATE: 05-07-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-142812  
FILING DATE: 05-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1643 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 964..1482  
US-08-852-730-15

Query Match 4.6%; Score 17; DB 3; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCCGGATCAT 177  
|||||  
DB 936 CAAAGTCCCGGATCAT 920

## RESULT 27

US-08-985-916-3/C  
Sequence 3, Application US/08985916  
Patent No. 6221636  
GENERAL INFORMATION:  
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
COUNTRY: VA  
ZIP: 22152  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,916  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325658  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869  
US-08-985-916-3

Query Match 4.6%; Score 17; DB 4; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 161 CAAAGTCCCGGATCAT 177  
|||||  
DB 936 CAAAGTCCCGGATCAT 920

## RESULT 28

US-08-985-916-4/C  
Sequence 4, Application US/08985916  
Patent No. 6221636  
GENERAL INFORMATION:  
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
COUNTRY: VA  
ZIP: 22152  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,916  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325658  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 217..1482  
US-08-985-916-4

Query Match 4.6%; Score 17; DB 4; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCCGGATCAT 177  
|||||  
DB 936 CAAAGTCCCGGATCAT 920

## RESULT 29

US-08-985-916-6/C  
Sequence 6, Application US/08985916  
Patent No. 6221636  
GENERAL INFORMATION:  
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
COUNTRY: VA  
ZIP: 22152  
COMPUTER READABLE FORM:



MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,916  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-325658  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: NORMAN F. OBLON  
REGISTRATION NUMBER: 24,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1643 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Brevibacterium lactofermentum  
STRAIN: ATCC 13869  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 964..1482  
US-08-985-916-6

Query Match 4.6%; Score 17; DB 4; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAGTGGCGGATCAT 177  
|||||  
DB 936 CAAGTGGCGGATCAT 920

RESULT 30  
US-08-836-022A-10/c  
Sequence 10, Application US/08836022A  
Patent No. 6001557  
GENERAL INFORMATION:  
APPLICANT: Trustees of the University of Pennsylvania  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Chen, Shu-Jen  
APPLICANT: Weltzman, Matthew  
TITLE OF INVENTION: Improved Adenovirus Virus and  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, P O Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,022A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/331,381  
FILING DATE: 28-OCT-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNPVN.008PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
US-08-836-022A-10

Query Match 4.6%; Score 17; DB 3; Length 19307;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAAGTATGAGCA 163  
|||||  
DB 3516 AAGAAGTATGAGCA 3500

RESULT 31  
US-09-427-048A-10/c  
Sequence 10, Application US/09427048A  
Patent No. 6203975  
GENERAL INFORMATION:  
APPLICANT: Trustees of the University of Pennsylvania  
APPLICANT: Wilson, James M.  
APPLICANT: Fisher, Krishna J.  
APPLICANT: Chen, Shu-Jen  
APPLICANT: Weltzman, Matthew  
TITLE OF INVENTION: Improved Adenovirus Virus and  
METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, P O Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/427,048A  
FILING DATE: 21-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,022  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNPVN.008PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-427-048A-10

Query Match 4.6%; Score 17; DB 4; Length 19307;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 AAGAGTGTGAGCA 163  
DB 3516 AAGAGTGTGAGCA 3500

## RESULT 32

US-09-094-287-8/c  
Sequence 8, Application US/09094287  
Patent No. 6084071  
GENERAL INFORMATION:  
APPLICANT: Racie, Lisa  
TITLE OF INVENTION: Human L105 Proteins and Polynucleotide  
TITLE OF INVENTION: Encoding Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,287  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15299  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-498-8224  
TELEFAX: 617-876-5851  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "EST sequence"  
US-09-094-287-8

Query Match 4.3%; Score 16; DB 3; Length 535;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGCTGCA 284  
DB 256 TGCATCAGCTGCTGCA 241

## RESULT 33

US-09-094-287-1/c  
Sequence 1, Application US/09094287  
Patent No. 6084071  
GENERAL INFORMATION:  
APPLICANT: Racie, Lisa  
TITLE OF INVENTION: Human L105 Proteins and Polynucleotide  
TITLE OF INVENTION: Encoding Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,287  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15299  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-498-8224  
TELEFAX: 617-876-5851  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 908 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 80..481

NAME/KEY: mat.peptide

LOCATION: 149..481

US-09-094-287-1

Query Match 4.3%; Score 16; DB 3; Length 908;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 269 TGCATCAGCTGCTGCA 284  
DB 342 TGCATCAGCTGCTGCA 327

## RESULT 34

US-09-094-287-3/c  
Sequence 3, Application US/09094287  
Patent No. 6084071  
GENERAL INFORMATION:  
APPLICANT: Racie, Lisa  
TITLE OF INVENTION: Human L105 Proteins and Polynucleotide  
TITLE OF INVENTION: Encoding Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,287  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15299  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-498-8224  
TELEFAX: 617-876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 932 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 85..519  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 154..519  
US-09-094-287-3

Query Match  
Best Local Similarity 100.0%; Score 16; DB 3; Length 932;  
Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATCAGCTGCTGCA 284  
|||||  
DB 347 TGCATCAGCTGCTGCA 332

RESULT 35  
US-09-612-964-1  
Sequence 1, Application US/09612964  
Patent No. 6403342  
GENERAL INFORMATION:  
APPLICANT: Gussatiner Mikhail Markovich  
APPLICANT: Lunts Maria Grigorievna  
APPLICANT: Kozlov Vuy Ivanovich  
APPLICANT: Ivanovskaya Larina Valerievna  
APPLICANT: Voroshilova Elvira Borisovna  
TITLE OF INVENTION: DNA CODING FOR MUTANT ISOPROPYLMALATE SYNTHASE,  
TITLE OF INVENTION: L-LEUCINE-PRODUCING MICROORGANISM AND METHOD FOR PRODUCING  
FILE REFERENCE: 193845USO  
CURRENT APPLICATION NUMBER: US/09/612,964  
CURRENT FILING DATE: 2000-07-10  
PRIOR APPLICATION NUMBER: RU 99114325  
PRIOR FILING DATE: 1999-07-09  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 1  
LENGTH: 1572  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1569)  
US-09-612-964-1

Query Match  
Best Local Similarity 100.0%; Score 16; DB 4; Length 1572;  
Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 ATCATCAGCGGCGCTGT 211  
|||||  
DB 547 ATCATCAGCGGCGCTGT 562

RESULT 36  
US-08-062-472B-2  
Sequence 2, Application US/08062472B  
Patent No. 5695954  
GENERAL INFORMATION:  
APPLICANT: Sherwood, Nancy G M

APPLICANT: Parker, David B  
APPLICANT: McRory, John E  
APPLICANT: Lescheid, David W  
TITLE OF INVENTION: DNA ENCODING TWO FISH NEUROPEPTIDES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KLARQUIST, SPARKMAN, CAMPBELL, LEIGH &  
ADDRESS: WHINSTON, LLP  
STREET: ONE WORLD TRADE CENTER, SUITE 1600, 121 S.W.  
CITY: PORTLAND  
STATE: OREGON  
COUNTRY: USA  
ZIP: 97204-2988  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/062,472B  
FILING DATE: 14-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: POLLEY, RICHARD J  
REGISTRATION NUMBER: 28107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2502 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-062-472B-2

Query Match  
Best Local Similarity 100.0%; Score 16; DB 1; Length 2502;  
Pred. No. 50;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 TTGCATCAGCTGCTGC 283  
|||||  
DB 1142 TTGCATCAGCTGCTGC 1157

RESULT 37  
US-09-461-697-359  
Sequence 359, Application US/09461697  
Patent No. 6277974  
GENERAL INFORMATION:  
APPLICANT: COSENT NEUROSCIENCE, Inc.  
APPLICANT: Lo, Donald C.  
APPLICANT: Barney, Shawn  
APPLICANT: Thomas, Mary Beth  
APPLICANT: Portbury, Stuart D.  
APPLICANT: Purnam, Kasturi  
APPLICANT: Katz, Lawrence C.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
FILE REFERENCE: 10001-005-999  
CURRENT APPLICATION NUMBER: US/09/461,697  
CURRENT FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 466  
SOFTWARE: fastseq for Windows Version 4.0  
SEQ ID NO 359  
LENGTH: 2702  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-461-697-359

Query Match 4.3%; Score 16; DB 4; Length 2702;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 260 AACTCAGTTTCATCA 275  
 |||||||  
 Db 2500 AACTCAGTTTCATCA 2515

## RESULT 38

US-09-453-702B-258  
 ; Sequence 258, Application US/09453702B  
 ; Patent No. 6365723  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blattner, Frederick R.  
 ; Burland, Nicole T.  
 ; Plunkett, Guy  
 ; Welch, Rod  
 ; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157  
 ; NUMBER OF SEQUENCES: 265  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Quarles & Brady  
 ; STREET: 1 South Pinckney Street  
 ; CITY: Madison  
 ; STATE: WI  
 ; COUNTRY: US  
 ; ZIP: 53701-2113  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 Inch, 1.44MB storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 8.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/453,702B  
 ; FILING DATE: 03-Dec-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/110,955  
 ; FILING DATE: 04-DEC-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Seay, Nicholas J.  
 ; REGISTRATION NUMBER: 27386  
 ; REFERENCE/DOCKET NUMBER: 960296,95017  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (608) 251-5000  
 ; TELEFAX: (608) 251-9166  
 ; INFORMATION FOR SEQ ID NO: 258:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8729 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 258:  
 ; US-09-453-702B-258

Query Match 4.3%; Score 16; DB 4; Length 8729;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 311 CCCAAGAAAGGGGAA 326  
 |||||||  
 Db 371 CCCAAGAAAGGGGAA 386

## RESULT 39

US-09-338-907-183/C  
 ; Sequence 183, Application US/09338907  
 ; Patent No. 6265546  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Daniel  
 ; APPLICANT: Blumenfeld, Marta

APPLICANT: Ilya, Chumakov  
 ; APPLICANT: Bougueleret, Lydie  
 ; TITLE OF INVENTION: PROSTATE CANCER GENE  
 ; FILE REFERENCE: GENSET, 18CPICP  
 ; CURRENT APPLICATION NUMBER: US/09/338,907  
 ; CURRENT FILING DATE: 1999-06-23  
 ; EARLIER APPLICATION NUMBER: 08/996,306  
 ; EARLIER FILING DATE: 1997-12-22  
 ; EARLIER APPLICATION NUMBER: 60/099,658  
 ; EARLIER FILING DATE: 1998-09-09  
 ; EARLIER APPLICATION NUMBER: 09/218,207  
 ; EARLIER FILING DATE: 1998-12-22  
 ; NUMBER OF SEQ ID NOS: 578  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 183  
 ; LENGTH: 37950  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 5259..5328  
 ; OTHER INFORMATION: exon2  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 12675..12791  
 ; OTHER INFORMATION: exon3  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 14621..14710  
 ; OTHER INFORMATION: exon4  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 19822..19912  
 ; OTHER INFORMATION: exon5  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 21789..21950  
 ; OTHER INFORMATION: exon6  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 23387..23510  
 ; OTHER INFORMATION: exon7  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 25520..26016  
 ; OTHER INFORMATION: exon8  
 ; US-09-338-907-183

Query Match 4.3%; Score 16; DB 4; Length 37950;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 TCAGAAGAGTGATG 157  
 |||||||  
 Db 34677 TCAGAAGAGTGATG 34662

## RESULT 40

US-09-218-207-183/C  
 ; Sequence 183, Application US/09218207  
 ; Patent No. 6346381  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Daniel  
 ; APPLICANT: Blumenfeld, Marta  
 ; APPLICANT: Ilya, Chumakov  
 ; APPLICANT: Bougueleret, Lydie  
 ; TITLE OF INVENTION: Prostate cancer gene  
 ; FILE REFERENCE: GENSET, 018CPI  
 ; CURRENT APPLICATION NUMBER: US/09/218,207  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 08/996,306  
 ; EARLIER FILING DATE: 1997-12-22  
 ; EARLIER APPLICATION NUMBER: 60/099,658

EARLIER FILING DATE: 1998-09-09

NUMBER OF SEQ ID NOS: 578

SOFTWARE: Patent.pm

SEQ ID NO 183

LENGTH: 37950

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: exon

LOCATION: 5259..5328

OTHER INFORMATION: exon2

FEATURE:

NAME/KEY: exon

LOCATION: 12675..12791

OTHER INFORMATION: exon3

FEATURE:

NAME/KEY: exon

LOCATION: 14621..14710

OTHER INFORMATION: exon4

FEATURE:

NAME/KEY: exon

LOCATION: 19822..19912

OTHER INFORMATION: exon5

FEATURE:

NAME/KEY: exon

LOCATION: 21789..21950

OTHER INFORMATION: exon6

FEATURE:

NAME/KEY: exon

LOCATION: 23387..23510

OTHER INFORMATION: exon7

FEATURE:

NAME/KEY: exon

LOCATION: 25520..26016

OTHER INFORMATION: exon8

US-09-218-207-183

# Query Match

Best Local Similarity 4.3%; Score 16; DB 4; Length 37950;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 TCAGAAAGAGTGTATG 157

DB 34677 TCAGAAAGAGTGTATG 34662

# RESULT 41

US-08-920-422-17

Sequence 17, Application US/08920422A

Patent No. 6255473

GENERAL INFORMATION:

APPLICANT: Vittek, Michael P.

APPLICANT: Mitsuda, No. 62554731ak1

APPLICANT: Roses, Allen D.

TITLE OF INVENTION: Presentin-1 Gene Promoter

FILE REFERENCE: VITEKPRESENTIN

CURRENT FILING DATE: 1997-08-29

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 17

LENGTH: 48974

TYPE: DNA

ORGANISM: Mus musculus

US-08-920-422-17

# Query Match

Best Local Similarity 4.3%; Score 16; DB 4; Length 48974;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 TGTGGAAGAAGTGA 155

DB 43070 TGTGGAAGAAGTGA 43085

# RESULT 42

US-09-009-913-1

Sequence 1, Application US/09009913

Patent No. 6087485

GENERAL INFORMATION:

APPLICANT: Axis Pharmaceuticals, Inc.

TITLE OF INVENTION: Asthma Related Genes

NUMBER OF SEQUENCES: 339

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Ave, Suite 200

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913

FILING DATE: 21-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677

REFERENCE/DOCKET NUMBER: SEQ-4P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-327-3231

TELEFAX: 650-327-3231

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 72928 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-09-009-913-1

# Query Match

Best Local Similarity 4.3%; Score 16; DB 3; Length 72928;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 AATCCAGTGTACCA 60

DB 42450 AATCCAGTGTACCA 42465

# RESULT 43

US-09-453-702B-57

Sequence 57, Application US/09453702B

Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.

APPLICANT: Burland, Valerie

APPLICANT: Perna, Nicole T.

APPLICANT: Plunkett, Guy

APPLICANT: Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Plunkett Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,702B  
FILING DATE: 03-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/110,955  
FILING DATE: 04-Dec-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296,95017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87563  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-09-453-702B-57

Query Match 4.3%; Score 16; DB 4; Length 87563;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 CCCAGAGAAAGGGGA 326  
|||||  
Db 19587 CCCAGAGAAAGGGGA 19602

RESULT 44  
US-08-368-803-21  
Sequence 21, Application US/08368803  
Patent No. 5733554  
GENERAL INFORMATION:  
APPLICANT: AUDONNET, Jean-Christophe F  
APPLICANT: BOULOT, Michel J  
APPLICANT: DARTIEL, Raphael J  
APPLICANT: DUINAT, Carole V  
APPLICANT: LAPLACE, Eliane L  
APPLICANT: RIVIERE, Michel A  
TITLE OF INVENTION: Avian Herpesvirus-based live recombinant avian  
TITLE OF INVENTION: vaccine, in particular against Gamboro disease  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LARSON AND TAYLOR  
STREET: 727 SOUTH 23RD STREET  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/368,803  
FILING DATE: 05-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SARRO, Thomas  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 920-7200

TELEFAX: (703) 892-8428  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-368-803-21

Query Match 4.1%; Score 15; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 GCATCATCAGCGGCC 208  
|||||  
Db 3 GCATCATCAGCGGCC 17

RESULT 45  
US-08-578-096A-22  
Sequence 22, Application US/08578096A  
Patent No. 5980906  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Avian herpesvirus-based live recombinant  
TITLE OF INVENTION: avian vaccine  
NUMBER OF SEQUENCES: 28  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,096A  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-578-096A-22

Query Match 4.1%; Score 15; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 GCATCATCAGCGGCC 208  
|||||  
Db 3 GCATCATCAGCGGCC 17

Search completed: November 7, 2002, 23:12:13  
Job time : 123.827 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 23:08:43 ; Search time 16.0364 Seconds  
(without alignments)  
8163.686 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369  
Sequence: 1 ggcacatttttgcgattgt.....ttgctccgcacacacatcct 369

Scoring table: OLIGO-MNC  
Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 10

Total number of hits satisfying chosen parameters: 83090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications-NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCN\_NEM\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEM\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEM\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEM\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEM\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEM\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEM\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	369	US-09-825-294-199	Sequence 199, App
2	315	85.4	1619	US-09-825-294-205	Sequence 205, App
3	315	85.4	1619	US-09-825-294-211	Sequence 211, App
4	315	85.4	1897	US-09-825-294-214	Sequence 214, App
5	281	76.2	396	US-09-825-294-9	Sequence 9, Appli
6	271	73.4	1010	US-09-825-294-212	Sequence 212, App
7	117	31.7	480	US-09-825-294-213	Sequence 213, App
8	55	14.9	430	US-09-867-701-4251	Sequence 4251, Ap
9	18	4.9	237	US-09-294-093B-5287	Sequence 5287, Ap
10	18	4.9	256	US-09-294-093B-5709	Sequence 5709, Ap
11	18	4.9	285	US-09-294-093B-5021	Sequence 5021, Ap
12	18	4.9	1791	US-09-416-384A-6	Sequence 6, Appli
13	17	4.6	1298	US-09-925-300-682	Sequence 682, App
14	17	4.6	1713	US-09-815-242-7853	Sequence 7853, Ap
15	17	4.6	2649	US-09-815-242-6571	Sequence 6571, Ap
16	17	4.6	6252	US-09-964-824A-313	Sequence 313, App
17	17	4.6	8033	US-09-070-927A-121	Sequence 121, App
18	17	4.6	11842	US-09-764-860-1187	Sequence 1187, Ap
19	16	4.3	124	US-09-815-242-2587	Sequence 2587, Ap

C	20	16	4.3	236	10	US-09-923-876-3098	Sequence 3098, Ap
	21	16	4.3	271	10	US-09-878-574-7775	Sequence 7775, Ap
	22	16	4.3	364	10	US-09-960-352-1111	Sequence 1111, Ap
	23	16	4.3	369	10	US-09-960-352-11486	Sequence 11486, A
	24	16	4.3	375	10	US-09-770-791-278	Sequence 278, App
	25	16	4.3	402	9	US-10-057-275-3	Sequence 3, Appli
	26	16	4.3	405	9	US-10-103-852-1	Sequence 1, Appli
	27	16	4.3	406	9	US-09-960-352-3690	Sequence 3690, Ap
	28	16	4.3	411	10	US-09-960-352-11005	Sequence 11005, A
	29	16	4.3	414	10	US-09-983-965-3483	Sequence 3483, Ap
	30	16	4.3	488	10	US-09-864-761-10902	Sequence 10902, A
	31	16	4.3	538	10	US-09-393-634-22	Sequence 22, Appli
	32	16	4.3	615	10	US-09-764-864-423	Sequence 423, Appl
	33	16	4.3	654	10	US-09-833-381-94	Sequence 94, Appl
	34	16	4.3	689	9	US-10-001-867-14	Sequence 14, Appl
	35	16	4.3	1172	10	US-09-815-242-4715	Sequence 4715, Ap
	36	16	4.3	1179	10	US-09-815-242-8625	Sequence 8625, Ap
	37	16	4.3	1549	10	US-09-813-358-34	Sequence 34, Appl
	38	16	4.3	1989	10	US-09-801-368-41	Sequence 41, Appl
	39	16	4.3	2053	10	US-09-822-849A-343	Sequence 343, Appl
	40	16	4.3	2165	10	US-09-802-669-94	Sequence 94, Appl
	41	16	4.3	2302	10	US-09-922-261-359	Sequence 359, Appl
	42	16	4.3	3212	10	US-09-834-291-1	Sequence 1, Appli
	43	16	4.3	3294	10	US-09-764-860-1156	Sequence 1156, Ap
	44	16	4.3	11749	10	US-09-764-877-2431	Sequence 2431, Ap
	45	16	4.3	17581	10	US-09-764-860-2170	Sequence 2170, Ap

#### ALIGNMENTS

RESULT 1  
US-09-825-294-199  
Sequence 199, Application US/09825294  
Patent No. US20020004921A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
FILE REFERENCE: 210121.484C5  
CURRENT APPLICATION NUMBER: US/09/825,294  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 199  
LENGTH: 369  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(369)  
OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-199

Query Match 100.0%; Score 369; DB 10; Length 369;  
Best Local Similarity 100.0%; Pred. No. 4.5e-188;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCAACTTTTGGCGATTGTTCTTCTTCAGAGCTTTGGCGTCAAAATCCAGTGTACCA	60
DB	1	GGCAACTTTTGGCGATTGTTCTTCTTCAGAGCTTTGGCGTCAAAATCCAGTGTACCA	60
QY	61	GTGTGAAGATTCCAGCTGAACAGACGCTCTCCCGAGTTCATTGTGATTCAC	120
DB	61	GTGTGAAGATTCCAGCTGAACAGACGCTCTCTCCCGAGTTCATTGTGATTCAC	120
QY	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGTGTAGAGCAAGTCCCGGATCATGTA	180
DB	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGTGTAGAGCAAGTCCCGGATCATGTA	180

```
QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTTGCGGGTACGAGTCTT 240
    |||||||
Db 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTTGCGGGTACGAGTCTT 240
QY 241 CTGCTTCCCGAGGAAAGTGAAGTCACTGATTTGATCAGCTGCTGCAACACCCCTTTGTAA 300
    |||||||
Db 241 CTGCTTCCCGAGGAAAGTGAAGTCACTGATTTGATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGCCCAAGAAAGGGAAGTTCCTGCTCGGCGCTTCANCCATGCTCCGCAC 360
    |||||||
Db 301 CGGGCCAAAGCCCAAGAAAGGGAAGTTCCTGCTCGGCGCTTCANCCATGCTCCGCAC 360
QY 361 CACCATCTCT 369
    |||||||
Db 361 CACCATCTCT 369
```

```
RESULT 2
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205
```

```
Query Match      85.4%; Score 315; DB 10; Length 1619;
Best Local Similarity 100.0%; Pred. No. 3,7e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
    |||||||
Db 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
QY 90 GCTCCTCCCCGAGTTCATTTGTGAATTGCACGGTGAACGTTCAAGCATGTGTCAAGAG 149
    |||||||
Db 90 GCTCCTCCCCGAGTTCATTTGTGAATTGCACGGTGAACGTTCAAGCATGTGTCAAGAG 149
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGATCCGCAAGTCTGTGATCATCAGCGGCT 209
    |||||||
Db 150 AAGTATGAGCAAAAGTCCGGGATCATGATCCGCAAGTCTGTGATCATCAGCGGCT 209
QY 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGAGGAAACTGAAGTGT 269
    |||||||
Db 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGAGGAAACTGAAGTGT 269
QY 270 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAGGCAAGAAAGGGGAAGTT 329
    |||||||
Db 270 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAGGCAAGAAAGGGGAAGTT 329
QY 330 CTGCTCTGCGGCTCA 344
    |||||||
Db 330 CTGCTCTGCGGCTCA 344
```

```
RESULT 3
US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211
```

```
Query Match      85.4%; Score 315; DB 10; Length 1619;
Best Local Similarity 100.0%; Pred. No. 3,7e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
    |||||||
Db 30 CAGGCTTTGGGCTGCAATTCAGTGTCTACAGTGTGAAGAATTCAGCTGAACAAGACT 89
QY 90 GCTCCTCCCCGAGTTCATTTGTGAATTGCACGGTGAACGTTCAAGCATGTGTCAAGAG 149
    |||||||
Db 90 GCTCCTCCCCGAGTTCATTTGTGAATTGCACGGTGAACGTTCAAGCATGTGTCAAGAG 149
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGATCCGCAAGTCTGTGATCATCAGCGGCT 209
    |||||||
Db 150 AAGTATGAGCAAAAGTCCGGGATCATGATCCGCAAGTCTGTGATCATCAGCGGCT 209
QY 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGAGGAAACTGAAGTGT 269
    |||||||
Db 210 GTCTCATCGGCTTGCGGGTACAGTCTCTGCTCCCGAGGAAACTGAAGTGT 269
QY 270 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAGGCAAGAAAGGGGAAGTT 329
    |||||||
Db 270 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAGGCAAGAAAGGGGAAGTT 329
QY 330 CTGCTCTGCGGCTCA 344
    |||||||
Db 330 CTGCTCTGCGGCTCA 344
```

```
RESULT 4
US-09-825-294-214
; Sequence 214, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214
```

```
Query Match      85.4%; Score 315; DB 10; Length 1897;
```



Best Local Similarity 100.0%; Pred. No. 3,7e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 30 CAGGCTTTCGCTGCAAAATCCAGTGTACCAATGTGAAGATTCACAGTGAACAGACT 89
    |||||||
Db 309 CAGGCTTTCGCTGCAAAATCCAGTGTACCAATGTGAAGATTCACAGTGAACAGACT 368
    |||||||
QY 90 GCTCCTCCCGGAGTTCATTTGTAATTTGCACGGTGAACGTTTCAAGACATGTGTAGAAG 149
    |||||||
Db 369 GCTCCTCCCGGAGTTCATTTGTAATTTGCACGGTGAACGTTTCAAGACATGTGTAGAAG 428
    |||||||
QY 150 AAGTATGAGCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
    |||||||
Db 429 AAGTATGAGCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 488
    |||||||
QY 210 GTCATCAGCTCTGCGGGGTACCAAGTCTTCTGCTCCCGGAAACTGAATCAGTTT 269
    |||||||
Db 489 GTCATCAGCTCTGCGGGGTACCAAGTCTTCTGCTCCCGGAAACTGAATCAGTTT 548
    |||||||
QY 270 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAGGCGCAAGAAAGGGAAGTT 329
    |||||||
Db 549 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAGGCGCAAGAAAGGGAAGTT 608
    |||||||
QY 330 CTGCTCGGCGCTCA 344
    |||||||
Db 609 CTGCTCGGCGCTCA 623
    |||||||
```

## RESULT 5

US-09-825-294-9  
Sequence 9, Application US/09825294

```
GENERAL INFORMATION:
PATENT NO. US20020004491A1
APPLICANT: Xu, Jiangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-9
```

Query Match 76.2%; Score 281; DB 10; Length 396;  
Best Local Similarity 100.0%; Pred. No. 5,8e-141;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 30 CAGGCTTTCGCTGCAAAATCCAGTGTACCAATGTGAAGATTCACAGTGAACAGACT 89
    |||||||
Db 40 CAGGCTTTCGCTGCAAAATCCAGTGTACCAATGTGAAGATTCACAGTGAACAGACT 99
    |||||||
QY 90 GCTCCTCCCGGAGTTCATTTGTAATTTGCACGGTGAACGTTTCAAGACATGTGTAGAAG 149
    |||||||
Db 100 GCTCCTCCCGGAGTTCATTTGTAATTTGCACGGTGAACGTTTCAAGACATGTGTAGAAG 159
    |||||||
QY 150 AAGTATGAGCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209
    |||||||
Db 160 AAGTATGAGCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 219
    |||||||
QY 210 GTCATCAGCTCTGCGGGGTACCAAGTCTTCTGCTCCCGGAAACTGAATCAGTTT 269
    |||||||
Db 220 GTCATCAGCTCTGCGGGGTACCAAGTCTTCTGCTCCCGGAAACTGAATCAGTTT 279
    |||||||
```

```
QY 270 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAG 310
    |||||||
Db 280 GCATCAGCTCTGCAACACCCCTTTGTAAAGGGCCCAAG 320
    |||||||
```

## RESULT 6

US-09-825-294-212  
Sequence 212, Application US/09825294

```
GENERAL INFORMATION:
PATENT NO. US20020004491A1
APPLICANT: Xu, Jiangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 212
LENGTH: 1010
TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-212
```

Query Match 73.4%; Score 271; DB 10; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 1,3e-135;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 31 AGGCTTTGCGCTGCAAAATCCAGTGTACCAATGTGAAGATTCACAGTGAACAGACT 90
    |||||||
Db 258 AGGCTTTGCGCTGCAAAATCCAGTGTACCAATGTGAAGATTCACAGTGAACAGACT 317
    |||||||
QY 91 CTCCTCCCGGAGTTCATTTGTAATTTGCACGGTGAACGTTTCAAGACATGTGTAGAAG 150
    |||||||
Db 318 CTCCTCCCGGAGTTCATTTGTAATTTGCACGGTGAACGTTTCAAGACATGTGTAGAAG 377
    |||||||
QY 151 AAGTATGAGCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 210
    |||||||
Db 378 AAGTATGAGCAAAATGCGGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 437
    |||||||
QY 211 TCTCATGCTCTGCGGGGTACCAAGTCTTCTGCTCCCGGAAACTGAATCAGTTT 270
    |||||||
Db 438 TCTCATGCTCTGCGGGGTACCAAGTCTTCTGCTCCCGGAAACTGAATCAGTTT 497
    |||||||
QY 271 CATCAGCTGTGCAACACCCCTTTTGTAA 301
    |||||||
Db 498 CATCAGCTGTGCAACACCCCTTTTGTAA 528
    |||||||
```

## RESULT 7

US-09-825-294-213  
Sequence 213, Application US/09825294

```
GENERAL INFORMATION:
PATENT NO. US20020004491A1
APPLICANT: Xu, Jiangchun
APPLICANT: Stolck, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4845
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 213
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
```

US-09-825-294-213

Query Match 31.7%: Score 117; DB 10; Length 480;  
Best Local Similarity 99.4%: Pred. No. 3,6e-53;  
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 30 CAGCCTTGGCGCTGCAATTCAGTGTACGAGTGAAGATTCAGCTGAACAAGACT 89  
|||||

DB 309 CAGCCTTGGCGCTGCAATTCAGTGTACGAGTGAAGATTCAGCTGAACAAGACT 368  
|||||

OY 90 GCTCCTCCCGAGTTCATTTGATTCGACGGTGAACGCTTCAAGACATGTGTGAGAAG 149  
|||||

DB 369 GCTCCTCCCGAGTTCATTTGATTCGACGGTGAACGCTTCAAGACATGTGTGAGAAG 428  
|||||

OY 150 AAGTATGAGCAAGTGCAGGCGATCATGTACCGCAAGTCTGTGCAT 197  
|||||

DB 429 AAGTATGAGCAAGTGCAGGCGATCATGTACCGCAAGTCTGTGCAT 476  
|||||

RESULT 8  
US-09-867-701-4251  
Sequence 4251, Application US/09867701  
Patent No. US2002013237A1  
GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.497

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4251

LENGTH: 430

TYPE: DNA

ORGANISM: Homo sapien

US-09-867-701-4251

Query Match 14.9%: Score 55; DB 10; Length 430;  
Best Local Similarity 100.0%: Pred. No. 5,6e-20;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 TCCCCAGGAACTGACATGCTTGCATCAGCTGTGCAACACCCCTCTTTGTA 299  
|||||

DB 1 TCCCCAGGAACTGACATGCTTGCATCAGCTGTGCAACACCCCTCTTTGTA 55  
|||||

RESULT 9  
US-09-294-093B-5287  
Sequence 5287, Application US/09294093B  
Patent No. US20010051335A1  
GENERAL INFORMATION:

APPLICANT: Laljudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

FILE REFERENCE: PL-0009 US

CURRENT FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/082,567

PRIORITY FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 5287

LENGTH: 237

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20010051335A1 700356180H1

NAME/KEY: unsure

LOCATION: 21

OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-5287

Query Match 4.9%: Score 18; DB 10; Length 237;  
Best Local Similarity 100.0%: Pred. No. 3,6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 GTGCATCATCAGCGGCT 209  
|||||

DB 44 GTGCATCATCAGCGGCT 61  
|||||

RESULT 10  
US-09-294-093B-5709  
Sequence 5709, Application US/09294093B  
Patent No. US20010051335A1  
GENERAL INFORMATION:

APPLICANT: Laljudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

FILE REFERENCE: PL-0009 US

CURRENT FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/082,567

PRIORITY FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 5709

LENGTH: 256

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20010051335A1 700382209H1

LOCATION: 19, 21, 234, 245

OTHER INFORMATION: a, t, c, g, or other

Query Match 4.9%: Score 18; DB 10; Length 256;  
Best Local Similarity 100.0%: Pred. No. 3,6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 GTGCATCATCAGCGGCT 209  
|||||

DB 77 GTGCATCATCAGCGGCT 94  
|||||

RESULT 11  
US-09-294-093B-5021  
Sequence 5021, Application US/09294093B  
Patent No. US20010051335A1  
GENERAL INFORMATION:

APPLICANT: Laljudi, Raghunath, V.

APPLICANT: Ito, Laura, Y.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

FILE REFERENCE: PL-0009 US

CURRENT FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/082,567

PRIORITY FILING DATE: April 21, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program

SEQ ID NO 5021

LENGTH: 286

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20010051335A1 700355590H1

NAME/KEY: unsure  
LOCATION: 8, 26, 57, 117, 124, 216, 248, 260  
OTHER INFORMATION: a, t, c, g, or other  
US-09-294-093B-5021

Query Match  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 GTCATCATCAGCGCCT 209  
|||||  
DB 58 GTCATCATCAGCGCCT 75

RESULT 12  
US-09-416-384A-6/C  
Sequence 6, Application US/09416384A  
Patent No. US20020081584A1  
GENERAL INFORMATION:  
APPLICANT: BLUMENFELD, Marta  
APPLICANT: BOUGELERET, Lydie  
APPLICANT: CHUMAKOV, Ilya  
APPLICANT: COHEN, Daniel  
APPLICANT: ESSILOUX, Laurent  
TITLE OF INVENTION: Genes, proteins and diallelic markers related to central...  
FILE REFERENCE: GENSET.043AUS  
CURRENT FILING DATE: 1999-10-12  
CURRENT APPLICATION NUMBER: US/09/416,384A  
PRIOR FILING DATE: 1999-10-30  
PRIOR APPLICATION NUMBER: 60/106,457  
PRIOR FILING DATE: 1998-10-12  
PRIOR APPLICATION NUMBER: 60/103,955  
PRIOR FILING DATE: 1998-10-12  
PRIOR APPLICATION NUMBER: 60/132,277  
PRIOR FILING DATE: 1999-05-03  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: Patent.pm  
SEQ ID NO 6  
LENGTH: 1791  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-416-384A-6

Query Match  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 ACGACTGCTCCTCCCGC 101  
|||||  
DB 695 ACGACTGCTCCTCCCGC 678

RESULT 13  
US-09-925-300-682  
Sequence 682, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/124,270  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 682  
LENGTH: 1298  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: misc feature  
LOCATION: (1294)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-682

Query Match  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCCGAGTTCATTGTGAA 114  
|||||  
DB 476 CCCGAGTTCATTGTGAA 492

RESULT 14  
US-09-815-242-7853  
Sequence 7853, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7853  
LENGTH: 1713  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1713)  
US-09-815-242-7853

Query Match  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 GCATCATCAGCGCCTG 210  
|||||  
DB 308 GCATCATCAGCGCCTG 324

RESULT 15  
US-09-815-242-6571  
Sequence 6571, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
PRIOR APPLICATION NUMBER: 2001-03-21  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 6571  
LENGTH: 2649  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(2649)  
US-09-815-242-6571

Query Match  
Best Local Similarity 100.0%; Score 17; DB 10; Length 2649;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AAGAGAGTGATGAGCA 162  
Db 2563 AAGAGAGTGATGAGCA 2579

RESULT 16  
US-09-964-824A-313  
Sequence 313, Application US/09964824A  
Patent No. US20020102531A1  
GENERAL INFORMATION:  
APPLICANT: Horrigan, Stephen  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
FILE REFERENCE: 689290-73  
CURRENT APPLICATION NUMBER: US/09/964,824A  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: US/60/236,033  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US/60/236,032  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US/60/236,028  
PRIOR FILING DATE: 2000-09-28  
NUMBER OF SEQ ID NOS: 583  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 313  
LENGTH: 6252  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-964-824A-313

Query Match  
Best Local Similarity 100.0%; Score 17; DB 10; Length 6252;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 CCCGAGTTCATGTGAA 114  
Db 3521 CCCGAGTTCATGTGAA 3537

RESULT 17  
US-09-070-927A-121  
Sequence 121, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunsch  
Patrick J. Dillon  
Steven Barash  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06  
APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB369  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8033 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-09-070-927A-121

Query Match  
Best Local Similarity 100.0%; Score 17; DB 10; Length 8033;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AAGAGAGTGATGAGCA 162  
Db 7402 AAGAGAGTGATGAGCA 7418

RESULT 18  
US-09-764-860-1187  
Sequence 1187, Application US/09764860  
Patent No. US20020094953A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC008  
CURRENT APPLICATION NUMBER: US/09/764,860

```

; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1187
; LENGTH: 11842
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1187

Query Match
Best Local Similarity 100.0%; Score 17; DB 10; Length 11842;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 CCTCTGCTCCCGAGG 253
Db 6500 CCTCTGCTCCCGAGG 6516

RESULT 19
US-09-815-242-2587
; Sequence 2587, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2587
; LENGTH: 124
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-2587

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 124;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AATCCAGTCTACGAG 61
Db 41 AATCCAGTCTACGAG 56

RESULT 20
US-09-923-876-3098/C
; Sequence 3098, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Itc)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 COR
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 3098
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700161660H1
US-09-923-876-3098

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 236;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 TCAGCTGCTGCACAC 288
Db 131 TCAGCTGCTGCACAC 116

RESULT 21
US-09-878-574-7775
; Sequence 7775, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 7775
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701100324H1
US-09-878-574-7775

Query Match
Best Local Similarity 100.0%; Score 16; DB 10; Length 271;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTACAGTCTCTGTG 243
Db 104 GGTACAGTCTCTGTG 119

RESULT 22
US-09-960-352-1111
; Sequence 1111, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
```

;; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
;; FILE REFERENCE: 16511.006/37-21(10298)C  
;; CURRENT APPLICATION NUMBER: US/09/960.352  
;; CURRENT FILING DATE: 2001-09-24  
;; NUMBER OF SEQ ID NOS: 15112  
;; SEQ ID NO 1111  
;; LENGTH: 364  
;; TYPE: DNA  
;; ORGANISM: Bos taurus  
;; OTHER INFORMATION: Clone ID: 05-LIB34-056-Q1-E1-B1  
US-09-960-352-1111

Query Match  
Best Local Similarity 100.0%; Score 16; DB 10; Length 364;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 CTGCAATCCAGTCT 56  
Db 194 CTGCAATCCAGTCT 209

RESULT 23  
US-09-960-352-11486  
Sequence 11486, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagesan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960.352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 11486  
LENGTH: 369  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 49-LIB34-018-Q1-E1-E10  
US-09-960-352-11486

Query Match  
Best Local Similarity 100.0%; Score 16; DB 10; Length 369;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 CTGCAATCCAGTCT 56  
Db 21 CTGCAATCCAGTCT 36

RESULT 24  
US-09-770-791-278/c  
Sequence 278, Application US/09770791  
Patent No. US20020062014A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Mathew, Abraham V.  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Woessner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Kricker, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.

;; APPLICANT: Allen, Keith  
;; APPLICANT: Hoffman, Neil  
;; APPLICANT: Hurban, Patrick  
;; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
;; FILE REFERENCE: 2029 (PARA-018PRV)  
;; CURRENT APPLICATION NUMBER: US/09/770.791  
;; CURRENT FILING DATE: 2001-01-26  
;; PRIOR APPLICATION NUMBER: 60/178,480  
;; PRIOR FILING DATE: 2000-01-27  
;; NUMBER OF SEQ ID NOS: 999  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 278  
;; LENGTH: 375  
;; TYPE: DNA  
;; ORGANISM: Arabidopsis thaliana  
US-09-770-791-278

Query Match  
Best Local Similarity 100.0%; Score 16; DB 10; Length 375;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 80 AACACGACTGCTCCT 95  
Db 323 AACACGACTGCTCCT 308

RESULT 25  
US-10-057-275-3/c  
Sequence 3, Application US/10057275  
Patent No. US2002015545A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/057,275  
FILING DATE: 25-Jan-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740A  
FILING DATE: February 17, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Human Pancreas  
CLONE: 226152  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-057-275-3

Query Match 4.3%; Score 16; DB 9; Length 402;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATCAGCTGCTGCA 284

DB 263 TGCATCAGCTGCTGCA 248

RESULT 26

US-10-103-859-1/c  
; Sequence 1, Application US/10103859  
; Patent No. US20020155094A1  
; GENERAL INFORMATION:  
; APPLICANT: White, J.R.  
; APPLICANT: Pelus, L.M.  
; TITLE OF INVENTION: Method of Treating Sepsis and ARDS Using Chemokine Beta-9  
; FILE REFERENCE: 1488,1520003 US/10/103,859  
; CURRENT APPLICATION NUMBER: US 09/496,273  
; PRIOR FILING DATE: 2000-02-01  
; PRIOR APPLICATION NUMBER: US 08/852,212  
; PRIOR FILING DATE: 1997-05-06  
; PRIOR APPLICATION NUMBER: US 60/017,871  
; PRIOR FILING DATE: 1996-05-14  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 405  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(405)  
; OTHER INFORMATION:  
US-10-103-859-1

Query Match 4.3%; Score 16; DB 9; Length 405;  
Best Local Similarity 100.0%; Pred. No. 43;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATCAGCTGCTGCA 284

DB 263 TGCATCAGCTGCTGCA 248

RESULT 27

US-09-960-352-3690  
; Sequence 3690, Application US/09960352  
; Patent No. US20020137159A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511,006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 3690  
; LENGTH: 406  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 16-LIB34-030-Q1-E1-D11  
US-09-960-352-3690

Query Match 4.3%; Score 16; DB 10; Length 406;  
Best Local Similarity 100.0%; Pred. No. 43;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CTGCAATTCAGTCT 56

DB 205 CTGCAATTCAGTCT 220

RESULT 28

US-09-960-352-11005  
; Sequence 11005, Application US/09960352  
; Patent No. US20020137159A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511,006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 11005  
; LENGTH: 411  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (333),(347),(373),(384)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 47-LIB34-011-Q1-E1-D4  
US-09-960-352-11005

Query Match 4.3%; Score 16; DB 10; Length 411;  
Best Local Similarity 100.0%; Pred. No. 43;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CTGCAATTCAGTCT 56

DB 389 CTGCAATTCAGTCT 404

RESULT 29

US-09-983-965-3483  
; Sequence 3483, Application US/09983965  
; Patent No. US20020137160A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 37-21(10297)C  
; CURRENT APPLICATION NUMBER: US/09/983,965  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: US 09/465,231  
; PRIOR FILING DATE: 1999-12-15  
; PRIOR APPLICATION NUMBER: US 60/113,678  
; PRIOR FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 5912  
; SEQ ID NO 3483  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (76),(81),(87)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 37-LIB3058-007-Q1-R1-B2  
US-09-983-965-3483

Query Match 4.3%; Score 16; DB 10; Length 414;

Best Local Similarity 100.0%; Pred. No. 43;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 TGTGATCGCTCTGCC 226  
|||||  
Db 219 TGTGATCGCTCTGCC 234

## RESULT 30

US-09-864-761-10902/C  
Sequence 10902, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon R.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecomica-X-1  
CURRENT FILING DATE: 2001-05-23/864,761  
PRIOR APPLICATION NUMBER: US/09/864,761  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 10902  
LENGTH: 488  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC003103.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.89  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1  
US-09-864-761-10902

Query Match 4.3%; Score 16; DB 10; Length 488;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 TGTGCTCCCGAGGA 254  
|||||  
Db 102 TGTGCTCCCGAGGA 87

## RESULT 31

US-09-393-634-22  
Sequence 22, Application US/09393634  
Patent No. US20020051997A1  
GENERAL INFORMATION:  
APPLICANT: Zuker, Charles S.  
APPLICANT: Adler, Jon Elliot  
APPLICANT: Ryba, Nick  
APPLICANT: Mueller, Ken  
APPLICANT: Hoon, Mark  
APPLICANT: The Regents of the University of California  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
TITLE OF INVENTION: SF, a NO. US20020051997A1el Family of Taste Receptors  
FILE REFERENCE: 02307E-098000US  
CURRENT APPLICATION NUMBER: US/09/393,634  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 538  
TYPE: DNA  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: mouse GR06  
US-09-393-634-22

Query Match 4.3%; Score 16; DB 10; Length 538;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 TGTGCGAAGAAGT 153  
|||||  
Db 175 TGTGCGAAGAAGT 190

## RESULT 32

US-09-764-864-423/C  
Sequence 423, Application US/09764864  
Patent No. US20020132753A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT223  
CURRENT APPLICATION NUMBER: US/09/764,864  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1792  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 423  
LENGTH: 615  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (513)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (536)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (569)



```
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (588)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (597)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (610)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-423

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 AAGAAAGGGAAGT 329
DB 565 AAGAAAGGGAAGT 550

RESULT 33
US-09-833-381-94
; Sequence 94, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 94
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-94

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCATGCTGCTGCA 284
DB 535 TGCATGCTGCTGCA 550

RESULT 34
US-10-001-887-14/c
; Sequence 14, Application US/10001887
; Patent No. US2002015464A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Carferkey, Robert
; APPLICANT: Liu, Yongming
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PR
; FILE REFERENCE: DEX-0269
; CURRENT APPLICATION NUMBER: US/10/001,887
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,998
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,563
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 689
```

```
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-887-14

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GGCCCAAGAAAGGG 324
DB 311 GGCCCAAGAAAGGG 296

RESULT 35
US-09-815-242-4715/c
; Sequence 4715, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4715
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4715

Query Match
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AATCCAGTCTACG 61
DB 992 AATCCAGTCTACG 977

RESULT 36
US-09-815-242-8625/c
; Sequence 8625, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
```

APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8625  
LENGTH: 1179  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1179)  
US-09-815-242-8625

Query Match  
Best Local Similarity 100.0%; Score 16; DB 10; Length 1179;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AATCCAGTCTACCAG 61  
Db 992 AATCCAGTCTACCAG 977

RESULT 37  
US-09-813-358-34  
Sequence 34, Application US/09813358  
Patent No. US20020048759A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Pyle, Ruth  
APPLICANT: Stolk, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER  
FILE REFERENCE: 210121.501  
CURRENT APPLICATION NUMBER: US/09/813,358  
CURRENT FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 222  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 34  
LENGTH: 1549  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1549)  
OTHER INFORMATION: n = A,T,C or G  
US-09-813-358-34

Query Match  
Best Local Similarity 100.0%; Score 16; DB 10; Length 1549;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 CTGCTGCAACACCCCT 292  
Db 57 CTGCTGCAACACCCCT 72

RESULT 38  
US-09-801-368-41  
Sequence 41, Application US/09801368  
Patent No. US20020128250A1  
GENERAL INFORMATION:  
APPLICANT: Busby, Robert  
APPLICANT: Call, Brian  
APPLICANT: Hecht, Peter  
APPLICANT: Holtzman, Doug  
APPLICANT: Madden, Kevin  
APPLICANT: Maxon, Mary  
APPLICANT: Milne, Todd  
APPLICANT: No. US20020128250A1man, Thea  
APPLICANT: Royer, John  
APPLICANT: Salama, Sofie  
APPLICANT: Sherman, Amir  
APPLICANT: Silva, Jeff  
APPLICANT: Summers, Eric  
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
FILE REFERENCE: 109272.147  
CURRENT APPLICATION NUMBER: US/09/801,368  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 09/487,558  
PRIOR FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: US 60/160,587  
PRIOR FILING DATE: 1999-10-20  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 41  
LENGTH: 1989  
TYPE: DNA  
ORGANISM: Aspergillus nidulans  
US-09-801-368-41

Query Match  
Best Local Similarity 100.0%; Score 16; DB 10; Length 1989;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 ACCGCAAGTCCTGTGC 195  
Db 1026 ACCGCAAGTCCTGTGC 1041

RESULT 39  
US-09-822-849A-343/C  
Sequence 343, Application US/09822849A  
Patent No. US20020045170A1  
GENERAL INFORMATION:  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fechtel, Kim  
APPLICANT: Agostino, Michael J.  
APPLICANT: Howes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakara  
APPLICANT: Graham, James R.  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6403  
CURRENT APPLICATION NUMBER: US/09/822,849A  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/195,582  
PRIOR FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 598  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 343  
LENGTH: 2053  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-849A-343

Query Match 4.3%; Score 16; DB 10; Length 2053;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGATCA 176  
|||||  
DB 1096 CAAAGTCCGGATCA 1081

RESULT 40  
US-09-802-669-94/c  
; Sequence 94, Application US/09802669  
; Patent No. US20020004490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcusson, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISFH-545  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US 09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 94  
; LENGTH: 2165  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1782)...(1813)  
US-09-802-669-94

Query Match 4.3%; Score 16; DB 10; Length 2165;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 CAAGCCCAAGAAAG 321  
|||||  
DB 2042 CAAGCCCAAGAAAG 2027

RESULT 41  
US-09-922-261-359  
; Sequence 359, Application US/09922261  
; Patent No. US2002011471A1  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Io, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US/09/922,261  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 359  
; LENGTH: 2702  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-922-261-359

Query Match 4.3%; Score 16; DB 10; Length 2702;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AACTCAGTTTGATCA 275  
|||||  
DB 2500 AACTCAGTTTGATCA 2515

RESULT 42  
US-09-834-291-1/c  
; Sequence 1, Application US/09834291  
; Patent No. US20020042064A1  
; GENERAL INFORMATION:  
; APPLICANT: Kramer, Peter  
; APPLICANT: Muller-Schilling, Martina  
; APPLICANT: Oren, Moshe  
; TITLE OF INVENTION: p53 Binding Areas  
; FILE REFERENCE: 4121-122  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: PCT/DE99/03343  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: DE 198 47 779.1  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3212  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-834-291-1

Query Match 4.3%; Score 16; DB 10; Length 3212;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 CAAGCCCAAGAAAG 321  
|||||  
DB 2487 CAAGCCCAAGAAAG 2472

RESULT 43  
US-09-764-860-1156  
; Sequence 1156, Application US/09764860  
; Patent No. US20020094953A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1156  
; LENGTH: 3294  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-860-1156

Query Match 4.3%; Score 16; DB 10; Length 3294;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTACAGTCTTCTG 243  
|||||  
DB 819 GGTACAGTCTTCTG 834

RESULT 44  
US-09-764-877-2431

```

; Sequence 2431, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2431
; LENGTH: 11749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2431

```

```

Query Match 4.3%; Score 16; DB 10; Length 11749;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 134 GACATGTCGAGAAAG 149
    |||
Db 4972 GACATGTCGAGAAAG 4987

```

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RESULT 45
US-09-764-869-2170
; Sequence 2170, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2170
; LENGTH: 17581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2170

```

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Query Match 4.3%; Score 16; DB 10; Length 17581;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 314 AAGAAAGGGGAGATT 329
    |||
Db 2661 AAGAAAGGGGAGATT 2676

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Job time : 41.0364 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:02:33 ; Search time 826.445 Seconds

(without alignments)  
11225.881 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggcacatttcgagatgtt.....tggctccgacaccacatcct 369

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Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5888026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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15: /cgn2_6/ptodata/1/pna/US019_COMB.seq: *
16: /cgn2_6/ptodata/1/pna/US020_COMB.seq: *
17: /cgn2_6/ptodata/1/pna/US021_COMB.seq: *
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19: /cgn2_6/ptodata/1/pna/US023_COMB.seq: *
20: /cgn2_6/ptodata/1/pna/US024_COMB.seq: *
21: /cgn2_6/ptodata/1/pna/US025_COMB.seq: *
22: /cgn2_6/ptodata/1/pna/US026_COMB.seq: *
23: /cgn2_6/ptodata/1/pna/US027_COMB.seq: *
24: /cgn2_6/ptodata/1/pna/US028_COMB.seq: *
25: /cgn2_6/ptodata/1/pna/US029_COMB.seq: *
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29: /cgn2_6/ptodata/1/pna/US033_COMB.seq: *
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33: /cgn2_6/ptodata/1/pna/US037_COMB.seq: *
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41: /cgn2_6/ptodata/1/pna/US045_COMB.seq: *
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Result No.	Score	% Query Match	Length	ID	Description
1	369	100.0	369	1 PCT-US01-45395-199	Sequence 199, App
2	369	100.0	369	2 US-09-656-668-199	Sequence 199, App
3	369	100.0	369	3 US-09-713-550-199	Sequence 199, App
4	369	100.0	369	4 US-09-825-294-199	Sequence 199, App
5	369	100.0	369	5 US-09-970-966-199	Sequence 199, App
6	369	100.0	369	6 US-10-212-677-283	Sequence 199, App
7	317	85.9	483	7 US-09-757-034-340	Sequence 199, App
8	317	85.9	483	8 US-10-235-954-340	Sequence 199, App
9	315	85.4	488	9 US-09-234-611-18421	Sequence 199, App
10	315	85.4	488	10 US-09-277-227-6800	Sequence 199, App
11	315	85.4	488	11 US-09-277-227-6800	Sequence 199, App
12	315	85.4	488	12 US-09-277-227-6800	Sequence 199, App
13	315	85.4	488	13 US-09-277-227-6800	Sequence 199, App
14	315	85.4	488	14 US-09-277-227-6800	Sequence 199, App
15	315	85.4	488	15 US-09-277-227-6800	Sequence 199, App
16	315	85.4	488	16 US-09-277-227-6800	Sequence 199, App
17	315	85.4	488	17 US-09-277-227-6800	Sequence 199, App
18	315	85.4	488	18 US-09-277-227-6800	Sequence 199, App
19	315	85.4	488	19 US-09-277-227-6800	Sequence 199, App
20	315	85.4	488	20 US-09-277-227-6800	Sequence 199, App
21	315	85.4	488	21 US-09-277-227-6800	Sequence 199, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

```

22 315 85.4 1524 42 US-10-216-167-15 Sequence 15, Appl
23 315 85.4 1524 42 US-10-218-168-15 Sequence 15, Appl
24 315 85.4 1524 42 US-10-218-612-15 Sequence 15, Appl
25 315 85.4 1524 42 US-10-218-631-15 Sequence 15, Appl
26 315 85.4 1524 42 US-10-218-765-15 Sequence 15, Appl
27 315 85.4 1524 42 US-10-218-784-15 Sequence 15, Appl
28 315 85.4 1524 42 US-10-218-849-15 Sequence 15, Appl
29 315 85.4 1524 42 US-10-218-930-15 Sequence 15, Appl
30 315 85.4 1524 42 US-10-218-956-15 Sequence 15, Appl
31 315 85.4 1524 42 US-10-219-003-15 Sequence 15, Appl
32 315 85.4 1524 42 US-10-219-010-15 Sequence 15, Appl
33 315 85.4 1524 42 US-10-219-060-15 Sequence 15, Appl
34 315 85.4 1524 42 US-10-219-061-15 Sequence 15, Appl
35 315 85.4 1524 42 US-10-219-062-15 Sequence 15, Appl
36 315 85.4 1524 42 US-10-219-063-15 Sequence 15, Appl
37 315 85.4 1524 42 US-10-219-064-15 Sequence 15, Appl
38 315 85.4 1524 42 US-10-219-065-15 Sequence 15, Appl
39 315 85.4 1524 42 US-10-219-066-15 Sequence 15, Appl
40 315 85.4 1524 42 US-10-219-067-15 Sequence 15, Appl
41 315 85.4 1524 42 US-10-219-068-15 Sequence 15, Appl
42 315 85.4 1524 42 US-10-219-069-15 Sequence 15, Appl
43 315 85.4 1524 42 US-10-219-070-15 Sequence 15, Appl
44 315 85.4 1524 42 US-10-219-071-15 Sequence 15, Appl
45 315 85.4 1524 42 US-10-219-072-15 Sequence 15, Appl

```

## ALIGNMENTS

RESULT 1  
PCT-US01-45395-199  
Sequence 199, Application PC/TUS0145395

```

: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molest, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.48401PC
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 29, 345
: OTHER INFORMATION: n = A,T,C or G
PCT-US01-45395-199

```

Query Match 100.0%; Score 369; DB 1; Length 369;  
Best Local Similarity 100.0%; Pred. No. 1.1e-188;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGGATTTGTTCTTTCAGAGCTTTGGCTGCAATTCAGTGTACCA 60
DB 1 GGCACCTTTTGGGATTTGTTCTTTCAGAGCTTTGGCTGCAATTCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGAGCAAGACGCTCCGCCGATTCATTTGTAATGCAC 120
DB 61 GTGTGAAGATTCAGCTGAGCAAGACGCTCCGCCGATTCATTTGTAATGCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
QY 181 CGCAAGTCCTGTGATCATCAGCGGCTGTCTCATCGCTTGC CGGGATCAGATCTT 240

```

```

DB 181 CGCAAGTCCTGTGATCATCAGCGGCTGTCTCATCGCTTGC CGGGATCAGATCTT 240
QY 241 CTGCTCCCGGAGAACTGAACAGTTCATCAGCTGTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCGGAGAACTGAACAGTTCATCAGCTGTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCANGCCATGCTCCGAC 360
QY 361 CACCATCTT 369
DB 361 CACCATCTT 369

```

RESULT 2  
US-09-656-668-199  
Sequence 199, Application US/0965668

```

: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
: FILE REFERENCE: 210121.484C3
: CURRENT FILING DATE: US/09/656,668
: NUMBER OF SEQ ID NOS: 199
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)-(369)
: OTHER INFORMATION: n = A,T,C or G
US-09-656-668-199

```

Query Match 100.0%; Score 369; DB 25; Length 369;  
Best Local Similarity 100.0%; Pred. No. 1.1e-188;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGGATTTGTTCTTTCAGAGCTTTGGCTGCAATTCAGTGTACCA 60
DB 1 GGCACCTTTTGGGATTTGTTCTTTCAGAGCTTTGGCTGCAATTCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGAGCAAGACGCTCCGCCGATTCATTTGTAATGCAC 120
DB 61 GTGTGAAGATTCAGCTGAGCAAGACGCTCCGCCGATTCATTTGTAATGCAC 120
QY 121 GGTGAACGTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACGTTCAAGACATGTGTGAGAAAGAGTGTGAGCAAAAGTCCGGGATCATGTA 180
QY 181 CGCAAGTCCTGTGATCATCAGCGGCTGTCTCATCGCTTGC CGGGATCAGATCTT 240
DB 181 CGCAAGTCCTGTGATCATCAGCGGCTGTCTCATCGCTTGC CGGGATCAGATCTT 240
QY 241 CTGCTCCCGGAGAACTGAACAGTTCATCAGCTGTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCGGAGAACTGAACAGTTCATCAGCTGTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCANGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCGGCCCTCANGCCATGCTCCGAC 360
QY 361 CACCATCTT 369
DB 361 CACCATCTT 369

```

RESULT 3

```

US-09-713-550-199
; Sequence 199, Application US/09713550
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-199

```

```

Query Match          100.0%; Score 369; DB 28; Length 369;
Best Local Similarity 100.0%; Pred. No. 1,1e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACCTTTTGGCGATGTTCTTGTCTTCAGGCTTTGGCGTGAATCCAGTGTACCA 60
DB 1 GGCACCTTTTGGCGATGTTCTTGTCTTCAGGCTTTGGCGTGAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACAGACAGCTGCTCTCCCGAGTTCATTTGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGCTGACAGACAGCTGCTCTCCCGAGTTCATTTGTAATTCAC 120
QY 121 GGTGAACCTTCAAGCATGTGTGACAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACCTTCAAGCATGTGTGACAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACAGTCTT 240
DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACAGTCTT 240
QY 241 CTGCTCCCCAGGAAAGTGAAGTCTGATCAGCTGCTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCCAGGAAAGTGAAGTCTGATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTCTGCTCGCCCTCANGCCATGCTCCGCAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTCTGCTCGCCCTCANGCCATGCTCCGCAC 360
QY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

```

RESULT 4
US-09-825-294-199
; Sequence 199, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Steven P.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

```

```

Query Match          100.0%; Score 369; DB 31; Length 369;
Best Local Similarity 100.0%; Pred. No. 1,1e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACCTTTTGGCGATGTTCTTGTCTTCAGGCTTTGGCGTGAATCCAGTGTACCA 60
DB 1 GGCACCTTTTGGCGATGTTCTTGTCTTCAGGCTTTGGCGTGAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACAGACAGCTGCTCTCCCGAGTTCATTTGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGCTGACAGACAGCTGCTCTCCCGAGTTCATTTGTAATTCAC 120
QY 121 GGTGAACCTTCAAGCATGTGTGACAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
DB 121 GGTGAACCTTCAAGCATGTGTGACAGAAAGATGATGAGACAAAGTCCGGGATCATGTA 180
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACAGTCTT 240
DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCCGGGTACAGTCTT 240
QY 241 CTGCTCCCCAGGAAAGTGAAGTCTGATCAGCTGCTGCAACACCCCTTTGTAA 300
DB 241 CTGCTCCCCAGGAAAGTGAAGTCTGATCAGCTGCTGCAACACCCCTTTGTAA 300
QY 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTCTGCTCGCCCTCANGCCATGCTCCGCAC 360
DB 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTCTGCTCGCCCTCANGCCATGCTCCGCAC 360
QY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

```

```

RESULT 5
US-09-970-966-199
; Sequence 199, Application US/0970966
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 29, 345
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-199

```

```

Query Match          100.0%; Score 369; DB 36; Length 369;
Best Local Similarity 100.0%; Pred. No. 1,1e-188;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACCTTTTGGCGATGTTCTTGTCTTCAGGCTTTGGCGTGAATCCAGTGTACCA 60
DB 1 GGCACCTTTTGGCGATGTTCTTGTCTTCAGGCTTTGGCGTGAATCCAGTGTACCA 60

```





```

; Sequence 340, Application US/10235954
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM002C1N
; CURRENT APPLICATION NUMBER: US/10/235,954
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/757,034
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 1440
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 340
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (367)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (443)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-235-954-340

```

```

Query Match      85.9%; Score 317; DB 42; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-160;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTGGCGGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGACT 89
DB 52 CAGGCTTGGCGGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGACT 111
QY 90 GCTCCTCCCGAGTTCATTGTGAATGACGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 112 GCTCCTCCCGAGTTCATTGTGAATGACGGTGAACGTTCAAGACATGTGTGAGAAAG 171
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 172 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 231
QY 210 GTCATCATGCTGCGGGGTACAGTCTGTGCTCCCGAGGAAACTGAAGTCACTGTT 269
DB 232 GTCATCATGCTGCGGGGTACAGTCTGTGCTCCCGAGGAAACTGAAGTCACTGTT 291
QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGAGTT 329
DB 292 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGAGTT 351
QY 330 CTGCTCTGCGGCTTCAG 346
DB 352 CTGCTCTGCGGCTTCAG 368

```

```

RESULT 9
US-10-212-677-283
; Sequence 283, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Panger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

```

```

; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-283

```

```

Query Match      85.4%; Score 315; DB 42; Length 414;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTGGCGGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGACT 89
DB 38 CAGGCTTGGCGGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGACT 97
QY 90 GCTCCTCCCGAGTTCATTGTGAATGACGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 98 GCTCCTCCCGAGTTCATTGTGAATGACGGTGAACGTTCAAGACATGTGTGAGAAAG 157
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 158 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 217
QY 210 GTCATCATGCTGCGGGGTACAGTCTGTGCTCCCGAGGAAACTGAAGTCACTGTT 269
DB 218 GTCATCATGCTGCGGGGTACAGTCTGTGCTCCCGAGGAAACTGAAGTCACTGTT 277
QY 270 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGAGTT 329
DB 278 GCATCAGCTGCTCAACACCCCTCTTTGTAAAGGGCCAGGCCCAAGAAAGGGAGTT 337
QY 330 CTGCTCTGCGGCTTCAG 344
DB 338 CTGCTCTGCGGCTTCAG 352

```

```

RESULT 10
US-09-234-611-18421
; Sequence 18421, Application US/09234611
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/234,611
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18421
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)-(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-234-611-18421

```

```

Query Match      85.4%; Score 315; DB 16; Length 488;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTGGCGGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGACT 89
DB 79 CAGGCTTGGCGGCAAAATCCAGTGTGACGAGTGAAGATTCACCTGAACAAGACT 138
QY 90 GCTCCTCCCGAGTTCATTGTGAATGACGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 139 GCTCCTCCCGAGTTCATTGTGAATGACGGTGAACGTTCAAGACATGTGTGAGAAAG 198

```

```

QY 150 AAGTATGAGCAAAAGTGCAGGATCATGTACCGAAGTCTCTGTCATCATCAGCGGCT 209
    |||||||
Db 199 AAGTATGAGCAAAAGTGCAGGATCATGTACCGAAGTCTCTGTCATCATCAGCGGCT 258
QY 210 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGTCCTCCCAAGGAACTGAAGTCTT 269
    |||||||
Db 259 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGTCCTCCCAAGGAACTGAAGTCTT 318
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
Db 319 GCATCAGCTGTGCAACACCCCTTTTGTACAGGGCCCAAGGCCCAAGAAAGGGAAGTT 378
QY 330 CTGCTCGGGCCCTCA 344
    |||||||
Db 379 CTGCTCGGGCCCTCA 393

```

RESULT 11  
US-09-277-227-6100

```

; Sequence 6100, Application US/09277227
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-766
; CURRENT APPLICATION NUMBER: US/09/277,227
; CURRENT FILING DATE: 1999-03-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6100
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-277-227-6100

```

Query Match 85.4%; Score 315; DB 16; Length 488;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAGGACT 89
    |||||||
Db 79 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAGGACT 138
QY 90 GCTCTCCCGCGAGTTCATTTGTAATGCAAGGTTGAACGTTCAAGACATGTGTCAAG 149
    |||||||
Db 139 GCTCTCCCGCGAGTTCATTTGTAATGCAAGGTTGAACGTTCAAGACATGTGTCAAG 198
QY 150 AAGTATGAGCAAAAGTGCAGGATCATGTACCGAAGTCTCTGTCATCATCAGCGGCT 209
    |||||||
Db 199 AAGTATGAGCAAAAGTGCAGGATCATGTACCGAAGTCTCTGTCATCATCAGCGGCT 258
QY 210 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGTCCTCCCAAGGAACTGAAGTCTT 269
    |||||||
Db 259 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGTCCTCCCAAGGAACTGAAGTCTT 318
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
Db 319 GCATCAGCTGTGCAACACCCCTTTTGTACAGGGCCCAAGGCCCAAGAAAGGGAAGTT 378
QY 330 CTGCTCGGGCCCTCA 344
    |||||||
Db 379 CTGCTCGGGCCCTCA 393

```

RESULT 12  
US-09-904-809-18421  
; Sequence 18421, Application US/09904809  
; GENERAL INFORMATION:

```

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/904,809
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/234,611
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18421
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-18421

```

Query Match 85.4%; Score 315; DB 34; Length 488;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 30 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAGGACT 89
    |||||||
Db 79 CAGGCTTTGGCGTCAATTCAGTGTACCAAGTGTGAAGAATTCAGCTGAACAGGACT 138
QY 90 GCTCTCCCGCGAGTTCATTTGTAATGCAAGGTTGAACGTTCAAGACATGTGTCAAG 149
    |||||||
Db 139 GCTCTCCCGCGAGTTCATTTGTAATGCAAGGTTGAACGTTCAAGACATGTGTCAAG 198
QY 150 AAGTATGAGCAAAAGTGCAGGATCATGTACCGAAGTCTCTGTCATCATCAGCGGCT 209
    |||||||
Db 199 AAGTATGAGCAAAAGTGCAGGATCATGTACCGAAGTCTCTGTCATCATCAGCGGCT 258
QY 210 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGTCCTCCCAAGGAACTGAAGTCTT 269
    |||||||
Db 259 GTCTCATCGCTCTGCGGGGTACCAAGTCTCTGTCCTCCCAAGGAACTGAAGTCTT 318
QY 270 GCATCAGCTGTGCAACACCCCTTTTGTACAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
Db 319 GCATCAGCTGTGCAACACCCCTTTTGTACAGGGCCCAAGGCCCAAGAAAGGGAAGTT 378
QY 330 CTGCTCGGGCCCTCA 344
    |||||||
Db 379 CTGCTCGGGCCCTCA 393

```

RESULT 13  
US-09-909-627-6100  
; Sequence 6100, Application US/09909627  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-766  
; CURRENT APPLICATION NUMBER: US/09/909,627  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 09/277,227  
; PRIOR FILING DATE: 1999-03-23  
; NUMBER OF SEQ ID NOS: 23680  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6100  
; LENGTH: 488  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(488)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-909-627-6100

Query Match	85.4%;	Score 315;	DB 34;	Length 488;
Best Local Similarity	100.0%;	Pred. NO. 2e-159;		
Matches 315;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	30	CAGGCTTGGCCCTGCACAAATCCAGTGTCTACACAGTGTGAAGAAATTCAGCTGAACAACGACT	89	
Db	79	CAGGTTTGGCGGTGCAAAATCCAGTGTCTACACAGTGTGAAGAAATTCAGCTGAACAACGACT	138	
QY	90	GCTCTCTCCCCGAGCTTCATTTGTAATTGCAGCGTGAACGTTTAAACATATGTTCAGAAG	149	
Db	139	GCTCTCTCCCCGAGCTTCATTTGTAATTGCACGGTGAACGTTTAAAGCATATGTTCAGAAG	198	
QY	150	AAGTATGAGACAAGTGGCGGGATCATGTACCGCAAGCTGTGCATCATGACGGCCT	209	
Db	199	AAGTATGAGACAAGTGGCGGGATCATGTACCGCAAGCTGTGCATCATGACGGCCT	258	
QY	210	GTCATCATGCGCTCTGCGGGGTACACAGTCTTGTCTTCCCAAGGAAATCTGAACCTCAGTTT	269	
Db	259	GTCATCATGCGCTCTGCGGGGTACACAGTCTTGTCTTCCCAAGGAAATCTGAACCTCAGTTT	318	
QY	270	GCATCAGCTGCTGCAACAACCCCTCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAAGTT	329	
Db	319	GCATCAGCTGCTGCAACAACCCCTCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAAGTT	378	
QY	330	CTGCCTGGGCCCTCA	344	
Db	379	CTGCCTGGGCCCTCA	393	

```

RESULT 14
US-10-119-480-15
; Sequence 15, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-15

```

Query Match	85.4%;	Score 315;	DB 40;	Length 1524;
Best Local Similarity	100.0%;	Pred. NO. 2e-159;		
Matches 315;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	30	CAGGGCTTGGCTGGAAATCCAGTCTACAGGTGGAAGATTCACGTGAACAACACT	89
Db	170	CAGGGCTTGGCTGGAAATCCAGTCTACAGGTGGAAGATTCACGTGAACAACACT	228
Qy	90	GGTCCCTCCCGCCAGTTCATTGTGAATTCACAGGCTGAACGTTCAAGACATGTTCAGAAG	149
Db	230	GCTCTCTCCCGCCAGTTCATTGTGAATTCACAGGCTGAACGTTCAAGACATGTTCAGAAG	289
Qy	150	AAGTATGAGCAAAAGTGC CGGGATCATGTACCGCAAGTCTGTGCATCATCAGGGCCT	209
Db	290	AAGTATGAGCAAAAGTGC CGGGATCATGTACCGCAAGTCTGTGCATCATCAGGGCCT	349
Qy	210	GTCTATGCGCTCTGCGGGGTACCAAGTCTTCTGCTCCCAAGGAAACTGAACCTCACTT	265

Accession	Sequence	Position
Db	GTCTCATATGCGCTCTGGCCGGGTACAGATCTTCTCTCCACGGGAAACTGAATCTAGTTT	409
Oy	GCATCAGCTGCTGCACACCCCTTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTT	329
Db	GCATCAGCTGCTGCAGAACCCCTCTTGTAAAGGGCCCAAGGCCCAAGAAAGGGGAAGTT	469
Oy	CTGCCTCGGCCCTCA	344
Db	CTGCCTCGGCCCTCA	484

```

RESULT 15
US-10-216-159A-15
: Sequence 15, Application US/10216159A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C6
: CURRENT APPLICATION NUMBER: US/10/216.159A
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 15
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-216-159A-15

```

	Query Match	Best Local Similarity	Score 315;	DB 42;	Length 1524;
	Matches 315;	Conservative	0;	Mismatches 0;	Indels 0;
					Gaps
Qy	30	CAGGCTTTGCGGTGCAAAATCCAGTCTACGATGTGAAGAAATTCACGCTGAACAAGACT	85.4%;	89	
Db	170	CAGGCTTTGCGGTGCAAAATCCAGTCTACGATGTGAAGAAATTCACGCTGAACAAGACT	100.0%;	228	
Qy	90	GCTCTCTCCCCGAGTTTCATTTGAAATTCGACGGTGAACGTTCAAGACATGTGTCAGAAG	85.4%;	149	
Db	230	GCTCTCTCCCCGAGTTTCATTTGAAATTCGACGGTGAACGTTCAAGACATGTGTCAGAAG	100.0%;	288	
Qy	150	AAGTAGTAGGCAAGAGTGGCGGGATCATGTACCCGAATCCTGTGATCATCAGCGGCT	85.4%;	209	

Db 290 AAGTGAAGAGCAAGTCCGGGATCAGTACCGCAAGTCTGTCAATCATCAGGGGCTT 349  
| 210 GTCTATGCGCTTCGCGGGATCAGTCTGTCTCCCAAGGAAATGAACTAGTTT 269  
| 350 GTCTCATGCGCTTCGCGGGATCAGTCTGTCTCCCAAGGAAATGAACTAGTTT 409  
| 270 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329  
| 410 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 469  
| 330 CTGCTCGGCGCTCA 344  
| 470 CTGCTCGGCGCTCA 484

RESULT 16  
US-10-216-160-15

Sequence 15, Application US/10216160  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Geritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
CURRENT APPLICATION NUMBER: US/10/216,160  
CURRENT FILING DATE: 2002-08-09  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-216-160-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCTGCAATTCAGTGTACGATGTAAGAAATTCAGCTGAACAAGACT 89  
| 170 CAGGCTTTGGCTGCAATTCAGTGTACGATGTAAGAAATTCAGCTGAACAAGACT 229  
| 90 GCTCTCTCCCGAGTTCATTGTGAATTCACAGGTAAGCTTCAAGACATGTGTCAAGAA 149  
| 230 GCTCTCTCCCGAGTTCATTGTGAATTCACAGGTAAGCTTCAAGACATGTGTCAAGAA 289  
| 150 AAGTGAAGAGCAAGTCCGGGATCAGTACCGCAAGTCTGTCAATCATCAGGGGCTT 209  
| 290 AAGTGAAGAGCAAGTCCGGGATCAGTACCGCAAGTCTGTCAATCATCAGGGGCTT 349  
| 210 GTCTATGCGCTTCGCGGGATCAGTCTGTCTCCCAAGGAAATGAACTAGTTT 269  
| 350 GTCTCATGCGCTTCGCGGGATCAGTCTGTCTCCCAAGGAAATGAACTAGTTT 409  
| 270 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329  
| 410 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 469  
| 330 CTGCTCGGCGCTCA 344  
| 470 CTGCTCGGCGCTCA 484

RESULT 17  
US-10-216-162-15

Sequence 15, Application US/10216162  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Geritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
CURRENT APPLICATION NUMBER: US/10/216,162  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-216-162-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGCTGCAATTCAGTGTACGATGTAAGAAATTCAGCTGAACAAGACT 89  
| 170 CAGGCTTTGGCTGCAATTCAGTGTACGATGTAAGAAATTCAGCTGAACAAGACT 229  
| 90 GCTCTCTCCCGAGTTCATTGTGAATTCACAGGTAAGCTTCAAGACATGTGTCAAGAA 149  
| 230 GCTCTCTCCCGAGTTCATTGTGAATTCACAGGTAAGCTTCAAGACATGTGTCAAGAA 289  
| 150 AAGTGAAGAGCAAGTCCGGGATCAGTACCGCAAGTCTGTCAATCATCAGGGGCTT 209  
| 290 AAGTGAAGAGCAAGTCCGGGATCAGTACCGCAAGTCTGTCAATCATCAGGGGCTT 349  
| 210 GTCTATGCGCTTCGCGGGATCAGTCTGTCTCCCAAGGAAATGAACTAGTTT 269  
| 350 GTCTCATGCGCTTCGCGGGATCAGTCTGTCTCCCAAGGAAATGAACTAGTTT 409  
| 270 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329  
| 410 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 469  
| 330 CTGCTCGGCGCTCA 344

Db 470 CTGCTCGGCCCTCA 484

RESULT 18

US-10-216-163-15

Sequence 15, Application US/10216163

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerltzen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530P1C5

CURRENT APPLICATION NUMBER: US/10/216,163

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 15

LENGTH: 1524

TYPE: DNA

ORGANISM: Homo Sapien

US-10-216-163-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30 CAGGCTTTGCGTGAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 89  
170 CAGGCTTTGCGTGAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 229  
Qy 90 GCTCTCCCGGAGTTCATTTGTAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 149  
Db 230 GCTCTCCCGGAGTTCATTTGTAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 289  
Qy 150 AAGTATGAGCAAGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 209  
Db 290 AAGTATGAGCAAGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 349  
Qy 210 GTCATGAGCGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 269  
Db 350 GTCATGAGCGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 409  
Qy 270 GTCATGAGCGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 329

Db 410 GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGCGCAAGGCCCAAGAAAGGCGAGTT 469  
Qy 330 CTGCTCGGCCCTCA 344  
Db 470 CTGCTCGGCCCTCA 484

RESULT 19

US-10-216-164-15

Sequence 15, Application US/10216164

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerltzen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530P1C5

CURRENT APPLICATION NUMBER: US/10/216,164

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 15

LENGTH: 1524

TYPE: DNA

ORGANISM: Homo Sapien

US-10-216-164-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30 CAGGCTTTGCGTGAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 89  
170 CAGGCTTTGCGTGAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 229  
Qy 90 GCTCTCCCGGAGTTCATTTGTAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 149  
Db 230 GCTCTCCCGGAGTTCATTTGTAATTCACAGTGTGGAAGATTCACCTGACCAACGACT 289  
Qy 150 AAGTATGAGCAAGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 209  
Db 290 AAGTATGAGCAAGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 349  
Qy 210 GTCATGAGCGTTCGCGGATCATGTATCCGCAAGTCTGTGCAATCAGCGGCT 269

Db 350 GTCATCGCTGCGGGGTACAGTCTTGTGCTGCCAGGGAACACTCACTCACTTT 409  
|||||  
QY 270 GCATCAGCTGCTGCAACACCCCTTTTGTAAACGGGCCAAGGCCAAGAAAGGGAGTT 329  
|||||  
Db 410 GCATCAGCTGCTGCAACACCCCTTTTGTAAACGGGCCAAGGCCAAGAAAGGGAGTT 469  
|||||  
QY 330 CTGCTCGGCCCTCA 344  
|||||  
Db 470 CTGCTCGGCCCTCA 484

## RESULT 20

US-10-216-165-15  
; Sequence 15, Application US/10216165  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephen, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C7  
; CURRENT APPLICATION NUMBER: US/10/216,165  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 15  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-216-165-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCCTTGGCTGCAATCCAGTGTGCAAGATTCACGCTGAACAGACT 89  
|||||  
Db 170 CAGCCTTGGCTGCAATCCAGTGTGCAAGATTCACGCTGAACAGACT 229  
|||||  
QY 90 GCTCCTCCCGAGTGTGTAATGCAAGGTAAGCTTCAAGACATGTGTGAGAA 149  
|||||  
Db 230 GCTCCTCCCGAGTGTGTAATGCAAGGTAAGCTTCAAGACATGTGTGAGAA 289  
|||||  
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGCTCCTGTGATCATCAGCGCT 209

Db 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGCTCCTGTGATCATCAGCGCT 349  
|||||  
QY 210 GTCATCGCTGCGGGGTACAGTCTTGTGCTGCCAGGGAACACTCACTCACTTT 269  
|||||  
Db 350 GTCATCGCTGCGGGGTACAGTCTTGTGCTGCCAGGGAACACTCACTCACTTT 409  
|||||  
QY 270 GCATCAGCTGCTGCAACACCCCTTTTGTAAACGGGCCAAGGCCAAGAAAGGGAGTT 329  
|||||  
Db 410 GCATCAGCTGCTGCAACACCCCTTTTGTAAACGGGCCAAGGCCAAGAAAGGGAGTT 469  
|||||  
QY 330 CTGCTCGGCCCTCA 344  
|||||  
Db 470 CTGCTCGGCCCTCA 484

## RESULT 21

US-10-216-166-15  
; Sequence 15, Application US/10216166  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephen, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C9  
; CURRENT APPLICATION NUMBER: US/10/216,166  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 15  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-216-166-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCCTTGGCTGCAATCCAGTGTGCAAGATTCACGCTGAACAGACT 89  
|||||  
Db 170 CAGCCTTGGCTGCAATCCAGTGTGCAAGATTCACGCTGAACAGACT 229  
|||||  
QY 90 GCTCCTCCCGAGTGTGTAATGCAAGGTAAGCTTCAAGACATGTGTGAGAA 149

|||||  
Db 230 GCTCTCCCCCAGTTTCATTTGTAATTCACGGTGAACGTTCAAGACATGTGTGAGAAG 289  
Oy 150 AAGTGTAGAGCAAAATGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 209  
Db 290 AAGTGTAGAGCAAAATGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 349  
Oy 210 GTCATATGCGCTCTGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 269  
Db 350 GTCATATGCGCTCTGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 409  
Oy 270 GCATAGCTGTGCAACACCCCTTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
Db 410 GCATAGCTGTGCAACACCCCTTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469  
Oy 330 CTGCTCGGCGCTCA 344  
Db 470 CTGCTCGGCGCTCA 484

RESULT 22  
US-10-216-167-15

Sequence 15, Application US/10216167  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC4  
CURRENT APPLICATION NUMBER: US/10/216,167  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-216-167-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
US-10-216-167-15

|||||  
Db 170 CAGGCTTTGCGCTGCAAAATCCAGTGTACAGTGAAGAAATCCAGCTGAACAGACT 229  
Oy 90 GCTCTCCCCCAGTTTCATTTGTAATTCACGGTGAACGTTCAAGACATGTGTGAGAAG 149  
Db 230 GCTCTCCCCCAGTTTCATTTGTAATTCACGGTGAACGTTCAAGACATGTGTGAGAAG 289  
Oy 150 AAGTGTAGAGCAAAATGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 209  
Db 290 AAGTGTAGAGCAAAATGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 349  
Oy 210 GTCATATGCGCTCTGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 269  
Db 350 GTCATATGCGCTCTGCGGGATCATGTACCGCAAGCTCTGTCATCAGCGGCT 409  
Oy 270 GCATAGCTGTGCAACACCCCTTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
Db 410 GCATAGCTGTGCAACACCCCTTTTGTACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469  
Oy 330 CTGCTCGGCGCTCA 344  
Db 470 CTGCTCGGCGCTCA 484

RESULT 23  
US-10-216-168-15

Sequence 15, Application US/10216168  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC10  
CURRENT APPLICATION NUMBER: US/10/216,168  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-216-168-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
US-10-216-168-15

Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGAGTGAAGACT 89  
DB 170 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGAGTGAAGACT 229  
QY 90 GCTCTCCCGCCGAGTTCATTGTGAATGCAAGGTGAAGCTTCAAGCATGTGTCAAGAA 149  
DB 230 GCTCTCCCGCCGAGTTCATTGTGAATGCAAGGTGAAGCTTCAAGCATGTGTCAAGAA 289  
QY 150 AAGTGTATGAGCAAAAGTGCAGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 209  
DB 290 AAGTGTATGAGCAAAAGTGCAGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 349  
QY 210 GTCATCAGCTCTGCGGAGTACAGTCTCTGCTGCCAGGAAATGACTAGTTT 269  
DB 350 GTCATCAGCTCTGCGGAGTACAGTCTCTGCTGCCAGGAAATGACTAGTTT 409  
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCGCAAGAAAGGGAAGTT 329  
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCGCAAGAAAGGGAAGTT 469  
QY 330 CTGCTCTGGGCTCTCA 344  
DB 470 CTGCTCTGGGCTCTCA 484

RESULT 24  
US-10-218-612-15

; Sequence 15, Application US/10218612

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Geritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530PIC21

; CURRENT APPLICATION NUMBER: US/10/218,612

; PRIORITY FILING DATE: 2002-08-12

; PRIORITY FILING DATE: 2002-04-09

; PRIORITY FILING DATE: 2002-04-09

; PRIORITY FILING DATE: 1997-09-17

; PRIORITY FILING DATE: 1997-09-17

; PRIORITY FILING DATE: 1997-10-17

; PRIORITY FILING DATE: 1997-10-17

; PRIORITY FILING DATE: 1997-10-28

; PRIORITY FILING DATE: 1997-10-31

; PRIORITY FILING DATE: 1997-10-31

; PRIORITY FILING DATE: 1997-12-17

; PRIORITY FILING DATE: 1997-12-17

; PRIORITY FILING DATE: 1998-03-20

; PRIORITY FILING DATE: 1998-03-25

; PRIORITY FILING DATE: 1998-03-25

; PRIORITY FILING DATE: 1998-03-26

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

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; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

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; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; ORGANISM: Homo Sapien  
US-10-218-612-15

Query Match

Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGAGTGAAGACT 89  
DB 170 CAGGCTTGGCGTGCAGAAATCCAGTGTACCAAGTGAAGATTCAGAGTGAAGACT 229  
QY 90 GCTCTCCCGCCGAGTTCATTGTGAATGCAAGGTGAAGCTTCAAGCATGTGTCAAGAA 149  
DB 230 GCTCTCCCGCCGAGTTCATTGTGAATGCAAGGTGAAGCTTCAAGCATGTGTCAAGAA 289  
QY 150 AAGTGTATGAGCAAAAGTGCAGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 209  
DB 290 AAGTGTATGAGCAAAAGTGCAGGATCATGTACCGCAAGTCCGTGATCATCAGCGGCT 349  
QY 210 GTCATCAGCTCTGCGGAGTACAGTCTCTGCTGCCAGGAAATGACTAGTTT 269  
DB 350 GTCATCAGCTCTGCGGAGTACAGTCTCTGCTGCCAGGAAATGACTAGTTT 409  
QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCGCAAGAAAGGGAAGTT 329  
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAACGGGCCCAAGGCGCAAGAAAGGGAAGTT 469  
QY 330 CTGCTCTGGGCTCTCA 344  
DB 470 CTGCTCTGGGCTCTCA 484

RESULT 25  
US-10-218-631-15

; Sequence 15, Application US/10218631

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Geritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530PIC14

; CURRENT APPLICATION NUMBER: US/10/218,631

; PRIORITY FILING DATE: 2002-08-12

; PRIORITY FILING DATE: 2002-04-09

; PRIORITY FILING DATE: 2002-04-09

; PRIORITY FILING DATE: 1997-09-17

; PRIORITY FILING DATE: 1997-09-17

; PRIORITY FILING DATE: 1997-10-17

; PRIORITY FILING DATE: 1997-10-17

; PRIORITY FILING DATE: 1997-10-28

; PRIORITY FILING DATE: 1997-10-31

; PRIORITY FILING DATE: 1997-10-31

; PRIORITY FILING DATE: 1997-12-17

; PRIORITY FILING DATE: 1997-12-17

; PRIORITY FILING DATE: 1998-03-20

; PRIORITY FILING DATE: 1998-03-25

; PRIORITY FILING DATE: 1998-03-25

; PRIORITY FILING DATE: 1998-03-26

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27

; PRIORITY FILING DATE: 1998-03-27



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; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-631-15

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCGTTTCCGCTGCAAAATCCAGTGTACGAGTGTGAAGATTCCAGCTGAACAGCACT 89
    |||
DB 170 CAGCGTTTCCGCTGCAAAATCCAGTGTACGAGTGTGAAGATTCCAGCTGAACAGCACT 229
    |||
QY 90 GCTCCCTCCCGGAGTTCATTTGTGAATTGCACGAGTGAACGTTCAAGACATGTGTAGAAAG 149
    |||
DB 230 GCTCCCTCCCGGAGTTCATTTGTGAATTGCACGAGTGAACGTTCAAGACATGTGTAGAAAG 289
    |||
QY 150 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGCCT 209
    |||
DB 290 AAGTGTGAGCAAAAGTCCGGGATCATGTACCGCAAGTCCCTGTGCATCATCAGCGCCT 349
    |||
QY 210 GTCTCATGCGCTCTGCGCGGATCATGTCTGTCTCCCGCAGGAAACTGACATCAGTTT 269
    |||
DB 350 GTCTCATGCGCTCTGCGCGGATCATGTCTGTCTCCCGCAGGAAACTGACATCAGTTT 409
    |||
QY 270 GCATCGCGCTGCTCAACACCCCTTTGTAAAGGGCCCAAGGGCCCAAGAAAGGAAAGTT 329
    |||
DB 410 GCATCGCGCTGCTCAACACCCCTTTGTAAAGGGCCCAAGGGCCCAAGAAAGGAAAGTT 469
    |||
QY 330 CTGCTCTGCGGCTCTCA 344
    |||
DB 470 CTGCTCTGCGGCTCTCA 484

RESULT 26
US-10-218-765-15
; Sequence 15, Application US/10218765
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltisen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218, 765
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
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PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/126773  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: 60/127887  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/131270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131445  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/140650  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/140723  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146222

PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146963  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/149320  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149638  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/151733  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/164418  
PRIOR FILING DATE: 1999-11-09  
PRIOR APPLICATION NUMBER: 60/166361  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/169445  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835  
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTGTACGAGTGTGAAGATTCCAGCTGACAGCACT 89  
DB 170 CAGGCTTGGCGCTGCAATCCAGTGTACGAGTGTGAAGATTCCAGCTGACAGCACT 229

QY 90 GCTCTCTCCCGGAGTTATTTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGA 149  
DB 230 GCTCTCTCCCGGAGTTATTTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGA 289

QY 150 AAGTGTGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATACGGGCT 209  
DB 290 AAGTGTGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTGTGATCATACGGGCT 349

QY 210 GTCATCGGCTGCGGATGACAGTCTTGTGCTCCAGGGAACGTACACTGTT 269  
DB 350 GTCATCGGCTGCGGATGACAGTCTTGTGCTCCAGGGAACGTACACTGTT 409

QY 270 GCATCAGCTGCTGCAACCCCTTTGTAAAGGCGCAAGGCGCAAGAAAGGAGT 329  
DB 410 GCATCAGCTGCTGCAACCCCTTTGTAAAGGCGCAAGGCGCAAGAAAGGAGT 469

QY 330 CTGCTCGGCGCTCA 344  
DB 470 CTGCTCGGCGCTCA 484

RESULT 27  
US-10-218-784-15  
; Sequence 15, Application US/10218784  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C18  
; CURRENT APPLICATION NUMBER: US/10/218,784  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090691  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095916  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096146  
PRIOR FILING DATE: 1998-08-11  
PRIOR APPLICATION NUMBER: 60/096791  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/097986  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098544  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100038

PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/126773  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: 60/127887  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/131270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131445  
PRIOR FILING DATE: 1999-04-28

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; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

```

```

Query Match          85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTGGCGCTGCAAAATCCAGTGTGCAAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
Db 170 CAGGCTTTGGCGCTGCAAAATCCAGTGTGCAAGTGTGAAGAAATTCAGCTGAACAACGACT 229
    |||||||
QY 90 GCTCCTCCCGGAGTTTATTTGTAATGTCAGCGTGAAGCTTCAAGACATGTGTAGAAAG 149
    |||||||
Db 230 GCTCCTCCCGGAGTTTATTTGTAATGTCAGCGTGAAGCTTCAAGACATGTGTAGAAAG 289
    |||||||
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
Db 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
    |||||||
QY 210 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACACTGATT 269
    |||||||
Db 350 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACACTGATT 409
    |||||||
QY 270 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329
    |||||||
Db 410 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 469
    |||||||
QY 330 CTGCTCTGGGCGCTCA 344
    |||||||
Db 470 CTGCTCTGGGCGCTCA 484

```

```

RESULT 28
US-10-218-849-15
; Sequence 15, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

```

```

; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC11
; CURRENT APPLICATION NUMBER: US/10/218.849
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-849-15

```

```

Query Match          85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTGGCGCTGCAAAATCCAGTGTGCAAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
Db 170 CAGGCTTTGGCGCTGCAAAATCCAGTGTGCAAGTGTGAAGAAATTCAGCTGAACAACGACT 229
    |||||||
QY 90 GCTCCTCCCGGAGTTTATTTGTAATGTCAGCGTGAAGCTTCAAGACATGTGTAGAAAG 149
    |||||||
Db 230 GCTCCTCCCGGAGTTTATTTGTAATGTCAGCGTGAAGCTTCAAGACATGTGTAGAAAG 289
    |||||||
QY 150 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 209
    |||||||
Db 290 AAGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCT 349
    |||||||
QY 210 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACACTGATT 269
    |||||||
Db 350 GTTCATCGGCTGCGGGGATCCAGTCTTCTCTCCCAAGGAACTGAACACTGATT 409
    |||||||
QY 270 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 329
    |||||||
Db 410 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGGCCCAAGGAAAGGGAAGTT 469
    |||||||
QY 330 CTGCTCTGGGCGCTCA 344
    |||||||
Db 470 CTGCTCTGGGCGCTCA 484

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```

RESULT 29
US-10-218-930-15
; Sequence 15, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC13
; CURRENT APPLICATION NUMBER: US/10/218.930
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-930-15

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PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
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PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/126773  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: 60/127887  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/131270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131445  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/140650  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/140723  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146963  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/149320  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149638

PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/151733  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/164418  
PRIOR FILING DATE: 1999-11-09  
PRIOR APPLICATION NUMBER: 60/166361  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/169445  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835  
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 CAGGCTTGGCGTGCAGATCCAGTGTACAGTGTGAGAAATTCAGCTGAACAGACT 89  
Db 170 CAGGCTTGGCGTGCAGATCCAGTGTACAGTGTGAGAAATTCAGCTGAACAGACT 229

Oy 90 GCTCCCTCCCGAGTTCAATTGTAATTCACGAGTGAAGTTCAAGACATGTGTGAGAAG 149  
Db 230 GCTCCCTCCCGAGTTCAATTGTAATTCACGAGTGAAGTTCAAGACATGTGTGAGAAG 289

Oy 150 AAGTATGAGCAAGTGTCCGGGATCATGTACCGCAATCTGTGATCATCAGCGGCT 209  
Db 290 AAGTATGAGCAAGTGTCCGGGATCATGTACCGCAATCTGTGATCATCAGCGGCT 349

Oy 210 GTCTCATGCGCTGCGCGGTACAGTCTCTGTGCTCCCGAGGAAATGAACTAGTTT 269  
Db 350 GTCTCATGCGCTGCGCGGTACAGTCTCTGTGCTCCCGAGGAAATGAACTAGTTT 409

Oy 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCAAAGCCCAAGAAAGGGAAGTT 329  
Db 410 GCATCAGCTGTGCAACACCCCTCTTTGTAAAGGGCCAAAGCCCAAGAAAGGGAAGTT 469

Oy 330 CTGCTCGGCGCTCA 344  
Db 470 CTGCTCGGCGCTCA 484

RESULT 31  
US-10-219-003-15  
; Sequence 15. Application US/10219003  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gunney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William J.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P9530P1C12  
; CURRENT APPLICATION NUMBER: US/10/219, 003  
; PRIOR FILING DATE: 2002-08-12  
; PRIOR APPLICATION NUMBER: 10/119, 480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873  
 PRIOR FILING DATE: 1997-12-17  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-27  
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 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081955  
 PRIOR FILING DATE: 1998-04-15  
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 PRIOR APPLICATION NUMBER: 60/084441  
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 PRIOR APPLICATION NUMBER: 60/085323  
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 PRIOR APPLICATION NUMBER: 60/086392  
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 PRIOR APPLICATION NUMBER: 60/090472  
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 PRIOR APPLICATION NUMBER: 60/090691  
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 PRIOR APPLICATION NUMBER: 60/090695  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/095302  
 PRIOR FILING DATE: 1998-08-04  
 PRIOR APPLICATION NUMBER: 60/095318  
 PRIOR FILING DATE: 1998-08-04  
 PRIOR APPLICATION NUMBER: 60/095916  
 PRIOR FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: 60/096146  
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 PRIOR APPLICATION NUMBER: 60/098544  
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 PRIOR APPLICATION NUMBER: 60/100385  
 PRIOR FILING DATE: 1998-09-15  
 PRIOR APPLICATION NUMBER: 60/100390  
 PRIOR FILING DATE: 1998-09-15  
 PRIOR APPLICATION NUMBER: 60/100627

PRIOR FILING DATE: 1998-09-16  
 PRIOR APPLICATION NUMBER: 60/100848  
 PRIOR FILING DATE: 1998-09-18  
 PRIOR APPLICATION NUMBER: 60/100919  
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 PRIOR FILING DATE: 1999-04-05  
 PRIOR APPLICATION NUMBER: 60/130232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: 60/131270  
 PRIOR FILING DATE: 1999-04-27  
 PRIOR APPLICATION NUMBER: 60/131291  
 PRIOR FILING DATE: 1999-04-27  
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 PRIOR FILING DATE: 1999-04-28  
 PRIOR APPLICATION NUMBER: 60/134287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 60/140650  
 PRIOR FILING DATE: 1999-06-22  
 PRIOR APPLICATION NUMBER: 60/140723

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1 FILE REFERENCE: P35301C10
2 CURRENT APPLICATION NUMBER: US/10/219,010
3 CURRENT FILING DATE: 2002-08-12
4
5 PRIOR APPLICATION NUMBER: 2002-04-09
6
7 PRIOR FILING DATE: 2002-04-09
8
9 PRIOR APPLICATION NUMBER: 60/059113
10
11 PRIOR FILING DATE: 1997-09-17
12
13 PRIOR APPLICATION NUMBER: 60/062287
14
15 PRIOR FILING DATE: 1997-10-17
16
17 PRIOR APPLICATION NUMBER: 60/063549
18
19 PRIOR FILING DATE: 1997-10-28
20
21 PRIOR APPLICATION NUMBER: 60/064103
22
23 PRIOR FILING DATE: 1997-10-31
24
25 PRIOR APPLICATION NUMBER: 60/069873
26
27 PRIOR FILING DATE: 1997-12-17
28
29 PRIOR APPLICATION NUMBER: 60/078910
30
31 PRIOR FILING DATE: 1998-03-20
32
33 PRIOR APPLICATION NUMBER: 60/079294
34
35 PRIOR FILING DATE: 1998-03-25
36
37 PRIOR APPLICATION NUMBER: 60/079656
38
39 PRIOR FILING DATE: 1998-03-26
40
41 PRIOR APPLICATION NUMBER: 60/079728
42
43 PRIOR FILING DATE: 1998-03-27
44
45 PRIOR APPLICATION NUMBER: 60/081819
46
47 PRIOR FILING DATE: 1998-04-15
48
49 PRIOR APPLICATION NUMBER: 60/081955

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PRIOR APPLICATION NUMBER: 60/082804

; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/084441

; PRIOR FILING DATE: 1998-05-06  
 ; PRIOR APPLICATION NUMBER: 60/085323

; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/085579

; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/086392  
 ; PRIOR FILING DATE: 1000-05-23

; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/089532  
 PRIOR FILING DATE: 1998-05-17

; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089538  
 ; PRIOR FILING DATE: 1998-06-17

; PRIOR FILING DATE: 1998-06-17  
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 ; PRIOR FILING DATE: 1998-06-18

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PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07

;; PRIOR APPLICATION NUMBER: 60/095302  
;; PRIOR FILING DATE: 1998-08-04

;; PRIOR APPLICATION NUMBER: 60/095318  
;; PRIOR FILING DATE: 1998-08-04

;  
; PRIOR APPLICATION NUMBER: 60/095916  
; PRIOR FILING DATE: 1998-08-10  
;

;; PRIOR APPLICATION NUMBER: 60/096146  
;; PRIOR FILING DATE: 1998-08-11

; PRIOR APPLICATION NUMBER: 60/096791  
 ; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: 60/097986  
 ; PRIOR FILING DATE: 1998-08-26

;; PRIOR APPLICATION NUMBER: 60/098544  
; PRIOR FILING DATE: 1998-08-31

; PRIOR APPLICATION NUMBER: 60/099596  
 ; PRIOR FILING DATE: 1998-09-09

;; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099803  
; PRIOR FILING DATE: 1998-09-10



PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
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PRIOR FILING DATE: 1998-09-10  
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PRIOR FILING DATE: 1999-04-05  
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PRIOR APPLICATION NUMBER: 60/131022

PRIOR FILING DATE: 1999-04-26  
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PRIOR FILING DATE: 1999-04-27  
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PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146963  
PRIOR FILING DATE: 1999-08-03  
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PRIOR FILING DATE: 1999-08-17  
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PRIOR FILING DATE: 1999-08-17  
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PRIOR APPLICATION NUMBER: 60/169445  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835  
PRIOR FILING DATE: 1999-12-07

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGCGTTGGCGCTCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAGCACT 89  
DB 170 CAGCGTTGGCGCTCAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAGCACT 229  
QY 90 GCTCCTCCCGGAGTTGATTTGATTCAGCGGTGAAGTTCAGATGTCAGAAAG 149  
DB 230 GCTCCTCCCGGAGTTGATTTGATTCAGCGGTGAAGTTCAGATGTCAGAAAG 289  
QY 150 AAGTGTGAGCAAGTCCCGGAGTATGATACCGAAGTCTGTGATCATCAGCGGCT 209  
DB 290 AAGTGTGAGCAAGTCCCGGAGTATGATACCGAAGTCTGTGATCATCAGCGGCT 349  
QY 210 GTCTCATGCGCTTGCCTCGGAGTACAGTCTTGTGCTCCCGAGGAAATGAACTAGTTT 269  
DB 350 GTCTCATGCGCTTGCCTCGGAGTACAGTCTTGTGCTCCCGAGGAAATGAACTAGTTT 409  
QY 270 GCATCAGTCTGTGCAACACCCCTTTTGTAAAGGGGCAAGGCCCAAGAAAGGGAAGTT 329  
DB 410 GCATCAGTCTGTGCAACACCCCTTTTGTAAAGGGGCAAGGCCCAAGAAAGGGAAGTT 469  
QY 330 CTGCGTGGGCGCTCA 344  
DB 470 CTGCGTGGGCGCTCA 484

RESULT 33  
US-10-219-060-15  
Sequence 15, Application US/10219060  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerltzen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William T.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC22  
CURRENT FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
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PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
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PRIOR APPLICATION NUMBER: 60/079728  
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PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
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PRIOR APPLICATION NUMBER: 60/095318  
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PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10

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PRIOR APPLICATION NUMBER: 60/123618
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PRIOR APPLICATION NUMBER: 60/125259
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PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

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Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 30 CAGGCTTTCCGCTGCAAAATTCAGTGTGTAAGAAATTCAGCTGAACAAGACT 89
DB 170 CAGGCTTTCCGCTGCAAAATTCAGTGTGTAAGAAATTCAGCTGAACAAGACT 229
QY 90 GCTCCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 230 GCTCCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAAAG 289
QY 150 AAGTGTGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 290 AAGTGTGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 349
QY 210 GTCATCAGCTGCTGCGGGGTACCAAGTCTCTGCTCCCGAGGAAACTGAACACTGATT 269
DB 350 GTCATCAGCTGCTGCGGGGTACCAAGTCTCTGCTCCCGAGGAAACTGAACACTGATT 409

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QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGCCCAAGAAAGGGAAGTT 329
DB 410 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGCCCAAGAAAGGGAAGTT 469
QY 330 CTGCTCGGCCCTCA 344
DB 470 CTGCTCGGCCCTCA 484

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RESULT 34
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; Sequence 15, Application US/10219061
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC16
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-061-15

```

```

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 30 CAGGCTTTCCGCTGCAAAATTCAGTGTGTAAGAAATTCAGCTGAACAAGACT 89
DB 170 CAGGCTTTCCGCTGCAAAATTCAGTGTGTAAGAAATTCAGCTGAACAAGACT 229
QY 90 GCTCCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAAAG 149
DB 230 GCTCCTCCCGGAGTTCATTTGTAATTCAGCGGTGAACGTTCAAGACATGTGTGAGAAAG 289
QY 150 AAGTGTGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 209
DB 290 AAGTGTGAGCAAAAGTCCCGGATCATGTATCCGCAAGTCTGTGCATCATCAGCGGCT 349

```



QY	90	GCTCCTCCCCGAGTTCATTGTAATTGCAAGCGTAACGTTCAAGACATGTCAGAAAG	149
Dp	230	GCTCCTCCCCGAGTTCATTGTAATTGCAAGCGTAACGTTCAAGACATGTCAGAAAG	289
QY	150	AAGTGATGAGCAAAAGTCCGGGATCATATGACCGCAAGTCTGTGCATCATCAGGCGCT	209
Dp	290	AAGTGATGAGCAAAAGTCCGGGATCATATGACCGCAAGTCTGTGCATCATCAGGCGCT	349
QY	210	GTCATCATGCGCTTCGCGGGATGACAGTCCTTCCTGCTCCCAAGGAAACTAATCAGTTT	269
Dp	350	GTCATCATGCGCTTCGCGGGATGACAGTCCTTCCTGCTCCCAAGGAAACTAATCAGTTT	409
QY	270	GCATCAGCTGCTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCAAGAAAAGGGGAATT	329
Dp	410	GCATCAGCTGCTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCAAGAAAAGGGGAATT	469
QY	330	CTGGCTGGGCGCCTCA	344
Dp	470	CTGGCTGGGCGCCTCA	484

RESULT 37  
US-10-219-064-15

```

? SEQUENCE ID: Application US/10219064
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Desnoyers, Luc
? APPLICANT: Gerritsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Smith, Victoria
? APPLICANT: Stephen, Jean-Philippe F.
? APPLICANT: Matanabe, Colin L.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3530PIC44
? CURRENT APPLICATION NUMBER: US/10/219,064
? PRIOR FILING DATE: 2002-08-13
? PRIOR APPLICATION NUMBER: 10/119,480
? PRIOR FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? REMAINING SEQ ID Application data removed - See File Wrapper or PALM.
? SEQ ID NO 15
? LENGTH: 1524
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-219-064-15

```

```
Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. NO. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	30	CAGGTTTGGCCCTCAATTCAGAGCTACCGGTGGAAGATTCACCTGAAACAAGACT	89
Db	170	CAGGTTTGGCCCTCAATTCAGAGCTACCGGTGGAAGATTCACCTGAAACAAGACT	229
QY	90	GCTCCTCCCCGAGTTCATTGTGTAATTCACGAGTGAAAGTTCAAGACATGTGTCAAG	149
Db	230	GCTCCTCCCCGAGTTCATTGTGTAATTCACGAGTGAAAGTTCAAGACATGTGTCAAG	289
QY	150	AAGTGAATGAGACAAAGTCCCGGAGTCAATGTACCGCAAGTCTGTGCATCAACGGGCT	209
Db	290	AAGTGAATGAGACAAAGTCCCGGAGTCAATGTACCGCAAGTCTGTGCATCAACGGGCT	349
QY	210	GTTTCATTCGCTCTGCGGGTACCAAGTCTTCTGCTCCCAAGGAAACTGAACCTGATTT	269
Db	350	GTTTCATTCGCTCTGCGGGTACCAAGTCTTCTGCTCCCAAGGAAACTGAACCTGATTT	409
QY	270	GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGGCCAAGGCCAAGAAAAGGGAGTT	329
Db	410	GCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGGCCAAGGCCAAGAAAAGGGAGTT	469
QY	330	CTGGCTCGGGCCCTCA 344	
Db	470	CTGGCTCGGGCCCTCA 484	

RESULT 38  
US-10-219-065-15

```

Sequence 15, Application US/10219065
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goodard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P5530PIC39
CURRENT APPLICATION NUMBER: US/10/219,065
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079566
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15

```

```

'      LENGTH: 1024
;      TYPE: DNA
;      ORGANISM: Homo Sapien
US-10-219-065-15

```



; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 15  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-067-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACAGTGTGAAGAAATTCACCTGAACAGCACT 89  
DB 170 CAGGCTTGGCGTGCAGAAATCCAGTGTACAGTGTGAAGAAATTCACCTGAACAGCACT 229  
QY 90 GCTCCCTCCCGAGTTCATTTGTGAATTCGACGGTGAACGTTCAAGACATGTGTAGAAAG 149  
DB 230 GCTCCCTCCCGAGTTCATTTGTGAATTCGACGGTGAACGTTCAAGACATGTGTAGAAAG 289  
QY 150 AAGTATGAGCAAGATGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 290 AAGTATGAGCAAGATGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 349  
QY 210 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 269  
DB 350 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 409  
QY 270 GCATCAGCTGCTGCACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 329  
DB 410 GCATCAGCTGCTGCACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 469  
QY 330 CTGCTCTGCGGCTCTCA 344  
DB 470 CTGCTCTGCGGCTCTCA 484

RESULT 41  
US-10-219-068-15

; Sequence 15, Application US/10219068  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerltzen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P350P1C31  
; CURRENT APPLICATION NUMBER: US/10/219,068  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 15  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-068-15

Query Match 85.4%; Score 315; DB 42; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 2e-159;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTGCAGAAATCCAGTGTACAGTGTGAAGAAATTCACCTGAACAGCACT 89  
DB 170 CAGGCTTGGCGTGCAGAAATCCAGTGTACAGTGTGAAGAAATTCACCTGAACAGCACT 229  
QY 90 GCTCCCTCCCGAGTTCATTTGTGAATTCGACGGTGAACGTTCAAGACATGTGTAGAAAG 149  
DB 230 GCTCCCTCCCGAGTTCATTTGTGAATTCGACGGTGAACGTTCAAGACATGTGTAGAAAG 289  
QY 150 AAGTATGAGCAAGATGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 290 AAGTATGAGCAAGATGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 349  
QY 210 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 269  
DB 350 GTCTCATCGCCTCTGCGGGGTACAGTCTTGTGCTCCCGCAGGAAACTGAACACTGATT 409  
QY 270 GCATCAGCTGCTGCACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 329  
DB 410 GCATCAGCTGCTGCACACCCCTTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAATT 469  
QY 330 CTGCTCTGCGGCTCTCA 344  
DB 470 CTGCTCTGCGGCTCTCA 484

RESULT 42  
US-10-219-069-15

; Sequence 15, Application US/10219069  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerltzen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P350P1C40  
; CURRENT APPLICATION NUMBER: US/10/219,069  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17

```

; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-069-15

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 89
Db 170 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 229

QY 90 GCTCTCCGCCGAGTTCATTGTGAATTGACGCTGAACGTTCAAGCATGTGCAGAAAG 149
Db 230 GCTCTCCGCCGAGTTCATTGTGAATTGACGCTGAACGTTCAAGCATGTGCAGAAAG 289

QY 150 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCATCAGGGCCT 209
Db 290 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCATCAGGGCCT 349

QY 210 GTCATCGGCTCTGCGGGTACAGTCTTGTCTCCCGAGGAAATGAACTCAGTTT 269
Db 350 GTCATCGGCTCTGCGGGTACAGTCTTGTCTCCCGAGGAAATGAACTCAGTTT 409

QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 329
Db 410 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 469

QY 330 CTGCTCGGGCCCTCA 344
Db 470 CTGCTCGGGCCCTCA 484

RESULT 43
US-10-219-070-15
; Sequence 15, Application US/10219070
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltzen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC42
; CURRENT APPLICATION NUMBER: US/10/219,070
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
```

```

; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-070-15

Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 89
Db 170 CAGGCTTGGCGTCAATCCAGTGTACAGTGAAGATCCAGCTGAACAGACT 229

QY 90 GCTCTCCGCCGAGTTCATTGTGAATTGACGCTGAACGTTCAAGCATGTGCAGAAAG 149
Db 230 GCTCTCCGCCGAGTTCATTGTGAATTGACGCTGAACGTTCAAGCATGTGCAGAAAG 289

QY 150 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCATCAGGGCCT 209
Db 290 AAGTATGAGCAAAATGCCGGGATCATGTACCGCAAGTCTTGATCATCATCAGGGCCT 349

QY 210 GTCATCGGCTCTGCGGGTACAGTCTTGTCTCCCGAGGAAATGAACTCAGTTT 269
Db 350 GTCATCGGCTCTGCGGGTACAGTCTTGTCTCCCGAGGAAATGAACTCAGTTT 409

QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 329
Db 410 GCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGGGAAGTT 469

QY 330 CTGCTCGGGCCCTCA 344
Db 470 CTGCTCGGGCCCTCA 484

RESULT 44
US-10-219-071-15
; Sequence 15, Application US/10219071
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltzen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC46
; CURRENT APPLICATION NUMBER: US/10/219,071
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
```



```
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; Remaining Prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO: 15
;; LENGTH: 1524
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-219-071-15
```

```
Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 30 CAGGCTTTGGCTGCAATATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
DB 170 CAGGCTTTGGCTGCAATATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 229

QY 90 GCTCCTCCCGGAGTTATTGTGAATTCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 149
    |||||||
DB 230 GCTCCTCCCGGAGTTATTGTGAATTCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 289

QY 150 AAGTATGAGCAAGAGTCCGGGATCATGTACCGCAAGTCCGTGCATCATCAGCGGCT 209
    |||||||
DB 290 AAGTATGAGCAAGAGTCCGGGATCATGTACCGCAAGTCCGTGCATCATCAGCGGCT 349

QY 210 GTCATCATGCTCTGCGGGATCAGTCTTCTGCTCCCGAGGAATCACTCAGTTT 269
    |||||||
DB 350 GTCATCATGCTCTGCGGGATCAGTCTTCTGCTCCCGAGGAATCACTCAGTTT 409

QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469

QY 330 CTGCTCGGCGCTCA 344
    |||||||
DB 470 CTGCTCGGCGCTCA 484
```

```
RESULT 45
US-10-219-072-15
; Sequence 15, Application us/10219072
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C45
; CURRENT FILING DATE: 2002-08-13
```

```
;; PRIOR APPLICATION NUMBER: 10/119,480
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; Remaining Prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO: 15
;; LENGTH: 1524
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-219-072-15
```

```
Query Match      85.4%; Score 315; DB 42; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 30 CAGGCTTTGGCTGCAATATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 89
    |||||||
DB 170 CAGGCTTTGGCTGCAATATCCAGTGTACAGTGTGAAGAAATTCAGCTGAACAACGACT 229

QY 90 GCTCCTCCCGGAGTTATTGTGAATTCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 149
    |||||||
DB 230 GCTCCTCCCGGAGTTATTGTGAATTCACGGTGAACGTTCAAGACATGTGTCAAGAAAG 289

QY 150 AAGTATGAGCAAGAGTCCGGGATCATGTACCGCAAGTCCGTGCATCATCAGCGGCT 209
    |||||||
DB 290 AAGTATGAGCAAGAGTCCGGGATCATGTACCGCAAGTCCGTGCATCATCAGCGGCT 349

QY 210 GTCATCATGCTCTGCGGGATCAGTCTTCTGCTCCCGAGGAATCACTCAGTTT 269
    |||||||
DB 350 GTCATCATGCTCTGCGGGATCAGTCTTCTGCTCCCGAGGAATCACTCAGTTT 409

QY 270 GCATCAGCTGTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 329
    |||||||
DB 410 GCATCAGCTGTGCAACACCCCTCTTTGTAAACGGGCCCAAGGCCCAAGAAAGGGAAGTT 469

QY 330 CTGCTCGGCGCTCA 344
    |||||||
DB 470 CTGCTCGGCGCTCA 484
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Search completed: November 8, 2002, 01:59:07
Job time : 834.445 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:16:33 : Search time 10.3091 Seconds  
(without alignments)  
3937.596 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369  
Sequence: 1 ggaacttttgcggattgt.....tgcctccgaccaccatcct 369

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 193892 seqs, 55004114 residues

Word size: 10

Total number of hits satisfying chosen parameters: 25490

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	85.4	1524	6	US-10-230-437-15
2	18	4.9	1587	6	US-10-092-411A-1425
3	18	4.9	1587	6	US-10-092-411A-2083
4	17	4.6	393	6	US-10-092-411A-263
5	16	4.3	111	5	US-09-513-999C-36268
6	16	4.3	397	6	US-10-266-131-144
7	16	4.3	433	5	US-09-513-999C-28601
8	16	4.3	577	5	US-09-513-999C-37773
9	15	4.1	250	5	US-09-513-999C-1336
10	15	4.1	465	5	US-09-513-999C-14500
11	15	4.1	481	5	US-09-513-999C-14500
12	15	4.1	579	6	US-10-240-425-140
13	15	4.1	686	6	US-10-240-425-710
14	15	4.1	940	1	PCT-US02-3203-35
15	15	4.1	1292	6	US-10-264-237-561
16	15	4.1	1542	6	US-10-264-237-1045
17	15	4.1	1733	6	US-10-264-237-315
18	15	4.1	1773	6	US-10-125-923A-555
19	15	4.1	1913	6	US-10-264-237-1252
20	15	4.1	3513	6	US-10-240-851-69
21	15	4.1	25020	6	US-10-192-280-1
22	15	4.1	36534	6	US-10-240-425-1461
23	15	4.1	74822	6	US-10-240-425-1121
24	14	3.8	25	7	US-60-417-190-4878
25	14	3.8	25	7	US-60-417-190-4878
26	14	3.8	25	7	US-60-417-190-4878

27	14	3.8	25	7	US-60-417-190-48790	Sequence 48790, A
28	14	3.8	25	7	US-60-417-190-48791	Sequence 48791, A
29	14	3.8	25	7	US-60-417-190-48792	Sequence 48792, A
30	14	3.8	25	7	US-60-417-190-48793	Sequence 48793, A
31	14	3.8	25	7	US-60-417-190-48794	Sequence 48794, A
32	14	3.8	25	7	US-60-417-190-48795	Sequence 48795, A
33	14	3.8	25	7	US-60-417-190-48796	Sequence 48796, A
34	14	3.8	25	7	US-60-417-190-48797	Sequence 48797, A
35	14	3.8	25	7	US-60-417-190-48798	Sequence 48798, A
36	14	3.8	25	7	US-60-417-190-48799	Sequence 48799, A
37	14	3.8	25	7	US-60-417-190-48800	Sequence 48800, A
38	14	3.8	25	7	US-60-417-190-48801	Sequence 48801, A
39	14	3.8	25	7	US-60-417-190-48802	Sequence 48802, A
40	14	3.8	25	7	US-60-417-190-48803	Sequence 48803, A
41	14	3.8	25	7	US-60-417-190-48804	Sequence 48804, A
42	14	3.8	25	7	US-60-417-190-48805	Sequence 48805, A
43	14	3.8	25	7	US-60-417-190-48806	Sequence 48806, A
44	14	3.8	25	7	US-60-417-190-48807	Sequence 48807, A
45	14	3.8	25	7	US-60-417-190-48808	Sequence 48808, A

ALIGNMENTS

RESULT 1  
US-10-230-437-15  
Sequence 15, Application US/10230437  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guirney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530P1C94  
CURRENT FILING DATE: 2002-08-28  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-230-437-15  
Query Match 85.4%; Score 315; DB 6; Length 1524;

Best Local Similarity 100.0%; Pred. No. 8.4e-166;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTTGGGCTCCCAATCCAGTGCACGAGTGTGAAGATTCCAGTCAACAACACT 89  
DB 170 CAGGCTTTGGGCTCCCAATCCAGTGCACGAGTGTGAAGATTCCAGTCAACAACACT 229  
QY 90 GCTCCCTCCCGAGTTCATTTGTGAATTCACAGGAGTGAACGTTTCAACATGTGTGAGAAG 149  
DB 230 GCTCCCTCCCGAGTTCATTTGTGAATTCACAGGAGTGAACGTTTCAACATGTGTGAGAAG 289  
QY 150 AAGTGAAGAGCAAAAGTCCGGGATCATGTATCCCAAGTCTGTGCATCATCAGCGGCT 209  
DB 290 AAGTGAAGAGCAAAAGTCCGGGATCATGTATCCCAAGTCTGTGCATCATCAGCGGCT 349  
QY 210 GTTCATCGGCTTGGCGGGATCACAGTCTGTGCTCCCGAGGAAACTGAATCAGTTT 269  
DB 350 GTTCATCGGCTTGGCGGGATCACAGTCTGTGCTCCCGAGGAAACTGAATCAGTTT 409  
QY 270 GCATCAGCTGCTGCACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAGTT 329  
DB 410 GCATCAGCTGCTGCACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAGTT 469  
QY 330 CTGGCTGGCGGCTCA 344  
DB 470 CTGGCTGGCGGCTCA 484

## RESULT 2

US-10-092-411A-1425  
Sequence 1425, Application US/10092411A  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: 032796-101  
CURRENT APPLICATION NUMBER: US/10/092.411A  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: US 09/134,001  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5676  
SEQ ID NO 1425  
LENGTH: 1587  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-10-092-411A-1425

Query Match 4.9%; Score 18; DB 6; Length 1587;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 AATTCACGCTGAACAACG 86  
DB 567 AATTCACGCTGAACAACG 584

## RESULT 3

US-10-092-411A-2083/C  
Sequence 2083, Application US/10092411A  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: 032796-101  
CURRENT APPLICATION NUMBER: US/10/092.411A  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: US 09/134,001  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5676  
SEQ ID NO 2083  
LENGTH: 1596  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-10-092-411A-2083

Query Match 4.9%; Score 18; DB 6; Length 1596;  
Best Local Similarity 100.0%; Pred. No. 0.74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGATCAGCTGCTGCAC 286  
DB 1308 TGATCAGCTGCTGCAC 1291

## RESULT 4

US-10-092-411A-263/C  
Sequence 263, Application US/10092411A  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: 032796-101  
CURRENT APPLICATION NUMBER: US/10/092.411A  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: US 09/134,001  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5676  
SEQ ID NO 263  
LENGTH: 393  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-10-092-411A-263

Query Match 4.6%; Score 17; DB 6; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 TCATGTGATTCGACG 121  
DB 389 TCATGTGATTCGACG 373

## RESULT 5

US-09-513-999C-36268/C  
Sequence 36268, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59 US2 REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 36268  
LENGTH: 111  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-36268

Query Match 4.3%; Score 16; DB 5; Length 111;

Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 258 TGAAGTCAGTTTCAT 273  
|||||  
DB 70 TGAAGTCAGTTTCAT 55

RESULT 6  
US-10-266-131-144/c  
Sequence 144, Application US/10266131  
GENERAL INFORMATION:  
APPLICANT: Friedlich, Glenn  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: Novel Murine Polynucleotide Tags and  
TITLE OF INVENTION: Mutant Cells and Mutant Animals Defined Thereby  
FILE REFERENCE: LEX-0030-USA  
CURRENT APPLICATION NUMBER: US/10/266,131  
CURRENT FILING DATE: 2002-10-07  
PRIOR APPLICATION NUMBER: US/09/617,675  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/143,878  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 2908  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 144  
LENGTH: 397  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-266-131-144

Query Match  
Best Local Similarity 4.3%; Score 16; DB 6; Length 397;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 TCTGCTCCCGAGGAA 255  
|||||  
DB 247 TCTGCTCCCGAGGAA 232

RESULT 7  
US-09-513-999C-28601/c  
Sequence 28601, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 28601  
LENGTH: 433  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 275  
OTHER INFORMATION: n-a, g, c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 309  
OTHER INFORMATION: r-a or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 310  
OTHER INFORMATION: r-a or g

Query Match  
Best Local Similarity 4.3%; Score 16; DB 5; Length 433;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCCGGATCA 176  
|||||  
DB 305 CAAAGTCCCGGATCA 290

RESULT 8  
US-09-513-999C-3777/c  
Sequence 3777, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 3777  
LENGTH: 577  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 73..474  
NAME/KEY: sig\_peptide  
LOCATION: 73..123  
OTHER INFORMATION: seq LALSLLIIVLAFG/IP  
US-09-513-999C-3777

Query Match  
Best Local Similarity 4.3%; Score 16; DB 5; Length 577;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 TGCAATCAGCTGCTGCA 284  
|||||  
DB 335 TGCAATCAGCTGCTGCA 320

RESULT 9  
US-09-513-999C-24773/c  
Sequence 24773, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 24773  
LENGTH: 250  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 182  
OTHER INFORMATION: s-g or c  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: 183  
OTHER INFORMATION: k=g or t  
US-09-513-999C-24773

Query Match  
Best Local Similarity 4.1%; Score 15; DB 5; Length 250;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GCTGCAATTCAGTG 54  
Db 39 GCTGCAATTCAGTG 25

RESULT 10  
US-09-513-999C-1336

Sequence 1336, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Mline Edwards, J.B.  
APPLICANT: Duclert, A.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 1336  
LENGTH: 466  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 141..464

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 197  
OTHER INFORMATION: m=a or c  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 198

OTHER INFORMATION: n=a, g, c or t  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 19  
OTHER INFORMATION: Xaa=Lys or Asn  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 20

OTHER INFORMATION: Xaa=Phe or Ile or Leu or Val  
US-09-513-999C-1336

Query Match  
Best Local Similarity 4.1%; Score 15; DB 5; Length 466;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 TGAAGAATTCAGCT 78  
Db 281 TGAAGAATTCAGCT 295

RESULT 11  
US-09-513-999C-14500/c

Sequence 14500, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Mline Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 14500  
LENGTH: 481  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 133  
OTHER INFORMATION: y=c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 325  
OTHER INFORMATION: r=a or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 326  
OTHER INFORMATION: w=a or t  
US-09-513-999C-14500

Query Match  
Best Local Similarity 4.1%; Score 15; DB 5; Length 481;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 AGTTCTGCTCGGCC 340  
Db 388 AGTTCTGCTCGGCC 374

RESULT 12  
US-10-240-425-140  
Sequence 140, Application US/10240425  
GENERAL INFORMATION:  
APPLICANT: Williams, Amanda  
APPLICANT: Boland, Joseph F.  
APPLICANT: Lord, Reginald V.  
APPLICANT: Alvarez, Chris  
APPLICANT: Wetzel, Jon C.  
APPLICANT: Scherf, Uwe  
APPLICANT: Vockley, Joseph G.

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
FILE REFERENCE: 44921-5026  
CURRENT APPLICATION NUMBER: US/10/240,425  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: PCT/US01/09847  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 60/193,446  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 1588  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 140  
LENGTH: 579  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 133  
OTHER INFORMATION: y=c or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 325  
OTHER INFORMATION: r=a or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 326  
OTHER INFORMATION: w=a or t  
US-10-240-425-140

Query Match  
Best Local Similarity 4.1%; Score 15; DB 6; Length 579;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 GCCAAGGCCCAAGAA 318  
Db 81 GCCAAGGCCCAAGAA 95

RESULT 13  
US-10-240-425-710  
; Sequence 710, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 710  
; LENGTH: 686  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AF634580  
; NAME/KEY: unsure  
; LOCATION: (1)..(686)  
; OTHER INFORMATION: n = a or c or g or t  
US-10-240-425-710

Query Match 4.1%; Score 15; DB 6; Length 686;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 GTCGAGAAGAGTGA 155  
DB 554 GTCGAGAAGAGTGA 568

RESULT 14  
PCT-US02-32032-35/C  
; Sequence 35, Application PC/TUS0232032  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: LEHR-MASON, Patricia M.  
; APPLICANT: TRAN, Uyen K.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: YANG, Junming  
; APPLICANT: XU, Yuming  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: CHAWLA, Nalinder K.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: FORSYTHE, Ian J.  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: ZEBARJADIAN, Yeganeh  
; APPLICANT: BAUGHN, Marian R.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: LEE, Soo Yeun  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: GORVAD, Ann E.  
; APPLICANT: KABLE, Amy E.  
; APPLICANT: LU, Dnyung Alina M.

; APPLICANT: BOROMSKY, Mark L.  
; TITLE OF INVENTION: SECRETED PROTEINS  
; FILE REFERENCE: PF-1217 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/32032  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 60/326,945  
; PRIOR FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: US 60/343,718  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/343,980  
; PRIOR FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: US 60/332,426  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PERL Program  
; SEQ ID NO 35  
; LENGTH: 940  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No: 7340485CBI  
PCT-US02-32032-35

Query Match 4.1%; Score 15; DB 1; Length 940;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 TGTGAGAGATTCCAG 76  
DB 303 TGTGAGAGATTCCAG 289

RESULT 15  
US-10-264-237-561/C  
; Sequence 561, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P431PI  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: Patent Ver. 3.1  
; SEQ ID NO 561  
; LENGTH: 1292  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (534)..(534)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-561

Query Match 4.1%; Score 15; DB 6; Length 1292;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCCAAGGCCCAAGAA 318  
DB 434 GCCAAGGCCCAAGAA 420

RESULT 16  
US-10-264-237-1045  
; Sequence 1045, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAL31PI  
CURRENT APPLICATION NUMBER: US/10/264,237  
CURRENT FILING DATE: 2002-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/16450  
PRIOR FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: US 60/205,515  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 2876  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 1045  
LENGTH: 1542  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1471)..(1471)  
OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-1045

Query Match 4.1%; Score 15; DB 6; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCTGC 44  
|||||  
DB 310 CAGGCTTGGCTGC 324

RESULT 17  
US-10-264-237-315/C  
Sequence 315, Application US/10264237  
GENERAL INFORMATION:  
APPLICANT: Blise et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PAL31PI  
CURRENT APPLICATION NUMBER: US/10/264,237  
CURRENT FILING DATE: 2002-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/16450  
PRIOR FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: US 60/205,515  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 2876  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 315  
LENGTH: 1733  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1459)..(1459)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1509)..(1509)  
OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-315

Query Match 4.1%; Score 15; DB 6; Length 1733;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 GTGTGAAGATTCCA 75  
|||||  
DB 1051 GTGTGAAGATTCCA 1037

RESULT 18  
US-10-125-923A-555/C  
Sequence 555, Application US/10125923A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P94301C79  
CURRENT APPLICATION NUMBER: US/10/125,923A  
CURRENT FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 555  
LENGTH: 1773  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-125-923A-555

Query Match 4.1%; Score 15; DB 6; Length 1773;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 TCAGCTGCTGCACCA 287  
|||||  
DB 1008 TCAGCTGCTGCACCA 994

RESULT 19  
US-10-264-237-1252  
Sequence 1252, Application US/10264237  
GENERAL INFORMATION:  
APPLICANT: Blise et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PAL31PI  
CURRENT APPLICATION NUMBER: US/10/264,237  
CURRENT FILING DATE: 2002-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/16450  
PRIOR FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: US 60/205,515  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 2876  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 1252  
LENGTH: 1913  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-264-237-1252

Query Match 4.1%; Score 15; DB 6; Length 1913;  
Best Local Similarity 100.0%; Pred. No. 35;



Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCCAAGCCCCAGAA 318  
|||||

DB 136 GCCAAGCCCCAGAA 150

## RESULT 20

US-10-240-851-69/C  
; Sequence 69, Application US/10240851  
; GENERAL INFORMATION:  
; APPLICANT: John P. Carulli et al.  
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
; FILE REFERENCE: 032796-021  
; CURRENT APPLICATION NUMBER: US/10/240,851  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: US 09/544,398  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 09/543,771  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 09/229,319  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,449  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/105,511  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 109  
; SEQ ID NO 69  
; LENGTH: 3513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-240-851-69

Query Match 4.1%; Score 15; DB 6; Length 3513;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 CAGCTGCTGCACAC 288  
|||||

DB 944 CAGCTGCTGCACAC 930

## RESULT 21

US-10-192-280-1  
; Sequence 1, Application US/10192280  
; GENERAL INFORMATION:  
; APPLICANT: Datta Gupta, Nanibhusan  
; APPLICANT: Shah, Ketan  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
; TITLE OF INVENTION: STREPTOCOCCUS AGALACTIAE CAPSULAR POLYSACCHARIDE SYNTHESIS  
; FILE REFERENCE: 475412001300  
; CURRENT APPLICATION NUMBER: US/10/192,280  
; CURRENT FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 25020  
; TYPE: DNA  
; ORGANISM: Streptococcus agalactiae  
US-10-192-280-1

Query Match 4.1%; Score 15; DB 6; Length 25020;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AAGAAGTGTGAGC 161  
|||||

DB 10941 AAGAAGTGTGAGC 10955

RESULT 22  
US-10-240-425-1461

; Sequence 1461, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1461  
; LENGTH: 36534  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. U73167  
US-10-240-425-1461

Query Match 4.1%; Score 15; DB 6; Length 36534;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CTGACTCAGTTGC 271  
|||||

DB 23250 CTGACTCAGTTGC 23264

## RESULT 23

US-10-240-425-1121  
; Sequence 1121, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1121  
; LENGTH: 74822  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AL049798  
US-10-240-425-1121

Query Match 4.1%; Score 15; DB 6; Length 74822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 ATGTCTCAGAAAGAA 151  
|||||

DB 70056 ATGTCTCAGAAAGAA 70070

```

RESULT 24
US-60-417-190-48787/c
; Sequence 48787, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48787

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 23 AAGATTCCAGCTG 10
|||||

```

```

; ORGANISM: Homo sapien
US-60-417-190-48789

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 20 AAGATTCCAGCTG 7
|||||

RESULT 27
US-60-417-190-48790/c
; Sequence 48790, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48790

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 19 AAGATTCCAGCTG 6
|||||

RESULT 28
US-60-417-190-48791/c
; Sequence 48791, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48791

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAGATTCCAGCTG 79
DB 18 AAGATTCCAGCTG 5
|||||

RESULT 29
US-60-417-190-48792/c
; Sequence 48792, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy

```

```

; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48792

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

OY 66 AAGATTCCAGCTG 79
Db 16 AAGATTCCAGCTG 3

RESULT 30
US-60-417-190-48793/c
; Sequence 48793, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48793
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48793

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

OY 66 AAGATTCCAGCTG 79
Db 15 AAGATTCCAGCTG 2

RESULT 31
US-60-417-190-94484/c
; Sequence 94484, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94484

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Gaps 0; Indels 0;
```

```

OY 143 CAGAAAGAGTGAT 156
Db 25 CAGAAAGAGTGAT 12

RESULT 32
US-60-417-190-94485/c
; Sequence 94485, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94485
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94485

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

OY 143 CAGAAAGAGTGAT 156
Db 24 CAGAAAGAGTGAT 11

RESULT 33
US-60-417-190-94486/c
; Sequence 94486, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94486
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94486

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02; Length 25;
Matches 14; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

OY 143 CAGAAAGAGTGAT 156
Db 23 CAGAAAGAGTGAT 10

RESULT 34
US-60-417-190-94487/c
; Sequence 94487, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
```

```
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94487
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94487
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 143 CAGAAAGAGTGAT 156
Db 22 CAGAAAGAGTGAT 9
```

```
RESULT 35
US-60-417-190-94488/C
; Sequence 94488, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
```

```
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94488
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 143 CAGAAAGAGTGAT 156
Db 20 CAGAAAGAGTGAT 7
```

```
RESULT 36
US-60-417-190-94489/C
; Sequence 94489, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
```

```
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94489
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-94489
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 7; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 143 CAGAAAGAGTGAT 156
Db 19 CAGAAAGAGTGAT 6
```

```
RESULT 37
US-09-513-999C-16171/C
; Sequence 16171, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16171
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16171
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Query Match
Best Local Similarity 100.0%; Score 14; DB 5; Length 80;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 93 CCTCCCCGAGTTC 106
Db 26 CCTCCCCGAGTTC 13
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RESULT 38
US-09-513-999C-17785
; Sequence 17785, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 17785
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 69
; OTHER INFORMATION: h-a or c or t
US-09-513-999C-17785
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Query Match
Best Local Similarity 100.0%; Score 14; DB 5; Length 100;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 161 CAAAGTCCGCGGAT 174
Db 43 CAAAGTCCGCGGAT 56
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RESULT 39
US-09-513-999C-19578
; Sequence 19578, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
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CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO: 19578  
LENGTH: 109  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-19578

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174  
DB 87 CAAAGTCCGGGAT 100

RESULT 40  
US-09-513-999C-23316  
Sequence 23316, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO: 23316  
LENGTH: 112  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-23316

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174  
DB 83 CAAAGTCCGGGAT 96

RESULT 41  
US-09-513-999C-18596/C  
Sequence 18596, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO: 18596  
LENGTH: 116  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-18596

Query Match 3.8%; Score 14; DB 5; Length 116;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174  
DB 95 CAAAGTCCGGGAT 82

RESULT 42  
US-09-513-999C-14544/C  
Sequence 14544, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO: 14544  
LENGTH: 125  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-14544

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CGCCTCTGCCGGGT 230  
DB 109 CGCCTCTGCCGGGT 96

RESULT 43  
US-09-513-999C-18527/C  
Sequence 18527, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO: 18527  
LENGTH: 129  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-18527

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 CAAAGTCCGGGAT 174  
DB 55 CAAAGTCCGGGAT 42

RESULT 44  
US-09-513-999C-28218  
Sequence 28218, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 28218  
 ; LENGTH: 138  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-513-999C-28218

Query Match 3.8%; Score 14; DB 5; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 TTCATTGTGAATTG 117  
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 Db 20 TTCATTGTGAATTG 33

RESULT 45  
 US-09-513-999C-25794  
 ; Sequence 25794, Application US/09513999C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 25794  
 ; LENGTH: 142  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-513-999C-25794

Query Match 3.8%; Score 14; DB 5; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 ACATGTGTCAGAAA 148  
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 Db 39 ACATGTGTCAGAAA 52

Search completed: November 8, 2002, 02:02:17  
 Job time : 69.3091 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 494.427 Seconds  
(without alignments)  
12086.984 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369  
Sequence: 1 ggcgaacttttgcgagtgt.....tggtccgcacacacacacct 369

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5082808

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rnd:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	315	85.4	704	BI919074
2	315	85.4	707	BI913989
3	315	85.4	920	AL538562
4	314	85.1	593	BE386060
5	307	83.2	747	BI917149
6	295	79.9	987	BO668420

7	284	77.0	690	13	BI669845
8	283	76.7	340	14	H06756
9	271	73.4	1010	12	BF345141
10	263	71.3	573	10	BE395206
11	262	71.0	548	10	BO882838
12	258	69.9	704	13	BI823714
13	237	64.2	570	13	BI831919
14	235	63.7	352	9	AA349894
15	224	60.7	670	12	BE753617
16	205	55.6	654	12	BE746601
17	196	53.1	698	13	BI554034
18	190	51.5	540	10	AW954549
19	175	47.4	433	9	AA582576
20	175	47.4	522	9	AI767459
21	175	47.4	541	14	BM974798
22	175	47.4	651	14	AV717094
23	175	47.4	652	14	BM980701
24	175	47.4	738	14	BM981455
25	174	47.2	890	12	BF125425
26	173	46.9	449	9	AI140655
27	167	45.3	878	12	BF125664
28	166	45.0	395	14	R20352
29	166	45.0	429	14	HI7189
30	151	40.9	434	9	AI299246
31	148	40.1	424	9	AI138793
32	145	39.3	435	10	AW014802
33	143	38.8	516	9	AA776783
34	143	38.8	794	12	BE731003
35	143	38.8	1134	12	BE730800
36	141	38.2	350	12	BE213586
37	141	38.2	484	12	BE184021
38	141	38.2	781	12	BE193459
39	140	37.9	424	12	BE188218
40	139	37.7	323	12	BE192926
41	139	37.7	323	12	BE210457
42	139	37.7	324	12	BE215210
43	139	37.7	330	12	BE200048
44	139	37.7	331	12	BE181955
45	139	37.7	331	12	BE204666

## ALIGNMENTS

RESULT 1  
BI919074  
LOCUS  
DEFINITION  
603180881F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5244956 5',  
mRNA sequence.  
BI919074  
BI919074.1 GI:16200128

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
1 (bases 1 to 704)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bms-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM1618 row: a column: 21  
High quality sequence start: 4  
High quality sequence stop: 702.  
Location/Qualifiers

## FEATURES

source

1. 704  
/organism="Homo sapiens"  
/db.xref="taxon:9606"  
/clone="IMAGE:5244956"  
/clone\_lib="NIH-MGC\_121"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

BASE COUNT 132 a 237 c 204 g 131 t

ORIGIN

Query Match 85.4%; Score 315; DB 13; Length 704;  
Best Local Similarity 100.0%; Pred. No. 1.7e-166;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTGTCTACAGTGTGAAGAAATTCAGTGAACAAGACT 89  
DB 347 CAGGCTTGGCGCTGCAATCCAGTGTCTACAGTGTGAAGAAATTCAGTGAACAAGACT 406  
QY 90 GCTCTCCCGCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 149  
DB 407 GCTCTCCCGCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 466  
QY 150 AAGTATGAGACAAAGTCCGCGGATCATGTACCCGAAGTCTGTGCATCATCAGCGGCT 209  
DB 467 AAGTATGAGACAAAGTCCGCGGATCATGTACCCGAAGTCTGTGCATCATCAGCGGCT 526  
QY 210 GTCTCATGCGCTGTGCGGGGTACAGTCTCTGTCTCCCGAGGAAATGAACTCAAGTT 269  
DB 527 GTCTCATGCGCTGTGCGGGGTACAGTCTCTGTCTCCCGAGGAAATGAACTCAAGTT 586  
QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
DB 587 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 646  
QY 330 CTGCTCGGGCCCTCA 344  
DB 647 CTGCTCGGGCCCTCA 661

RESULT 2  
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LOCUS DEFINITION 603180565F1 NIH-MGC\_121 Homo sapiens cDNA clone IMAGE:5244569 5',  
mRNA sequence.  
ACCESSION BI913989  
VERSION BI913989.1 GI:16178286  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 707)  
NIH-MGC <http://imgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Plate: L1AM11617 row: a column: 18  
High quality sequence stop: 698.  
Location/Qualifiers  
1. 707  
/organism="Homo sapiens"  
/db.xref="taxon:9606"  
/clone="IMAGE:5244569"  
/clone\_lib="NIH-MGC\_121"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

BASE COUNT 133 a 233 c 209 g 132 t

ORIGIN

Query Match 85.4%; Score 315; DB 13; Length 707;  
Best Local Similarity 100.0%; Pred. No. 1.7e-166;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCGCTGCAATCCAGTGTCTACAGTGTGAAGAAATTCAGTGAACAAGACT 89  
DB 315 CAGGCTTGGCGCTGCAATCCAGTGTCTACAGTGTGAAGAAATTCAGTGAACAAGACT 374  
QY 90 GCTCTCCCGCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 149  
DB 375 GCTCTCCCGCGAGTTCATTTGTGAATTCACAGGTGAACGTTCAAGACATGTGTGAGAAG 434  
QY 150 AAGTATGAGACAAAGTCCGCGGATCATGTACCCGAAGTCTGTGCATCATCAGCGGCT 209  
DB 435 AAGTATGAGACAAAGTCCGCGGATCATGTACCCGAAGTCTGTGCATCATCAGCGGCT 494  
QY 210 GTCTCATGCGCTGTGCGGGGTACAGTCTCTGTCTCCCGAGGAAATGAACTCAAGTT 269  
DB 495 GTCTCATGCGCTGTGCGGGGTACAGTCTCTGTCTCCCGAGGAAATGAACTCAAGTT 554  
QY 270 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 329  
DB 555 GCATCAGCTGCTGCAACACCCCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAGGGAAGTT 614  
QY 330 CTGCTCGGGCCCTCA 344  
DB 615 CTGCTCGGGCCCTCA 629

RESULT 3  
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LOCUS DEFINITION AL538562 L11-F1013.FBn1 Homo sapiens cDNA clone CSODF024Y004 5  
Prime, mRNA sequence.  
ACCESSION AL538562  
VERSION AL538562.1 GI:12866967  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 920)  
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [segreff@genoscope.cns.fr](mailto:segreff@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr).  
Location/Qualifiers  
1. 920

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source



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/organism="Homo sapiens"
/db_xref="taxon:9606"
//clone="CS0DF024Y004"
/clone_1lb="LTI_FLO13_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

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Query Match	Similarity	Score	DB 9:	Length	920:
Best Local	Similarity 100.0%	Pred. No. 1.8e-166			
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Db	308	CAGGCTTGGCCCTCGCAATTCACAGTCTACCAAGTGTGAAGAAATTCACAGCTGAACAACGACT	367		
QY	90	GCTCTCTCCCCGAGTTCAATTGTGAATTCACAGGTGAACGTTCCAGACACTGTGTGAGAAAG	149		
Db	368	GCTCTCTCCCCGAGTTCAATTGTGAATTCACAGGTGAACGTTCCAGACACTGTGTGAGAAAG	427		
QY	150	AAGTATGAGACAAAGTACCGGGATCATGTACCGCAATCTCTGTGCATCATCAGCGGCT	209		
Db	428	AAGTATGAGACAAAGTACCGGGATCATGTACCGCAATCTCTGTGCATCATCAGCGGCT	487		
QY	210	GTCATCATGCGCTCTGTCGCGGGTACCAAGTCTCTTGTGCTCCCAAGGAACTGAATCAGTTT	269		
Db	488	GTCATCATGCGCTCTGTCGCGGGTACCAAGTCTCTTGTGCTCCCAAGGAACTGAATCAGTTT	547		
QY	270	GCATCAGCTGCTGCAACACCCCTCTTTGTGAACGGGSCCAAGGCCCAAGAAAGGGGAGCTT	329		
Db	548	GCATCAGCTGCTGCAACACCCCTCTTTGTGAACGGGSCCAAGGCCCAAGAAAGGGGAGCTT	607		
QY	330	CTGCCCTGGGCGCCTCA 344			
Db	608	CTGCCCTGGGCGCCTCA 622			
RESULT 4					
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LOCUS	601276753F1 NIH_MGC_20	Homo sapiens	CDNA clone IMAGE:3617749 5'		
DEFINITION	mRNA sequence.				
ACCESSION	BE386060				
VERSION	BE386060.1	GI:9331425			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (bases 1 to 593)				
REFERENCE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished (1999)				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>				
	Tissue Procurement: ATCC/DC/DTF				
	CDNA Library Preparation: Ling Hong/Rubin Laboratory				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">image.llnl.gov</a>				

Plate:	ILCM285	row:	1	column:	14
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	/clone="IMAGE:3617749"				
	/clone_lib="NHL_MGC_20"				
	/tissue_type="melanotic melanoma"				
	/lab_host="DH10B (phage-resistant)"				
	/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."				
BASE COUNT	139	a	166	c	183
ORIGIN	g 105 t				

	Query	March	85.1%	Score	314	DB	10	Length	593	
	Best	Local Similarity	100.0%	Pred.	No.	5	9e-166			
	Matches	314	Conservative	0	Mismatches	0	Indels	0	Gaps	0
OY	31	AGGCTTTGGCGGTGCATAATCCAGTGGCTACAGTGTAAGAATTCACGTGAACAACGACTG	90							
Db	246	AGGCTTTGGCGGTGCATAATCCAGTGGCTACAGTGTAAGAATTCACGTGAACAACGACTG	305							
OY	91	CTCCTCCCCCGAGTTCATTGTGAATTCACAGGTGAACGTTCAAGCATGTGNCAGAAAGA	150							
Db	306	CTCCCTCCCCCGAGTTCATTGTGAATTCACAGGTGAACGTTCAAGCATGTGNCAGAAAGA	365							
OY	151	AGTGAATGAGCAAGAGGCCGGAGTATGATGACGGCAAGTCCTTGATCATCATCAGCGCCTG	210							
Db	366	AATGATGAGCAAGAGGCCGGAGTATGATGACGGCAAGTCCTTGATCATCATCAGCGCCTG	425							
OY	211	TCTCATCGGCTCTGCCGGGTACCAAGTCTTGTCTGCCAGGGAATCACTACAGTTTG	270							
Db	426	TCTCATCGGCTCTGCCGGGTACCAAGTCTTGTCTGCCAGGGAATCACTACAGTTTG	485							
OY	271	CATCAGCTGCTGCACACCCCCTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAAGTTC	330							
Db	486	CATCAGCTGCTGCACACCCCCTTTGTAAAGGGGCCAAGGCCCAAGAAAGGGGAAGTTC	545							
OY	331	TGCTCGGGCCTCA	344							
Db	546	TGCTCGGGCCTCA	559							

[illegible]

Found through the I.M.A.G.E. Consortium/LLNL at:  
 http://lmlm1619.row.n column: 17  
 Plate: LMLM1619  
 High quality sequence stop: 737.

FEATURES  
 source  
 1. 747  
 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5245648"  
 /clone\_lib="NIH\_MGC\_121"  
 /lab\_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

BASE COUNT 140 a 245 c 216 g 146 t  
 ORIGIN

Query Match 83.28; Score 307; DB 13; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-162;  
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

30 CAGCCTTTGGCGCTCAATCCAGTGTACCAAGTGAAGAAATTCACCTGCAACAGCACT 89  
 354 CAGCCTTTGGCGCTCAATCCAGTGTACCAAGTGAAGAAATTCACCTGCAACAGCACT 413  
 90 GCTCTCTCCCGAGATTGTTGAATTCACAGGTCGTCATGATGTCAGAAAG 149  
 414 GCTCTCTCCCGAGATTGTTGAATTCACAGGTCGTCATGATGTCAGAAAG 473  
 150 AAGTATGAGGCAAGAGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
 474 AAGTATGAGGCAAGAGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 533  
 210 GTCATCATCGGCTGTGCGGGTACCAAGTCTGTGATCATCAGCGGCAAGTCAACTGATT 269  
 534 GTCATCATCGGCTGTGCGGGTACCAAGTCTGTGATCATCAGCGGCAAGTCAACTGATT 593  
 270 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGCGCCCAAGAAAAGGGAAGTT 329  
 594 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGCGCCCAAGAAAAGGGAAGTT 653  
 330 CTGCTCT 336  
 654 CTGCTCT 660

RESULT 6  
 B0668420 987 bp mRNA linear EST 15-JUL-2002  
 LOCUS B0668420  
 DEFINITION AGENCOURT\_8301981 NIH\_MGC\_102 Homo sapiens cDNA clone IMAGE:6275121  
 5' mRNA sequence.  
 ACCESSION B0668420  
 VERSION B0668420.1 GI:21778667  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 987)  
 AUTHORS NIH-MGC http://mgc.nhl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://lmlm2457.row.n column: 10  
 Plate: LLM2457  
 High quality sequence stop: 583.

FEATURES  
 source  
 1. 987  
 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6275121"  
 /clone\_lib="NIH\_MGC\_102"  
 /tissue\_type="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: salivary gland; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 196 a 314 c 285 g 191 t 1 others  
 ORIGIN

Query Match 79.98; Score 295; DB 14; Length 987;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-155;  
 Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

30 CAGCCTTTGGCGCTCAATCCAGTGTACCAAGTGAAGAAATTCACCTGCAACAGCACT 89  
 301 CAGCCTTTGGCGCTCAATCCAGTGTACCAAGTGAAGAAATTCACCTGCAACAGCACT 360  
 90 GCTCTCTCCCGAGATTGTTGAATTCACAGGTCGTCATGATGTCAGAAAG 149  
 361 GCTCTCTCCCGAGATTGTTGAATTCACAGGTCGTCATGATGTCAGAAAG 420  
 150 AAGTATGAGGCAAGAGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
 421 AAGTATGAGGCAAGAGCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 480  
 210 GTCATCATCGGCTGTGCGGGTACCAAGTCTGTGATCATCAGCGGCAAGTCAACTGATT 269  
 481 GTCATCATCGGCTGTGCGGGTACCAAGTCTGTGATCATCAGCGGCAAGTCAACTGATT 540  
 270 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGCGCCCAAGAAAAGGGAAGTT 324  
 541 GCATCAGCTCTGCAACACCCCTTTTGTAAAGGCGCCCAAGAAAAGGGAAGTT 595

RESULT 7  
 B1669845 690 bp mRNA linear EST 12-SEP-2001  
 LOCUS B1669845  
 DEFINITION 603293440F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5312889 5',  
 mRNA sequence.  
 ACCESSION B1669845  
 VERSION B1669845.1 GI:15584078  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 690)  
 AUTHORS NIH-MGC http://mgc.nhl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: L1M11792 row: p column: 10  
 High quality sequence stop: 690.  
 Location/Qualifiers

## FEATURES

## SOURCE

1. 690

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5312889"  
 /clone\_lib="NIH\_MGC\_96"  
 /tissue\_type="hypothalamus"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pBluescript (modified  
 pluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
 size-selected for average insert size 2.3 kb and  
 normalized to 50% of total. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NIMH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."

## BASE COUNT

127 a 231 c 202 g 130 t

Query Match 77.0%; Score 284; DB 13; Length 690;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-149; Mismatches 0; Indels 0; Gaps 0;  
 Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

61 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 120  
 |||||||  
 363 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 422

121 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 180  
 |||||||  
 423 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 482

181 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 240  
 |||||||  
 483 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 542

241 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 300  
 |||||||  
 543 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 602

301 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 360  
 |||||||  
 603 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 660

361 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 420  
 |||||||  
 663 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 720

421 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 480  
 |||||||  
 723 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 780

481 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 540  
 |||||||  
 783 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 840

541 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 600  
 |||||||  
 843 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 900

601 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 960  
 |||||||  
 903 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 960

961 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 1020  
 |||||||  
 1023 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 1080

1081 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 1140  
 |||||||  
 1143 GTGTGAAGATTCAGCTGGAACAAGACTGCTCCCTCCAGTTCATTGTAATGAC 1200

## FEATURES

## SOURCE

1. 340

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 Insert Size: 1737  
 High quality sequence stop: 312  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 1737 Std Error: 0.00  
 Seq primer: M13Rpl  
 High quality sequence stop: 312.  
 Location/Qualifiers

## BASE COUNT

77 a 95 c 89 g 79 t

Query Match 76.7%; Score 283; DB 14; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-148; Mismatches 0; Indels 0; Gaps 0;  
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

30 CAGGCTTTGGCTGCAATTCAGTCTACCAAGTGAAGATTCAGTGAACAAGACT 89  
 |||||||  
 20 CAGGCTTTGGCTGCAATTCAGTCTACCAAGTGAAGATTCAGTGAACAAGACT 79

90 GCTCTCTCCCGGAGTATTTGTAATGACAGGAGGAGTTCAGTGAACAAGACT 149  
 |||||||  
 80 GCTCTCTCCCGGAGTATTTGTAATGACAGGAGGAGTTCAGTGAACAAGACT 139

150 AAGTGAAGAGCAAGAGTTCAGTGAACAAGACTGCTGTCATCATCAGCGGCT 209  
 |||||||  
 140 AAGTGAAGAGCAAGAGTTCAGTGAACAAGACTGCTGTCATCATCAGCGGCT 199

210 GCTCATGCGCTTGGCGGATACCAAGTCTCTGCTCCCAAGGAACTGAACTGTT 269  
 |||||||  
 200 GCTCATGCGCTTGGCGGATACCAAGTCTCTGCTCCCAAGGAACTGAACTGTT 259

270 GCAATCAGCTGCTGCAACACCCCTTTGTAAGGCGCAAGGCC 312  
 |||||||  
 260 GCAATCAGCTGCTGCAACACCCCTTTGTAAGGCGCAAGGCC 302

## RESULT 9

## LOCUS

BF345141 1010 bp mRNA linear EST 22-NOV-2000

602018318F1 NCL\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4153684  
 5', mRNA sequence.

ACCESSION BF345141  
 VERSION BF345141.1 GI:11292606

KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 1 (bases 1 to 1010)  
 NIH-MGC http://imgc.nhl.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

## FEATURES

## source

1. 1010  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4153684"  
/issue\_type="anaplastic oligodendroglioma with 1p/19q loss"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT  
ORIGIN

266 a 344 c 254 g 146 t

## Query Match

Best Local Similarity 73.4%; Score 271; DB 12; Length 1010;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGGCTTGGCCCTGCAATCCAGTGTACAGTGAAGAAATTCAGCTGAACAACGACTG 90  
DB 258 AGGCTTGGCCCTGCAATCCAGTGTACAGTGAAGAAATTCAGCTGAACAACGACTG 317  
QY 91 CTGCTCCCGGAGTCTATTGTGAATTCACAGCTGACAGCTTCAAGACATGTGTCAAGAAGA 150  
DB 318 CTGCTCCCGGAGTCTATTGTGAATTCACAGCTGACAGCTTCAAGACATGTGTCAAGAAGA 377  
QY 151 AGTATGAGACAAAGTCCGGGATCATGTACCCGAATCTCTGTGATCATCAGGGGCTG 210  
DB 378 AGTATGAGACAAAGTCCGGGATCATGTACCCGAATCTCTGTGATCATCAGGGGCTG 437  
QY 211 TCTCATGCGCTTGGCCGGGTACAGTCTCTCTCCCAAGGAAACTGAAGTCAAGTTTG 270  
DB 438 TCTCATGCGCTTGGCCGGGTACAGTCTCTCTCTCCCAAGGAAACTGAAGTCAAGTTTG 497  
QY 271 CATCAGCTGCTGCAACACCCCTTTGTATAC 301  
DB 498 CATCAGCTGCTGCAACACCCCTTTGTATAC 528

RESULT 10  
LOCUS BE395206 573 bp mRNA linear EST 21-JUL-2000  
DEFINITION 60130955881 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3631047 5',  
ACCESSION BE395206  
VERSION BE395206.1 GI:9340571  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory

## FEATURES

## source

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM320 row: c column: 16  
High quality sequence stop: 573.  
Location/Qualifiers  
1. 573  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3631047"  
/issue\_type="NIH\_MGC\_44"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT  
ORIGIN

119 a 192 c 154 g 108 t

## Query Match

Best Local Similarity 71.3%; Score 263; DB 10; Length 573;  
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CAAGACTGCTCCCTCCCGGATTCATTGTAATTCAGCGGTGAACGTTCAAGCATGTG 141  
DB 1 CAAGACTGCTCCCTCCCGGATTCATTGTAATTCAGCGGTGAACGTTCAAGCATGTG 60  
QY 142 TCAGAAAGAGTATGAGCAAAAGTCCGGGATCATACCGCAAGTCTGTGATCATC 201  
DB 61 TCAGAAAGAGTATGAGCAAAAGTCCGGGATCATACCGCAAGTCTGTGATCATC 120  
QY 202 AGCGGCTGTCTCATGCTCTGCGGATTCAGTCTCTGCTCCCAAGGAAACTGAA 261  
DB 121 AGCGGCTGTCTCATGCTCTGCGGATTCAGTCTCTGCTCCCAAGGAAACTGAA 180  
QY 262 CTCAGTTGATCATGCTGTGCAACACCCCTTTGTATACGGGGCAAGGCAAGAAAG 321  
DB 181 CTCAGTTGATCATGCTGTGCAACACCCCTTTGTATACGGGGCAAGGCAAGAAAG 240  
QY 322 GGGAGTTTGTGCTCCGGGCTCA 344  
DB 241 GGGAGTTTGTGCTCCGGGCTCA 263

RESULT 11  
LOCUS B0882838 948 bp mRNA linear EST 16-AUG-2002  
DEFINITION AGENCOURT\_8627686 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:6291960  
ACCESSION B0882838  
VERSION B0882838.1 GI:22274846  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLM2492 row: k column: 01  
 High quality sequence stop: 533.  
 Location/Qualifiers

# FEATURES

source

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1. 948
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_43"
/issue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: eye; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

BASE COUNT 183 a 288 c 286 g 190 t 1 others  
 ORIGIN

Query Match 71.0%; Score 262; DB 14; Length 948;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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30 CAGGCTTGGCGTCAATTCAGTGTACAGTGTGAAGAATTCAGTGAACACGACT 89
|||||
298 CAGGCTTGGCGTCAATTCAGTGTACAGTGTGAAGAATTCAGTGAACACGACT 357
|||||
90 GCTCTCCCGGAGTTCATTGTGAATTCAGCGGTGAACATGTCAGAAAG 149
|||||
358 GCTCTCCCGGAGTTCATTGTGAATTCAGCGGTGAACATGTCAGAAAG 417
|||||
150 AAGTATGAGACAAAGTCCGGGATCATGACCGCAAGTCTGTGATCATCAGCGCCT 209
|||||
418 AAGTATGAGACAAAGTCCGGGATCATGACCGCAAGTCTGTGATCATCAGCGCCT 477
|||||
210 GTCTCATCGCTTCGCGGGTACGAGTCTGTGATCATCAGCGCCT 269
|||||
478 GTCTCATCGCTTCGCGGGTACGAGTCTGTGATCATCAGCGCCT 537
|||||
270 GCATCAGCTGCTGCACACCC 291
|||||
538 GCATCAGCTGCTGCACACCC 559

```

RESULT 12  
 BI823714 704 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603040833F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5181585 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI823714  
 VERSION BI823714.1 GI:15935264  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 704)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLM11453 row: a column: 10  
 High quality sequence stop: 692.  
 Location/Qualifiers

# FEATURES

source

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1. 704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_115"
/issue_type="normal pigmented retinal epithelium"
/lab_host="DH10B"
/Note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORE6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research genetics tracking code
021. Note: this is a NIH_MGC Library."

```

BASE COUNT 135 a 227 c 205 g 137 t  
 ORIGIN

Query Match 69.9%; Score 258; DB 13; Length 704;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-134;  
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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30 CAGGCTTGGCGTCAATTCAGTGTACAGTGTGAAGAATTCAGTGAACACGACT 89
|||||
309 CAGGCTTGGCGTCAATTCAGTGTACAGTGTGAAGAATTCAGTGAACACGACT 368
|||||
90 GCTCTCCCGGAGTTCATTGTGAATTCAGCGGTGAACATGTCAGAAAG 149
|||||
369 GCTCTCCCGGAGTTCATTGTGAATTCAGCGGTGAACATGTCAGAAAG 428
|||||
150 AAGTATGAGACAAAGTCCGGGATCATGACCGCAAGTCTGTGATCATCAGCGCCT 209
|||||
429 AAGTATGAGACAAAGTCCGGGATCATGACCGCAAGTCTGTGATCATCAGCGCCT 488
|||||
210 GTCTCATCGCTTCGCGGGTACGAGTCTGTGATCATCAGCGCCT 269
|||||
489 GTCTCATCGCTTCGCGGGTACGAGTCTGTGATCATCAGCGCCT 548
|||||
270 GCATCAGCTGCTGCACAC 287
|||||
549 GCATCAGCTGCTGCACAC 566

```

RESULT 13  
 BI831919 570 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603078792F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5170606 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI831919  
 VERSION BI831919.1 GI:15943469  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 570)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLM11424 row: g column: 23

High quality sequence stop: 566.  
Location/Qualifiers

# FEATURES

1..570

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="5170606"  
/clone\_lib="NIH\_MGC\_119"  
/tissue\_type="medulla"  
/lab\_host="DH10B"

/note="Organ: brain; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb. Insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."

BASE COUNT 130 a 170 c 137 g 133 t

## ORIGIN

Query Match 64.2%; Score 237; DB 13; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.9e-122;  
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CACGACTGCTCTCCGCCGAGTTCATTTGTAATGCAAGGTAAGATCAAGACATGTG 141  
DB 1 CACGACTGCTCTCTCCGCCGAGTTCATTTGTAATGCAAGGTAAGATCAAGACATGTG 60  
QY 142 TCAGAAAGAGTATGAGGCAAGGCGGATCATGTACCGCAAGTCTGTGCATCATC 201  
DB 61 TCAGAAAGAGTATGAGGCAAGGCGGATCATGTACCGCAAGTCTGTGCATCATC 120  
QY 202 AGCGGCTGTCTCATCGCTCTGCGGATCATGTACCGCAAGTCTGTGCATCATC 261  
DB 121 AGCGGCTGTCTCATCGCTCTGCGGATCATGTACCGCAAGTCTGTGCATCATC 180  
QY 262 CTCAGTTGCATCAGCTGCTCAACACCCCTCTTTGTAACGGGCCCAAGCCCAAGAA 318  
DB 181 CTCAGTTGCATCAGCTGCTCAACACCCCTCTTTGTAACGGGCCCAAGCCCAAGAA 237

## RESULT 14

AA349894 352 bp mRNA linear EST 21-APR-1997  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AA349894 352 bp mRNA linear EST 21-APR-1997  
DEFINITION Infant brain Homo sapiens CDNA 5' end, mRNA sequence.  
ACCESSION AA349894  
VERSION AA349894.1 GI:2002213  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 352)  
Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.  
3,400 expressed sequence tags identify diversity of transcripts  
from human brain  
Nat. Genet. 4, 256-267 (1993)  
9364420  
Other-ESTs: EST56848 THC106611  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/cdb/ngi/ngi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..352

## FEATURES

1..352

/organism="Homo sapiens"  
/db\_xref="ATCC (Inhost):150796"  
/db\_xref="taxon:9606"  
/clone\_lib="Infant brain"  
/sex="female"  
/dev\_stage="infant"  
/note="Organ: brain; Vector: lafmid BA; Site\_1: HindIII; Site\_2: NotI"

BASE COUNT 76 a 111 c 85 g 77 t 3 others

## ORIGIN

Query Match 63.7%; Score 235; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.2e-121;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GTGAATTGCAGCGGTGAACCTTCACAGCATGTGTCAAGAAAGATGAGGCAAGTGC 169  
DB 1 GTGAATTGCAGCGGTGAACCTTCACAGCATGTGTCAAGAAAGATGAGGCAAGTGC 60  
QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTGCTGCGGG 229  
DB 61 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTGCTGCGGG 120  
QY 230 TACAGTCTCTGCTGCCCGGCAAGCAAGTCAAGTTCATGATCAGCTGCAACACC 289  
DB 121 TACAGTCTCTGCTGCCCGGCAAGTCAAGTTCATGATCAGCTGCAACACC 180  
QY 290 CCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGGAAGTTGCTCGGCCCTCA 344  
DB 181 CCTCTTTGTAACGGGCCCAAGGCCCAAGAAAGGGGAAGTTGCTCGGCCCTCA 235

## RESULT 15

BG753617 670 bp mRNA linear EST 15-MAY-2001  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BG753617 670 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602732803F1 NIH\_MGC\_43 Homo sapiens CDNA clone IMAGE:4876392 5',  
ACCESSION BG753617  
VERSION BG753617.1 GI:14064270  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 670)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM1759 row: e column: 01  
High quality sequence stop: 585.  
Location/Qualifiers  
1..670

## FEATURES

1..670

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="4876392"  
/clone\_lib="NIH\_MGC\_43"  
/tissue\_type="normal pigmented retinal epithelium"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit



```

QY 269 TGCATCAGCTGTCGACACCCCTCTTTGTAACGGGCGCCAGGCCCAAGAAAGGGAGCT 328
      |||||||
Db 547 TGCATCAGCTGTCGACACACCCCTCTTTGTAACGGGCGCCAGGCCCAAGAAAGGGAGCT 606
      |||||||
QY 329 TCGGCTCGGGCCCTCA 344
      |||||||
Db 607 TCGGCTCGGGCCCTCA 622
      |||||||

RESULT 18
AW954549 540 bp mRNA linear EST 01-JUN-2000
LOCUS EST366619 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION AW954549
VERSION AW954549.1 GI:8144232
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 540)
AUTHORS Hegde,P., Ol,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
          I.E., Seed,A.I., Sharov,V., Lee,N.H., Yeatman,F.J. and
          Quackenbush,J.
          Assessment of gene expression patterns in a model of colon tumor
          metastasis using a 19,200 element cDNA microarray
          Unpublished (2000)
          Contact: John Quackenbush
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 3528
          Fax: 301 838 0208
          Email: johnd@tigr.org
          Plate: 65
          Seq primer: Reverse.
FEATURES
          source
          location/Qualifiers
          1..540
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="MAGE resequences, MAGC"
            /note="Vector: pBluescriptSKm"
BASE COUNT 122 a 150 c 134 g 134 t
ORIGIN
Query Match 51.5%; Score 190; DB 10; Length 540;
Best Local Similarity 100.0%; Pred. No. 6.5e-96;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ATGAGCAAGTGGCGGATCATGTACCGAAGTCCCTGTCATCATCATAGCGGCTGTCTC 214
      |||||||
Db 56 ATGAGCAAGTGGCGGATCATGTACCGAAGTCCCTGTCATCATCATAGCGGCTGTCTC 115
      |||||||
QY 215 ATGCGCTTGGCGGATACAGTCTCTGCTCCCAAGGAACTGAATCAGTTTGCATC 274
      |||||||
Db 116 ATGCGCTTGGCGGATACAGTCTCTGCTCCCAAGGAACTGAATCAGTTTGCATC 175
      |||||||
QY 275 AGCTGTGCAACACCCCTCTTTGTAACGGGCGCCAGGCCCAAGAAAGGGAGCTTCC 334
      |||||||
Db 176 AGTGTGTGCAACACCCCTCTTTGTAACGGGCGCCAGGCCCAAGAAAGGGAGTTCGCC 235
      |||||||
QY 335 TCGGCCCTCA 344
      |||||||
Db 236 TCGGCCCTCA 245
      |||||||

RESULT 19
AA582576 433 bp mRNA linear EST 26-SEP-1997
LOCUS AA582576
DEFINITION n55e03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087804 3',
          mRNA sequence.
ACCESSION AA582576
VERSION AA582576.1 GI:2359936

```

```

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
          Emmer-Buck, M.D., Ph.D.
          CDNA Library Preparation: Stratagene, Inc.
          CDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          www-bio.lnl.gov/bdrip/image/image.html
          Insert length: 904 Std Error: 0.00
          Seq primer: -40m13 fwd. ET from Amersham
          High quality sequence stop: 407.
FEATURES
          source
          location/Qualifiers
          1..433
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="1087804"
            /clone_lib="NCL_CGAP_Kid6"
            /sex="mixed"
            /tissue_type="kidney tumor"
            /lab_host="SOLR (kanamycin resistant)"
            /note="Organ: kidney; Vector: Bluescript SK-; Site:1.
            EcoRI; Site:2: xhoI; Cloned unidirectionally. Primer:
            Oligo df. Pooled kidney tumors. 5' adaptor sequence: 5'
            GAATTCGGCAGAG 3' 3' adaptor sequence: 5'
            CTCGAGTCTTTTCTTTTCTTTT 3' Average insert size: 1.0 kb."
BASE COUNT 98 a 112 c 104 g 119 t
ORIGIN
Query Match 47.4%; Score 175; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.8e-87;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGGATCATGTACCGCAAGTCTGTGTCATCATCAGCGGCTGTCTATCGGCTGCGGG 229
      |||||||
Db 258 GGGATCATGTACCGCAAGTCTGTGTCATCATCAGCGGCTGTCTATCGGCTGCGGG 317
      |||||||
QY 230 TACCACTCTCTTCTGCTCCCAAGGAACTGACTGATTCATCAGCTGCTGCAACACC 289
      |||||||
Db 318 TACCACTCTCTTCTGCTCCCAAGGAACTGACTGATTCATCAGCTGCTGCAACACC 377
      |||||||
QY 290 CCTCTTTGTAACGGGCGCCAGAACGAAAGGGAAGTTCTGCTGGGCCCTCA 344
      |||||||
Db 378 CCTCTTTGTAACGGGCGCCAGAACGAAAGGGAAGTTCTGCTGGGCCCTCA 432
      |||||||

RESULT 20
A1767459 522 bp mRNA linear EST 20-DEC-1999
LOCUS A1767459
DEFINITION wh26h03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2381909 3',
          mRNA sequence.
ACCESSION A1767459
VERSION A1767459.1 GI:5233968
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 522)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index

```



JOURNAL  
COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LUNL at:  
www.bio.lnlnl.gov/db/rp/image/image.html  
Insert length: 877 Std Error: 0.00  
Seq primer: -40UP from Glibco  
High quality sequence stop: 470.

FEATURES  
source

Location/Qualifiers  
1..522  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2381909"  
/clone\_lib="NCI CGAP\_Kid11"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP\_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN

Query Match 47.4%; Score 175; DB 9; Length 522;  
Best Local Similarity 100.0%; Pred. No. 1.9e-87;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

170 GGATCATGTCAGCCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCGCGGG 229  
|||||  
286 GGGATCATGTCAGCCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCGCGGG 345  
|||||  
230 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGTCATGTCGTCGACAC 289  
|||||  
346 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGTCATGTCGTCGACAC 405  
|||||  
290 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCTCTCA 344  
|||||  
406 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCTCTCA 460  
|||||

RESULT 21  
LOCUS

BM974798 541 bp mRNA linear EST 21-MAR-2002  
UI-CF-EC1-acd-1-10-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone

## DEFINITION

UI-CF-EC1-acd-1-10-0-UI 3', mRNA sequence.

## ACCESSION

BM974798  
BM974798.1 GI:19592389

## VERSION

EST.

## KEYWORDS

human.

## SOURCE

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 541)  
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

## AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene

## TITLE

discovery  
Genome Res. 6 (9), 791-806 (1996)

## JOURNAL

97044477  
Contact: McCreay, PB

## MEDLINE

McCreay Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

FEATURES  
source

Location/Qualifiers  
1..541  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EC1-acd-1-10-0-UI"  
/clone\_lib="UI-CF-EC1"  
/tissue\_type="Lung"  
/dev\_stage="Adult and Fetal"  
/lab\_host="DH10B (Life Technologies) (71 phage resistant)"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTCTTAC.

BASE COUNT  
ORIGIN

Query Match 47.4%; Score 175; DB 14; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.9e-87;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

170 GGATCATGTCAGCCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCGCGGG 229  
|||||  
296 GGGATCATGTCAGCCAGTCTGTCATCATCAGCGGCTGTCATGCGCTTCGCGGG 355  
|||||  
230 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGTCATGTCGTCGACAC 289  
|||||  
356 TACCAGTCTTTCGCTCCCGCAGGAAGTGAAGTTCATGTCATGTCGTCGACAC 415  
|||||  
290 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCTCTCA 344  
|||||  
416 CCTCTTTGTAACGGGCGCAAGGCCAAGAAAGGGAAGTTCTGCTCGGCTCTCA 470  
|||||

RESULT 22  
LOCUS

AV171094/c 651 bp mRNA linear EST 16-OCT-2000  
AV171094 DCB Homo sapiens cDNA clone DCBAZD04 5', mRNA sequence.

## DEFINITION

AV171094  
AV171094.1 GI:10814246

## ACCESSION

AV171094

## VERSION

EST.

## KEYWORDS

human.

## SOURCE

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 651)  
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

## AUTHORS

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,



Fax: 319 356 7171  
Email: paul-mccravy@iowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)).  
Seq primer: M13 FORWARD  
POLY-A-tails

## FEATURES

**Source**

```

FEATURES
SOURCE
Location/Qualifiers
1..738
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-adh-b-10-0-0"
/clone_1lb="UI-CF-EN1"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker: Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-805,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAAGT.
TAG_1lb=UI-CF-EN1
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_SBO=CTGCTCAAGT"
151 a 199 c 164 g 221 t 3 others

```

RESULT 25	
LOCUS	BF125425
DEFINITION	BF125425 890 bp mRNA linear EST 24-OCT-2000 601765551.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026252.5', mRNA sequence.
ACCESSION	BF125425
VERSION	BF125425.1 GI:10964465
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 890) NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

## FEATURES

**Source**

```

SOURCE
1. .090
/organism="Homo sapiens"
/db_xref="caxon:9606"
/clone="IMAGE:4026252"
/clone_lib="NTL_MGC_20"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/ncore="organ : skin; Vector: pORF7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

FEATURES	source
RESULT 26	
LOCUS	AI140655
DEFINITION	AI140655 449 bp mRNA linear EST 29-OCT-1996
ACCESSION	U62209.1 Soares_fetal_lung.NBHL19w Homo sapiens cDNA clone
VERSION	IMAGE:1739728 3, mRNA sequence.
KEYWORDS	AI140655
SOURCE	AI140655.1 GI:3648112
ORGANISM	EST.
REFERENCE	human.
AUTHORS	Homo sapiens
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 449) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP). Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapsf.rem@nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium ( <a href="mailto:info@image.lnl.gov">info@image.lnl.gov</a> ) for further information. Insert length: 896 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 429. Location/Qualifiers 1..449

Query Match	46.9%	Score 173	DB 9	Length 449	
Best Local Similarity	100.0%	Pred. No. 2.5e-86			
Matches 173	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
Db	170	GGGATCATGATACCCGAACTGCTGTCATCATCAGCGGCTGTCTCATCGCCTTCGCGGG	229		
Db	277	GGGATCATGTAACCGAAGTCCGTCATCATCAGCGGCTGTCTCATCGCCTTCGCGGG	336		
Qy	230	TACAGTCCTTTCGTCTGCCCAAGGAACTGAAGTTCGATCGATCGCTGCTGCACAC	289		
Db	337	TACAGTCCTTTCGTCTGCCCAAGGAACTGAAGTTCGATCGATCGCTGCTGCACAC	396		
Qy	290	CCTCTTTTAAACGGGCAAGGCCCAAGAAAGGGGAAAGTTCGCTCGGCGCT	342		
Db	397	CCTCTTTTAAACGGGCAAGGCCCAAGAAAGGGGAAAGTTCGCTCGGCGCT	449		
RESULT 27					
LOCUS	BF125664	878 bp	mRNA	linear	EST 24-OCT-2000
DEFINITION	601763237P1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4026320 5',				
LOCUS	BF125664				
ACCESSION	BF125664.1	GI:10964704			
VERSION					
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 878)				
AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .				
TITLE	National Institutes of Health. Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-rt@mail.nih.gov">cgabbs-rt@mail.nih.gov</a> Tissue Procurement: ATCC/DCTD/DTF CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">image.lnl.gov</a> Plate: LNCM856 row: 1 column: 09 High quality sequence stop: Ph.D. Location/Qualifiers 1. 878 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4026320" /clone_lib="NIH_MGC_20" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:				

BASE COUNT		278 a	194 c	251 g	155 t	EcORI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."	
ORIGIN	Query Match	45.38;	Score 167;	DB 12;	Length 878;		
	Best Local Similarity	100.0%;	Pred. No. 7.3e-83;				
	Matches 167;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Oy	86	GACGCTCCCTCCCGGAGATTCATGTGAATGCAGCGGATCAAGACATGTGTAC	145				
Db	300	GACTGCTCTCTCCCGAGATTTCATGTGAATGCAGCGGATCAAGACATGTGTAC	359				
Oy	146	AAAGAAGTAGTAGGAGCAAAAGTCCGGGATCATATGCCGAAGTCTGTGATCATACGC	205				
Db	360	AAAGAAGTAGTAGGAGCAAAAGTCCGGGATCATATGCCGAAGTCTGTGATCATACGC	419				
Oy	206	GCGCTGTCATATGCGCTGCGGGATCCAGTCATTCCTGCTCCGACG	252				
Db	420	GCTGTCTCATATGCGCTGCGGGATCCAGTCATTCCTGCTCCGACG	466				
RESULT 28							
R20352	LOCUS	R20352	395 bp	mRNA	linear	EST 17-APR-1995	
DEFINITION	yg20f09.r1 Soares infant brain IN1B Homo sapiens cDNA clone						
ACCESSION	R20352						
VERSION	R20352.1	GI:774986					
KEYWORDS	EST.						
SOURCE	human.						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
REFERENCE	1 (bases 1 to 395)						
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucab,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wobldmann,P. and Wilson,R.						
TITLE	The WashU-Merck EST Project						
JOURNAL	Unpublished (1995)						
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu						
	Insert Size: 1628						
	High quality sequence stops: 326						
	Source: IMAGE Consortium, LNL						
	This clone is available royalty-free through LNL; contact the						
	IMAGE Consortium (info@image.llnl.gov) for further information.						
	Insert Length: 1628						
	Std Error: 0.00						
	Seq primer: M13RP1						
	High quality sequence stop: 326.						
FEATURES	Location/Qualifiers						
source	1..395						
	/organism="Homo sapiens"						
	/db_xref="GDB:405062"						
	/db_xref="taxon:9606"						
	/clone="IMAGE:32715"						
	/clone_11b="Soares Infant brain IN1B"						
	/sex="female"						
	/dev_stage="73 days post natal"						
	/lab_host="DH10B (ampicillin resistant)"						
	/note="Organ: Whole brain; Vector: lambdaB; Site:1: Not						
	I; Site:2: Hind III; 1st strand cDNA was primed with a NOT						
	I - oligo(dT) primer [5'						
	AACGCGAAGAAATTCGCGCCGACGAATTTTTTTTTTTTTTTT 3'];						



Query Match 40.9%; Score 151; DB 9; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 6,6e-74;  
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATCGCTTCCGCGG 229  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 280 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATCGCTTCCGCGG 339  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Y 230 TACCAAGTCTTCTGCTCCCGCAAGGAACTGAATCTGATTCATCATCAGCTGCTGCACACC 289  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 340 TACCAAGTCTTCTGCTCCCGCAAGGAACTGAATCTGATTCATCATCAGCTGCTGCACACC 399  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Y 290 CCTCTTTGTACAGGCGCCCAAGGCCAAGAAA 320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 400 CCTCTTTGTACAGGCGCCCAAGGCCAAGAAA 430  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 31  
 LOCUS A1138793 424 bp mRNA linear EST 28-OCT-1998  
 DEFINITION qd98e07.x1 Soares\_testis\_NHT Homo sapiens CDNA clone IMAGE:1737540  
 3', mRNA sequence.  
 ACCESSION A1138793  
 VERSION A1138793.1 GI:3644765  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 424)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
 Ph.D.  
 'CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbtrp/image/image.html  
 Insert length: 960 std Error: 0.00  
 Seq primer: -40m13 fwd. RT from Amersham  
 High quality sequence stop: 420.  
 Location/Qualifiers  
 1..424  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1737540"  
 /clone\_1lb="Soares\_testis\_NHT"  
 /sex="male"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech Laboratories  
 Inc. and primed with a Not I - oligo(dT) primer [5'  
 TGTTCATCATCTGAAGTGGAGCGGCCCAATTTTCTTTTCTTTT 3'].  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization to Cot5, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 96 a 108 c 96 g 124 t  
 ORIGIN

Query Match 40.1%; Score 148; DB 9; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 3,2e-72;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATCGCTTCCGCGG 229

DB 277 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCGCTGTCTCATCGCTTCCGCGG 336  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Y 230 TACCAAGTCTTCTGCTCCCGCAAGGAACTGAATCTGATTCATCATCAGCTGCTGCACACC 289  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 337 TACCAAGTCTTCTGCTCCCGCAAGGAACTGAATCTGATTCATCATCAGCTGCTGCACACC 396  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Y 290 CCTCTTTGTACAGGCGCCCAAGGCCAAGA 317  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 397 CCTCTTTGTACAGGCGCCCAAGGCCAAGA 424  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 32  
 LOCUS AW014802 435 bp mRNA linear EST 10-SEP-1999  
 DEFINITION UI-H-B10-aag-b-04-0-UI.s1 NCI-CGAP\_Sub1 Homo sapiens CDNA clone  
 IMAGE:2709078 3', mRNA sequence.  
 ACCESSION AW014802  
 VERSION AW014802.1 GI:5863559  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 435)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 NCI-CGAP clone distribution information can be found through the  
 I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbtrp/image/image.html  
 Seq primer: M13 Forward  
 POLYA-Yes.  
 Location/Qualifiers  
 1..435  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2709078"  
 /clone\_1lb="NCI-CGAP\_Sub1"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; The  
 NCI-CGAP\_Sub1 library is a subtracted library derived from  
 BI. BI constitutes a mixture of 21 normalized or  
 subtracted NCI-CGAP libraries: NCI-CGAP\_Co4,  
 NCI-CGAP\_Pr22, NCI-CGAP\_Pr28, NCI-CGAP\_Co10, NCI-CGAP\_Co16  
 , NCI-CGAP\_Kid5, NCI-CGAP\_Kid12, NCI-CGAP\_Kid3,  
 NCI-CGAP\_Kid11, NCI-CGAP\_Lm22, NCI-CGAP\_Br2, NCI-CGAP\_Kid3,  
 NCI-CGAP\_Co11, NCI-CGAP\_Le12, NCI-CGAP\_Brn23, NCI-CGAP\_Co8,  
 NCI-CGAP\_Lm24, NCI-CGAP\_Lm19, NCI-CGAP\_Gc4, NCI-CGAP\_Gc6  
 , NCI-CGAP\_Brn25. These 21 libraries were pooled and a  
 single-stranded DNA preparation of the resulting mixture  
 was used as a tracer in a subtractive hybridization with a  
 driver whose composition is detailed below: NCI-CGAP\_Kid3  
 pool 1 L1AM 3334-3337, 3682-3683, 3799-3803 (IMAGE  
 CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855  
 ) NCI-CGAP\_Kid5 pool 1 L1AM 3338-3342, 3722-3723,  
 3776-3778 (IMAGE CloneIDs 1323912-1325831,  
 1471368-1472903, 1492104-1493255) NCI-CGAP\_Lm5 pool 1 L1AM  
 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,  
 1520904-1522439) NCI-CGAP\_Gc4 pool 1 L1AM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,  
 1469064-1470983, 1475592-1476743) NCI-CGAP\_Pr22 pool 1  
 L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs  
 985608-986759, 1101192-1101959, 1217928-1220615)  
 NCI-CGAP\_Co10 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE

CloneIDs 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 530,000 recombinants. Subtraction was performed as previously described [Bonaldo & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. genome Research 6, 791-806.

Research 6, 791-806.  
TAG\_LIB-NCI-CGAP\_K1d5  
TAG\_TISSUE-Kidney  
TAG\_SEQ-ATTC"

BASE COUNT 95 a 109 c 95 g 136 t

Query Match 39.3%; Score 145; DB 10; Length 435;  
Best Local Similarity 100.0%; Pred. No. 1.6e-70;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGCCTCTTCATCGCTTCCGGG 229

DB 291 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGCCTCTTCATCGCTTCCGGG 350

QY 230 TACCACTCCTTCCTGCTCCCGAGGAAGTCACTGATTCATCAGCTGCTGCAACACC 289

DB 351 TACCACTCCTTCCTGCTCCCGAGGAAGTCACTGATTCATCAGCTGCTGCAACACC 410

QY 290 CCTCTTTGTACGCGGCCCAAGGCCCA 314

DB 411 CCTCTTTGTACGCGGCCCAAGGCCCA 435

# RESULT 33

LOCUS AA776783

DEFINITION ah36904.s1 Soares\_testis\_NHT Homo sapiens cDNA clone 1276662 3', mRNA sequence.

ACCESSION AA776783

VERSION AA776783.1

KEYWORDS GI:2836117

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnlnl.gov/bdrp/image/image.html

Insert Length: 941 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 510.

Location/Qualifiers

1, 516

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="1276662"

/clone\_lib="Soares\_testis\_NHT"

/sex="male"

/lab\_host="DH10B"

/note="Vector: pT773D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'

TCCTACATCTGAGTGGAGGCGGCCCAATTTTCTTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 117 a 139 c 121 g 139 t

Query Match 38.8%; Score 143; DB 9; Length 516;

Best Local Similarity 100.0%; Pred. No. 2.3e-69;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGCCTCTTCATCGCTTCCGGG 229

DB 268 GGGATCATGACCGCAAGTCCCTGTCATCATCAGCGCCTCTTCATCGCTTCCGGG 327

QY 230 TACCACTCCTTCCTGCTCCCGAGGAAGTCACTGATTCATCAGCTGCTGCAACACC 289

DB 328 TACCACTCCTTCCTGCTCCCGAGGAAGTCACTGATTCATCAGCTGCTGCAACACC 387

QY 290 CCTCTTTGTACGCGGCCCAAGGCCCA 312

DB 388 CCTCTTTGTACGCGGCCCAAGGCCCA 410

# RESULT 34

LOCUS BE731003

DEFINITION 601570968F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:384540 5', mRNA sequence.

ACCESSION BE731003

VERSION BE731003.1

KEYWORDS GI:10144995

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL NIH-MGC http://imgc.ncbi.nlm.nih.gov/

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/NIH Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at: image.lnlnl.gov

Plate: LINC543 row: h column: 17

High quality sequence stop: 642.

Location/Qualifiers

1, 794

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:384540"

/clone\_lib="NIH\_MGC\_21"

/tissue\_type="Choriocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: Placenta; Vector: pOTB7; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(5). Size-selected >500bp

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 195 a 227 c 217 g 155 t

Query Match 38.8%; Score 143; DB 12; Length 794;

Best Local Similarity 100.0%; Pred. No. 2.6e-69;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CAGGCTTGGCTGCAATCCAGTCTACCACTGTAAGAAATTCACGTCGACACACT 89

```

DB 284 CAGCCTTGGCGTCAATCAATCCAGTGTACAGTGTGAAGATTCCAGTGAACACGACT 343
|||||
QY 90 GCTCCTCCCGCAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAA 149
|||||
DB 344 GCTCCTCCCGCAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAA 403
|||||
QY 150 AAGTATGGAGCAAGTCCCGG 172
|||||
DB 404 AAGTATGGAGCAAGTCCCGG 426
|||||

RESULT 35
BE730800 1134 bp mRNA linear EST 15-SEP-2000
LOCUS 601570755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845557 5',
DEFINITION mRNA sequence.
ACCESSION BE730800
VERSION BE730800.1 GI:10144792
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1134)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rt@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at: Image.liml.gov
Plate: L10M543 row: m column: 14
High quality sequence stop: 640.

FEATURES
Source location/Qualifiers
1..1134
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3845557"
/clone_id="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: placenta; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming,
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(6). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 329 a 320 c 308 g 177 t
ORIGIN
```

```

Query Match 38.8%; Score 143; DB 12; Length 1134;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 30 CAGGCTTTCGCGTCAATCAATCCAGTGTACAGTGTGAAGATTCCAGTGAACACGACT 89
|||||
DB 284 CAGCCTTGGCGTCAATCAATCCAGTGTACAGTGTGAAGATTCCAGTGAACACGACT 343
|||||
QY 90 GCTCCTCCCGCAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAA 149
|||||
DB 344 GCTCCTCCCGCAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAA 403
|||||
QY 150 AAGTATGGAGCAAGTCCCGG 172
|||||
DB 404 AAGTATGGAGCAAGTCCCGG 426
|||||
```

```

RESULT 36
BG213596 350 bp mRNA linear EST 21-APR-2001
LOCUS BG213596
DEFINITION R373211 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG213596
VERSION BG213596.1 GI:13735283
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 350)
AUTHORS Harrington,J.,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: sca@atersys.com
High quality sequence stop: 350.

FEATURES
Source location/Qualifiers
1..350
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/clone_id="HT1080"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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BASE COUNT 98 a 93 c 84 g 75 t
ORIGIN
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Query Match 38.2%; Score 141; DB 12; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.8e-68;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 30 CAGGCTTTCGCGTCAATCAATCCAGTGTACAGTGTGAAGATTCCAGTGAACACGACT 89
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DB 19 CAGCCTTTCGCGTCAATCAATCCAGTGTACAGTGTGAAGATTCCAGTGAACACGACT 78
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QY 90 GCTCCTCCCGCAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAA 149
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DB 79 GCTCCTCCCGCAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAAGAA 138
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QY 150 AAGTATGGAGCAAGTCCCG 170
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DB 139 AAGTATGGAGCAAGTCCCG 159
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RESULT 37
BG184021 484 bp mRNA linear EST 21-APR-2001
LOCUS BG184021
DEFINITION RST2936 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG184021
VERSION BG184021.1 GI:13705708
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 484)
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**AUTHORS**  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
J., Danzig, J. and Ducar, M.

**TITLE**  
Creation of genome-wide protein expression libraries using random  
activation of gene expression

**JOURNAL**  
Nat. Biotechnol. 19 (5), 440-445 (2001)

**MEDLINE**  
21227151

**COMMENT**  
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Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athersys.com

**FEATURES**  
High quality sequence stop: 482.  
Location/Qualifiers  
1..484  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

**BASE COUNT**  
137 a 122 c 107 g 118 t

**ORIGIN**

Query Match 38.2%; Score 141; DB 12; Length 484;  
Best Local Similarity 100.0%; Pred. No. 3e-68;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 30 CAGGCTTGGCGTCAAAATCAGTGTACCAAGTGAAGATTGCACTGACAGCAACT 89  
|||||  
**DB** 5 CAGGCTTGGCGTCAAAATCAGTGTACCAAGTGAAGATTGCACTGACAGCAACT 64  
|||||

**QY** 90 GCTCTTCCCGCCGAGTTCATTGTGAATTGACGCGTGAACGTTCAAGACATGTGTGAGAAG 149  
|||||  
**DB** 65 GCTCTTCCCGCCGAGTTCATTGTGAATTGACGCGTGAACGTTCAAGACATGTGTGAGAAG 124  
|||||

**QY** 150 AAGTGATGGAGCAAAAGTCCG 170  
|||||

**DB** 125 AAGTGATGGAGCAAAAGTCCG 145  
|||||

**RESULT 38**  
BG193459 781 bp mRNA linear EST 21-APR-2001  
**LOCUS**  
RST12532 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
**ACCESSION**  
BG193459  
**VERSION**  
BG193459.1 GI:13715146  
**KEYWORDS**  
EST.  
**SOURCE**  
human.  
**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 781)  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
J., Danzig, J. and Ducar, M.

**TITLE**  
Creation of genome-wide protein expression libraries using random  
activation of gene expression

**JOURNAL**  
Nat. Biotechnol. 19 (5), 440-445 (2001)

**MEDLINE**  
21227151

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Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900

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Email: scain@athersys.com  
High quality sequence stop: 322.  
Location/Qualifiers  
1..781  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

**BASE COUNT**  
187 a 180 c 193 g 221 t

**ORIGIN**

Query Match 38.2%; Score 141; DB 12; Length 781;  
Best Local Similarity 100.0%; Pred. No. 3.5e-68;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 30 CAGGCTTGGCGTCAAAATCAGTGTACCAAGTGAAGATTGCACTGACAGCAACT 89  
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|||||

**QY** 90 GCTCTTCCCGCCGAGTTCATTGTGAATTGACGCGTGAACGTTCAAGACATGTGTGAGAAG 149  
|||||  
**DB** 97 GCTCTTCCCGCCGAGTTCATTGTGAATTGACGCGTGAACGTTCAAGACATGTGTGAGAAG 156  
|||||

**QY** 150 AAGTGATGGAGCAAAAGTCCG 170  
|||||

**DB** 157 AAGTGATGGAGCAAAAGTCCG 177  
|||||

**RESULT 39**  
BG188218 424 bp mRNA linear EST 21-APR-2001  
**LOCUS**  
RST7232 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
**ACCESSION**  
BG188218  
**VERSION**  
BG188218.1 GI:13709905  
**KEYWORDS**  
EST.  
**SOURCE**  
human.  
**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 424)  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
J., Danzig, J. and Ducar, M.

**TITLE**  
Creation of genome-wide protein expression libraries using random  
activation of gene expression

**JOURNAL**  
Nat. Biotechnol. 19 (5), 440-445 (2001)

**MEDLINE**  
21227151

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**FEATURES**  
High quality sequence stop: 424.  
Location/Qualifiers  
1..424  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

Query Match 37.9%; Score 140; DB 12; Length 424;

Best Local Similarity 100.0%; Pred. No. 1,1e-67;

Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 33 GCTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGTGAACAGCAGTCT 92  
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 39 GCTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGTGAACAGCAGTCT 98  
 |||||||  
 93 CTTCCCGGAGTTCATTGTGAATTCAGCGGTGAACGTTCAAGACATGTCTCAAGAAAG 152  
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 99 CTTCCCGGAGTTCATTGTGAATTCAGCGGTGAACGTTCAAGACATGTCTCAAGAAAG 158  
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 Oy 153 TGATGAGCAAAAGTCCGGG 172  
 |||||||  
 Db 159 TGATGAGCAAAAGTCCGGG 178

RESULT 40  
 BG192926 323 bp mRNA linear EST 21-APR-2001  
 LOCUS  
 DEFINITION RST12050 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG192926  
 VERSION BG192926.1 GI:13714613  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 1 (bases 1 to 323)  
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,  
 E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,  
 J., Danzig,J. and Ducar,M.  
 Creation of genome-wide protein expression libraries using random

TITLE  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL  
 MEDLINE 21227151

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 Fax: 216 361 9596  
 Email: scaine@atersys.com

High quality sequence stop: 323.  
 Location/Qualifiers

FEATURES  
 source 1..323  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

BASE COUNT 90 a 84 c 78 g 71 t

Query Match 37.7%; Score 139; DB 12; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 3,6e-67;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 34 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGTGAACAGCAGTCTC 93  
 |||||||  
 Db 1 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGTGAACAGCAGTCTC 60

Oy 94 CTTCCCGGAGTTCATTGTGAATTCAGCGGTGAACGTTCAAGACATGTCTCAAGAAAGT 153  
 |||||||  
 Db 61 CTTCCCGGAGTTCATTGTGAATTCAGCGGTGAACGTTCAAGACATGTCTCAAGAAAGT 120  
 |||||||  
 Oy 154 GATGAGCAAAAGTCCGGG 172  
 |||||||  
 Db 121 GATGAGCAAAAGTCCGGG 139

RESULT 41  
 BG210457 323 bp mRNA linear EST 21-APR-2001  
 LOCUS  
 DEFINITION RST30002 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG210457  
 VERSION BG210457.1 GI:13732144  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 1 (bases 1 to 323)  
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,  
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,  
 E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,  
 J., Danzig,J. and Ducar,M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL  
 MEDLINE 21227151

COMMENT  
 Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scaine@atersys.com  
 High quality sequence stop: 323.  
 Location/Qualifiers

FEATURES  
 source 1..323  
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 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

BASE COUNT 90 a 83 c 78 g 72 t

Query Match 37.7%; Score 139; DB 12; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 3,6e-67;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 34 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGTGAACAGCAGTCTC 93  
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 Db 1 CTTTGGCGGCAAAATCCAGTGTACAGTGTGAAGAATTCACAGTGAACAGCAGTCTC 60  
 |||||||  
 Oy 94 CTTCCCGGAGTTCATTGTGAATTCAGCGGTGAACGTTCAAGACATGTCTCAAGAAAGT 153  
 |||||||  
 Db 61 CTTCCCGGAGTTCATTGTGAATTCAGCGGTGAACGTTCAAGACATGTCTCAAGAAAGT 120  
 |||||||

Oy 154 GATGAGCAAAAGTCCGGG 172  
 |||||||  
 Db 121 GATGAGCAAAAGTCCGGG 139

RESULT 42  
 BG215210 324 bp mRNA linear EST 21-APR-2001  
 LOCUS  
 DEFINITION RST34874 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG215210  
 VERSION BG215210.1 GI:13741231  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 324)  
 AUTHORS Harrington, J., J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,  
 E., Veloso, N., Kikka, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
 J., Danzig, J., and Ducar, M.  
 TITLE Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scalin@athersys.com  
 High quality sequence stop: 324.  
 Location/Qualifiers  
 1..324  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."  
 BASE COUNT 90 a 83 c 79 g 72 t  
 ORIGIN  
 Query Match 37.7%; Score 139; DB 12; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-67;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 34 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGAACACAGCTGCTC 93  
 Db 1 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGAACACAGCTGCTC 60  
 Oy 94 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 153  
 Db 61 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 120  
 Oy 154 GATGAGCAAAAGTCCGGG 172  
 Db 121 GATGAGCAAAAGTCCGGG 139  
 RESULT 43  
 BG200048/c 330 bp mRNA linear EST 21-APR-2001  
 LOCUS RS719350 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BG200048  
 ACCESSION BG200048  
 VERSION BG200048.1 GI:13721735  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 330)  
 AUTHORS Harrington, J., J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,  
 E., Veloso, N., Kikka, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
 J., Danzig, J., and Ducar, M.

TITLE Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scalin@athersys.com  
 High quality sequence stop: 330.  
 Location/Qualifiers  
 1..330  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."  
 BASE COUNT 71 a 80 c 86 g 93 t  
 ORIGIN  
 Query Match 37.7%; Score 139; DB 12; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-67;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 34 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGAACACAGCTGCTC 93  
 Db 330 CTTTCGGTGCAGAAATCCAGTGTACCAAGTGTGAAGATTCCAGCTGAACACAGCTGCTC 271  
 Oy 94 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 153  
 Db 270 CTCGCCGAGTTCATTGTGAATTGCACGGTGAACCTTCAAGACATGTGTCAAGAAAGACT 211  
 Oy 154 GATGAGCAAAAGTCCGGG 172  
 Db 210 GATGAGCAAAAGTCCGGG 192  
 RESULT 44  
 BG181955/c 331 bp mRNA linear EST 21-APR-2001  
 LOCUS RS7815 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BG181955  
 ACCESSION BG181955  
 VERSION BG181955.1 GI:13703642  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 331)  
 AUTHORS Harrington, J., J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,  
 E., Veloso, N., Kikka, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
 J., Danzig, J., and Ducar, M.  
 TITLE Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scalin@athersys.com  
 High quality sequence stop: 331.  
 Location/Qualifiers  
 1..331

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."  
 expressed in HT1080 under normal circumstances."

## BASE COUNT

74 a 81 c 87 g 89 t

## ORIGIN

Query Match 37.7%; Score 139; DB 12; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-67;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CTTTGGCGTCAATCCAGTGTACCGAGTGTGAAGATTCCAGCTGAACAGCACTGCTC 93  
 DB 331 CTTTGGCGTCAATCCAGTGTACCGAGTGTGAAGATTCCAGCTGAACAGCACTGCTC 272  
 QY 94 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGAGT 153  
 DB 271 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGAGT 212  
 QY 154 GATGGAGCAAAAGTCCGGG 172  
 DB 211 GATGGAGCAAAAGTCCGGG 193

## RESULT 45

## BG204666/c

LOCUS 331 bp mRNA linear EST 21-APR-2001  
 DEFINITION RST24065 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG204666  
 VERSION BG204666.1 GI:13726337  
 KEYWORDS EST.

## SOURCE

## ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,  
 Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,  
 E., Veloso, N., Klika, A., Hess, J., Coltrien, K., Lo, K., Offenbacher,  
 J., Danzig, J. and Ducar, M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

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 Athersys, Inc.  
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 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
 High quality sequence stop: 331.

## FEATURES

## source

1. .331

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="Athersys RAGE Library"

/cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

## BASE COUNT

73 a 81 c 86 g 91 t

## ORIGIN

Query Match 37.7%; Score 139; DB 12; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-67;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CTTTGGCGTCAATCCAGTGTACCGAGTGTGAAGATTCCAGCTGAACAGCACTGCTC 93  
 DB 331 CTTTGGCGTCAATCCAGTGTACCGAGTGTGAAGATTCCAGCTGAACAGCACTGCTC 272  
 QY 94 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGAGT 153  
 DB 271 CTCCTCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTGAGAAAGAGT 212  
 QY 154 GATGGAGCAAAAGTCCGGG 172  
 DB 211 GATGGAGCAAAAGTCCGGG 193

Search completed: November 7, 2002, 23:07:28  
 Job time : 503.427 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 938.618 Seconds  
(without alignments)  
11441.218 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369  
Sequence: 1 ggcgaacttttcgagattgt.....tggtccgcacacacatcct 369

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: GenEmbl:\*
- 2: gb\_da:\*
- 3: gb\_hg:\*
- 4: gb\_in:\*
- 5: gb\_om:\*
- 6: gb\_ov:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_da:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_hg\_hum:\*
- 31: em\_hg\_inv:\*
- 32: em\_hg\_other:\*
- 33: em\_hg\_mus:\*
- 34: em\_hg\_pln:\*
- 35: em\_hg\_rtd:\*
- 36: em\_hg\_mam:\*
- 37: em\_hg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_hgo\_hum:\*
- 40: em\_hgo\_mus:\*
- 41: em\_hgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	99.5	369	6	AX093381 Sequence
2	365.4	99.0	466	6	BC017318 Homo sapi
3	365.4	99.0	1524	6	AX358762 Sequence
4	365.4	99.0	1524	6	AX362255 Sequence
5	365.4	99.0	1832	6	AK094501 Homo sapi
6	365.4	99.0	1890	6	AX136281 Sequence
7	343.4	93.1	396	6	AX093191 Sequence
8	336.4	91.2	2528	6	AX319944 Sequence
9	305.2	82.7	1797	10	AB041649 Mus muscu
10	284	77.0	591	6	AX136556 Sequence
11	198.2	53.7	129676	9	AC079773 Homo sapi
12	159	43.1	209885	2	AC124493 Mus muscu
13	145.6	39.5	147131	9	AC010974 Homo sapi
14	80.2	21.7	136799	2	AC110334 Rattus no
15	80.2	21.7	190503	2	AC128363 Rattus no
16	38.4	10.4	90060	9	AC111928 Rattus no
17	37.2	10.1	150724	9	AP000550 Homo sapi
18	37.2	10.1	180884	9	AC008018 Homo sapi
19	36.8	10.0	177088	2	AC096395 Rattus no
20	36.4	9.9	235593	2	AL772296 Mus muscu
21	36.4	9.9	293387	2	AL807802 Mus muscu
22	36.2	9.8	3405	4	BTEAG1
23	36.2	9.8	3486	4	BTEAG2
24	36.2	9.8	168181	2	AC115890 Homo sapi
25	36.2	9.8	191141	9	AC073424 Homo sapi
26	36.2	9.8	44032	2	AC014006 Drosophi
27	36	9.8	160089	3	AC007813 Drosophi
28	36	9.8	255624	3	AE003723 Drosophi
29	35.8	9.7	157226	9	AC018902 Homo sapi
30	35.8	9.7	163135	9	AC098218 Rattus no
31	35.8	9.7	184157	2	AC073438 Homo sapi
32	35.6	9.6	36424	2	AL390015 Homo sapi
33	35.6	9.6	168767	9	AC099562 Homo sapi
34	35.2	9.5	65280	9	AC118549 Homo sapi
35	35.2	9.5	179854	9	AC007437 Homo sapi
36	35.2	9.5	188561	2	AC110739 Mus muscu
37	35	9.5	38491	3	LMFL8138 Leishman
38	35	9.5	40620	3	AF239995 Leishman
39	34.8	9.4	164462	2	AC106546 Rattus no
40	34.6	9.4	169123	2	AC130865 Rattus no
41	34.6	9.4	199450	2	AC124918 Rattus no
42	34.6	9.4	204767	2	AC097561 Rattus no
43	34.4	9.3	187023	2	AC120749 Rattus no
44	34.2	9.3	2817	3	AF015539 Mytilus e
45	34.2	9.3	64958	2	AC090905 Homo sapi

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AX093381	Sequence 199 from Patent WO0118046.	AX093381	AX093381	AX093381.1	GI:13509829	human.	Homo sapiens	1 (bases 1 to 369)	Xu, J. and Stolk, J. A.	Ovarian tumor sequences and methods of use therefor	Patent: WO 0118046-A 199 15-MAR-2001;
AX093381	Sequence 199 from Patent WO0118046.	AX093381	AX093381	AX093381.1	GI:13509829	human.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				

FEATURES	CORIXA CORPORATION (US)	Location/Qualifiers
source	1.369	/organism="Homo sapiens" /db_xref="taxon:9606"
misc_feature	1.369	/note="n = A,T,C or G"
BASE COUNT	82 a 109 c 90 g 86 t	2 others
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Best Local Similarity	100.0%	Pred. No. 3.7e-96;
Matches 369; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	GGCACTTTTGGGGAAATGTTCTTGGCTTTCAGAGCTTTGGCGTGCAGAAATCCAGTCTACCA 60
Db	1	GGCACTTTTGGCGAATGTTCTTTCAGAGCTTTGGCGTGCAGAAATCCAGTCTACCA 60
QY	61	GTTGTAAGAAATTCACAGTCAACACACATGCTCCCTCCCGAGTTGATGTGAATTCAC 120
Db	61	GTTGTAAGAAATTCACAGTCAACACACATGCTCCCTCCCGAGTTGATGTGAATTCAC 120
QY	121	GGTGAACGTTTCAAGACATGTGTTCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
Db	121	GGTGAACGTTTCAAGACATGTGTTCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTA 180
QY	181	CCGCAAGTCTGTGCATTCATCAGCGGCGCTGTCTCATCGCTGCCGGGTACCACTCTT 240
Db	181	CCGCAAGTCTGTGCATTCATCAGCGGCGCTGTCTCATCGCTGCCGGGTACCACTCTT 240
QY	241	CTGCTCCCCAGGGAAGTCACTCACTGTTGCATCAGCTGCTGCAACACCCCTCTTTGTAA 300
Db	241	CTGCTCTCCCAAGGGAAGTCACTCACTGTTGCATCAGCTGCTGCAACACCCCTCTTTGTAA 300
QY	301	CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCCTCCCGCGCCCTCAAGCCATGGCTCCGAC 360
Db	301	CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCCTCCCGCGCCCTCAAGCCATGGCTCCGAC 360
QY	361	CACCATCTT 369
Db	361	CACCATCTT 369
RESULT 2		
LOCUS	BC017318	946 bp mRNA linear PRI 09-NOV-2001
DEFINITION	Homo sapiens, clone MGC:29643 IMAGE:3641660, mRNA, complete cds.	
ACCESSION	BC017318	
VERSION	BC017318.1	GI:16878239
KEYWORDS	MGC.	
SOURCE	Homo sapiens.	
ORGANISM	Homo sapiens.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 946)	
TITLE	Strausberg, R.	
JOURNAL	Direct Submission	
REMARK	Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
COMMENT	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@nrl.nih.gov">nisc_mgc@nrl.nih.gov</a> Shevchenko, Y., Wettherby, K.D. Beckstrom-Sternberg, S.M.,	

FEATURES	source
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <a href="http://Image.liml.gov">http://Image.liml.gov</a>	
Series: IRAL Plate: 39 Row: b Column: 19	
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.	
Location/Qualifiers	
1. 946	
/organism="Homo sapiens"	
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/clone="MGC:29643 IMAGE:3641660"	
/tissue_type="Pancreas, adenocarcinoma"	
/clone_lib="NIH-MGC_39"	
/lab_host="DH10B-R"	
/note="Vector: pOT7"	
261. 686	
/codon_start=1	
/product="Unknown (protein for MGC:29643)"	
/protein_id="AAH17318.1"	
/db_xref="GI:16878240"	
/translation="MNVLGIAATFCGLFLPGLALQICYCEEFOLNDDCSSEPIV TCLVNMDCOMEVEIOSAGIIMYRKSSACSIASAGYGFSPGLNLSVCSICCN TFLCNGPPRRKGSASALRGLRIITFLKLALESFHC"	
BASE COUNT	197 a 292 c 261 g 196 t
ORIGIN	
Query Match	99.0%; Score 365.4; DB 9; Length 946;
Best Local Similarity	99.2%; Pred. No. 1.1e-95;
Matches 366; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
1 GGCACATTTTGGGATTTGTTCTGCTTCACAGCTTTGGGCGCAAAATCCAGTGTACCA 60	
281 GGCACATTTTGGGATTTGTTCTGCTTCACAGCTTTGGGCGCAAAATCCAGTGTACCA 340	
61 GGTGGAAGAAATTCACAGCTGACATGCTCTCCCGAGTTCAATGTAATTGCAC 120	
341 GGTGGAAGAAATTCACAGCTGACATGCTCTCCCGAGTTCAATGTAATTGCAC 400	
121 GGTGGAAGCTTCAAGACATGTGTCAAGAAAGATGTATGAGCAAAAGTGGCGGATCATGTA 180	
401 GGTGGAAGCTTCAAGACATGTGTCAAGAAAGATGTATGAGCAAAAGTGGCGGATCATGTA 460	
181 CGGCAAGTCTTGTGATCATACGCGGCTGTCTATATGCGCTCTGCGGGATCCAGTCTTT 240	
461 CGGCAAGTCTTGTGATCATACGCGGCTGTCTATATGCGCTCTGCGGGATCCAGTCTTT 520	
241 CTGCTCTCCCGAGGAAGTCACTAGTTTGGATCATGAGTGTGCAAAACCCCTCTTTGTA 300	
521 CTGCTCTCCCGAGGAAGTCACTAGTTTGGATCATGAGTGTGCAAAACCCCTCTTTGTA 580	
301 CGGGCCAGAGCCCAAGAAAGGGAAGTTGTGCTCGGCTCTCANGCCATGAGCTCCGAC 360	
581 CGGGCCAGAGCCCAAGAAAGGGAAGTTGTGCTCGGCTCTCANGCCATGAGCTCCGAC 640	
361 CACCATCTCT 369	
641 CACCATCTCT 649	
RESULT 3	
LOCUS	AX358762
DEFINITION	Sequence 15 from Patent WO0193983.
ACCESSION	AX358762
VERSION	AX358762.1 GI:18675282

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

REFERENCE 1  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0193983-A 15 13-DEC-2001;  
Genentech Inc. (US)

FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 321 a 433 c 435 g 335 t

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Query Match 99.0%; Score 365.4; DB 6; Length 1524;  
Best Local Similarity 99.2%; Pred. No. 1.1e-95;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGATGTTCTTCTTCATCAGGCTTTGGCTGCAATCCAGTGTACCA 60  
Db 141 GGCACATTTTGGGATGTTCTTCTTCATCAGGCTTTGGCTGCAATCCAGTGTACCA 200

QY 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGAGTTGATTTGATTCAC 120  
Db 201 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGAGTTGATTTGATTCAC 260

QY 121 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTCCGGGATCATGTA 180  
Db 261 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTCCGGGATCATGTA 320

QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTTCCGGGTACAGTCTTT 240  
Db 321 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTTCCGGGTACAGTCTTT 380

QY 241 CTGCTCCCGAGGAACTGAACCTGATTCATCAGTGTGCAACACCCCTTTGTAA 300  
Db 381 CTGCTCCCGAGGAACTGAACCTGATTCATCAGTGTGCAACACCCCTTTGTAA 440

QY 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCTCCGCAC 360  
Db 441 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCTCCGCAC 500

QY 361 CACCATCTT 369  
Db 501 CACCATCTT 509

RESULT 4  
AX362255 1524 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 15 from Patent WO0208288.  
ACCESSION AX362255  
VERSION AX362255.1 GI:18694585  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

REFERENCE 1  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;  
Genentech, Inc. (US)

FEATURES  
source  
Location/Qualifiers  
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BASE COUNT 321 a 433 c 435 g 335 t

ORIGIN

Query Match 99.0%; Score 365.4; DB 6; Length 1524;  
Best Local Similarity 99.2%; Pred. No. 1.1e-95;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGATGTTCTTCTTCATCAGGCTTTGGCTGCAATCCAGTGTACCA 60  
Db 141 GGCACATTTTGGGATGTTCTTCTTCATCAGGCTTTGGCTGCAATCCAGTGTACCA 200

QY 61 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGAGTTGATTTGATTCAC 120  
Db 201 GTGTGAAGAAATTCAGCTGAACACGACTGCTCTCCCGAGTTGATTTGATTCAC 260

QY 121 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTCCGGGATCATGTA 180  
Db 261 GGTGAACGTTTCAGACATGTGTCAAGAAAGATGAGCAAGTCCGGGATCATGTA 320

QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTTCCGGGTACAGTCTTT 240  
Db 321 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGGCTTCCGGGTACAGTCTTT 380

QY 241 CTGCTCCCGAGGAACTGAACCTGATTCATCAGTGTGCAACACCCCTTTGTAA 300  
Db 381 CTGCTCCCGAGGAACTGAACCTGATTCATCAGTGTGCAACACCCCTTTGTAA 440

QY 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCTCCGCAC 360  
Db 441 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCTGCTCGGCGCTCAGGCTCCGCAC 500

QY 361 CACCATCTT 369  
Db 501 CACCATCTT 509

RESULT 5  
AK094501 1832 bp mRNA linear PRI 15-JUL-2002  
DEFINITION Homo sapiens cDNA FLJ37182 fls, clone BRAL22001350, weakly similar to Homo sapiens Gz-selective GTPase-activating protein (RGS20) mRNA.  
ACCESSION AK094501  
VERSION AK094501.1 GI:21753575  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

REFERENCE 1  
AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagaitsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Negaharui, K., Masuno, Y., Nagai, K., and Isogai, T.  
TITLE NED0 human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1832)  
Isogai, T. and Yamamoto, J.  
Direct Submission  
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team): 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology (RAB) (supported by Japan construction: Helix Research Institute (HRI) (supported by Japan Technology Center etc.); 5'-3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.  
Location/Qualifiers

## FEATURES

source

1. .1832

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="BRAL22001350"

/issue\_type="alzheimer cortex"

/clone\_11b="BRAL22"

/note="Cloning vector: pME18FLJ3"

215. .640

/note="unnamed protein product"

/codon\_start=1

/protein\_id="BAC04368.1"

/db\_xref="GI:21735376"

/translation="MWVIGIAATFCGLFLPGLFALQIQCYOCSEFQLNNDSSPEFIV  
NCTVAVDMQCEVMEQSAQIMYRRKSCASSACLIASAGYOSFCSPGKLNISVCSCN  
TPLCNGPPKRRGSSASALRPLRTIILFLKLALFSAHC"

BASE COUNT 411 a 501 c 513 g 407 t

ORIGIN

Query Match 99.0%; Score 365.4; DB 9; Length 1832;  
Best Local Similarity 99.2%; Pred. No. 1.1e-95;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTTCGGATGTTCTTCTTCAGGCTTGGCGTCAAAATCCAGTCTACCA 60  
DB 235 GGCACTTTTTCGGATGTTCTTCTTCAGGCTTGGCGTCAAAATCCAGTCTACCA 294  
QY 61 GTGTGAAGATTCACGCTGAACACGAGTCTCTCCCGAGTTCAATTTGAATGCAC 120  
DB 295 GTGTGAAGATTCACGCTGAACACGAGTCTCTCCCGAGTTCAATTTGAATGCAC 354  
QY 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGTATGAGAGAAAGTCCGGATCATGTA 180  
DB 355 GGTGAACGTTCAAGCATGTGTGCAAGAAAGTATGAGAGAAAGTCCGGATCATGTA 414  
QY 181 CCGCAAGTCTGTGCATCATCATCAGCGGCTGTCTCATCGCTCCGCGGTACCACTCTT 240  
DB 415 CCGCAAGTCTGTGCATCATCATCAGCGGCTGTCTCATCGCTCCGCGGTACCACTCTT 474  
QY 241 CTGCTCCCGAGGAAATCACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 475 CTGCTCCCGAGGAAATCACTGATGATGATGATGATGATGATGATGATGATGATGAT 534  
QY 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTTCGCTCGGCTTCANGCATGAGTCCGAC 360  
DB 535 CGGGCCAAAGGCCCAAGAAAGGGGAGTTCGCTCGGCTTCANGCATGAGTCCGAC 594  
QY 361 CACCATCTT 369  
DB 595 CACCATCTT 603

RESULT 6  
AX136281  
LOCUS AX136281 1890 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 203 from Patent EPI067182.  
ACCESSION AX136281  
VERSION AX136281.1 GI:14272687  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE 1 (bases 1 to 1890)  
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and  
Hayashi, K.  
TITLE Secretory protein or membrane protein  
JOURNAL Patent: EP 1067182-A 203 10-JAN-2001;  
FEATURES Helix Research Institute (JP)  
Location/Qualifiers

source

1. .1890

/organism="Homo sapiens"

/db\_xref="taxon:9606"

274. .771

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAC39782.1"

/db\_xref="GI:14272688"

/translation="MWVIGIAATFCGLFLPGLFALQIQCYOCSEFQLNNDSSPEFIV  
NCTVAVDMQCEVMEQSAQIMYRRKSCASSACLIASAGYOSFCSPGKLNISVCSCN  
TPLCNGPPKRRGSSASALRPLRTIILFLKLASSRHTALKEPPPALFRQSPPT  
PILPE"

BASE COUNT 419 a 528 c 533 g 410 t

ORIGIN

Query Match 99.0%; Score 365.4; DB 6; Length 1890;  
Best Local Similarity 99.2%; Pred. No. 1.1e-95;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTTCGGATGTTCTTCTTCAGGCTTGGCGTCAAAATCCAGTCTACCA 60  
DB 294 GGCACTTTTTCGGATGTTCTTCTTCAGGCTTGGCGTCAAAATCCAGTCTACCA 353  
QY 61 GTGTGAAGATTCACGCTGAACACGAGTCTCTCCCGAGTTCAATTTGAATGCAC 120  
DB 354 GTGTGAAGATTCACGCTGAACACGAGTCTCTCCCGAGTTCAATTTGAATGCAC 413  
QY 121 GGTGAACGTTCAAGCATGTGTGCAAGAAAGTATGAGAGAAAGTCCGGATCATGTA 180  
DB 414 GGTGAACGTTCAAGCATGTGTGCAAGAAAGTATGAGAGAAAGTCCGGATCATGTA 473  
QY 181 CCGCAAGTCTGTGCATCATCATCAGCGGCTGTCTCATCGCTCCGCGGTACCACTCTT 240  
DB 474 CCGCAAGTCTGTGCATCATCATCAGCGGCTGTCTCATCGCTCCGCGGTACCACTCTT 533  
QY 241 CTGCTCCCGAGGAAATCACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 534 CTGCTCCCGAGGAAATCACTGATGATGATGATGATGATGATGATGATGATGATGAT 593  
QY 301 CGGGCCAAAGGCCCAAGAAAGGGGAGTTCGCTCGGCTTCANGCATGAGTCCGAC 360  
DB 594 CGGGCCAAAGGCCCAAGAAAGGGGAGTTCGCTCGGCTTCANGCATGAGTCCGAC 653  
QY 361 CACCATCTT 369  
DB 654 CACCATCTT 662

RESULT 7  
AX093191  
LOCUS AX093191 396 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 9 from Patent WO0118046.  
ACCESSION AX093191  
VERSION AX093191.1 GI:13509640  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE 1 (bases 1 to 396)  
AUTHORS Xu, J., and Stolk, J. A.  
TITLE Ovarian tumor sequences and methods of use therefor  
JOURNAL Patent: WO 0118046-A 9 15-MAR-2001;  
FEATURES CORIXA CORPORATION (US)  
Location/Qualifiers  
source 1. .396  
misc\_feature 1. .396  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="n = A, T, C or G"  
BASE COUNT 90 a 117 c 95 g 92 t 2 others  
ORIGIN





/db.xref="taxon:10090"  
 /clone="MNCB-0671"  
 /sex="female"  
 /clone\_lib="Sugano mouse brain mcb"  
 /dev\_stage="adult"  
 325..750  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="BAA95101.1"  
 /db.xref="GI:7670500"  
 /translation="MWLGIAATFCGLFWLPGLALQIOCYOCSEFQNLNNDSSPEFIV  
 NCTVNDQCKREVEQASAGIMYRKSSAACLITASAGYOSFCSPKINSVCISCN  
 TPLCGPPKRGSSAISIRPLITLLFFHLALCLALHC"

BASE COUNT 391 a 487 c 511 g 408 t  
 ORIGIN

Query Match 82.7%; Score 305.2; DB 10; Length 1797;  
 Best Local Similarity 89.1%; Pred. No. 4.1e-78;  
 Matches 328; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 2 GCACCTTTTGGGATTTGCTTTCAGGCTTTGAGGCTTGCACAAATCCAGTACACG 61  
 DB 346 GCACTTTTGGGATTTGCTTTCAGGCTTGCAGGCTTGCACAAATCCAGTACACG 405  
 QY 62 TGTGAAGATTCACGTGACAGAGCTGCTCCCGAGTTCATTGTGAATTCACG 121  
 DB 406 TGTGAAGATTCACGTGACAGAGCTGCTCCCGAGTTCATTGTGAATTCACG 465  
 QY 122 GTGAAGCTTCAAGACATGTGTGAGAAAGATGAGAGCAAGTCCGGGATTCATGAC 181  
 DB 466 GTGAAGCTTCAAGACATGTGTGAGAAAGATGAGAGCAAGTCCGGGATTCATGAC 525  
 QY 182 CGCAAGCTTCTGATCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATTCATGAC 241  
 DB 526 CGCAAGCTTCTGATCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATTCATGAC 585  
 QY 242 TGTCTCCCGAGGAACTGACTGATGCTGATGCTGCTGACACACCCCTTTGTAC 301  
 DB 586 TGTCTCCCGAGGAACTGACTGATGCTGATGCTGCTGACACACCCCTTTGTAC 645  
 QY 302 GGGCCAAAGCCCAAGAAAGGGAAGTTCCTGCTGCGCCCTCANGCCATGCTCCGAC 361  
 DB 646 GGGCCAAAGCCCAAGAAAGGGAAGTTCCTGCTGCGCCCTCANGCCATGCTCCGAC 705  
 QY 362 ACCATCTCT 369  
 DB 706 ACTCTCTCT 713

RESULT 10  
 AX136556 591 bp DNA linear PAT 30-MAY-2001  
 LOCUS AX136556  
 DEFINITION Sequence 478 from Patent EP1067182.  
 ACCESSION AX136556  
 VERSION AX136556.1 GI:14272960  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 591)  
 AUTHORS Ota, T., Isega, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.  
 TITLE Secretory protein or membrane protein  
 JOURNAL Patent: EP 1067182-A 478 10-JAN-2001;  
 Helix Research Institute (JP)  
 FEATURES  
 source 1..591  
 /organism="Homo sapiens"  
 /db.xref="taxon:9606"

BASE COUNT 108 a 198 c 173 g 109 t 3 others  
 ORIGIN

Query Match 77.0%; Score 284; DB 6; Length 591;  
 Best Local Similarity 99.3%; Pred. No. 6.2e-72;  
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATTTGCTTTCAGGCTTTGAGGCTTGCACAAATCCAGTACCA 60  
 DB 294 GGCACCTTTTGGGATTTGCTTTCAGGCTTTGAGGCTTGCACAAATCCAGTACCA 353  
 QY 61 GTGTGAAGATTCACGTGACAGAGCTGCTCCCGAGTTCATTGTGAATTCACG 120  
 DB 354 GTGTGAAGATTCACGTGACAGAGCTGCTCCCGAGTTCATTGTGAATTCACG 413  
 QY 121 GTGAAGCTTCAAGACATGTGTGAGAAAGATGAGAGCAAGTCCGGGATTCATG 180  
 DB 414 GTGAAGCTTCAAGACATGTGTGAGAAAGATGAGAGCAAGTCCGGGATTCATG 473  
 QY 181 CCGCAAGCTTCTGATCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATTCATG 240  
 DB 474 CCGCAAGCTTCTGATCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATTCATG 533  
 QY 241 CTGTCTCCCGAGGAACTGACTGATGCTGATGCTGCTGACACCTGCTGAC 286  
 DB 534 CTGTCTCCCGAGGAACTGACTGATGCTGATGCTGCTGACACCTGCTGAC 579

RESULT 11  
 AC079773/c 129676 bp DNA linear PRI 09-JAN-2002  
 LOCUS AC079773  
 DEFINITION Homo sapiens BAC clone RP11-258B17 from 2, complete sequence.  
 ACCESSION AC079773  
 VERSION AC079773.8 GI:15145561  
 KEYWORDS HTG.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 129676)  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 PUBMED 99063792  
 REFERENCE 2 (bases 1 to 129676)  
 AUTHORS Shah, N., Meyer, R., Boyer, E. and Dignan, G.  
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 129676)  
 AUTHORS Waterson, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 4 (bases 1 to 129676)  
 REFERENCE 4 (bases 1 to 129676)  
 AUTHORS Waterson, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-AUG-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 5 (bases 1 to 129676)  
 REFERENCE 5 (bases 1 to 129676)  
 AUTHORS Waterson, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Aug 9, 2001 this sequence version replaced gi:14488388.  
 COMMENT  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc  
 Contact: saplens@wustl.wustl.edu  
 Summary Statistics  
 Center project name: H\_NH0258B17

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repeat_region	/rpt_family="ERV1"	18434. .18801
repeat_region	/rpt_family="ERV1"	18933. .19074
repeat_region	/rpt_family="ERV1"	19144. .19250
repeat_region	/rpt_family="ERV1"	19260. .19628
repeat_region	/rpt_family="ERV1"	20104. .20145
repeat_region	/rpt_family="(TG)n"	20170. .20305
repeat_region	/rpt_family="MER1_type"	20618. .20756
repeat_region	/rpt_family="MER1_type"	21300. .21325
repeat_region	/rpt_family="(A)n"	21428. .21796
misc_feature	/note="match to EST BF821779 (MID:g1261303)"	23084. .23228
repeat_region	/rpt_family="MIR"	23967. .24256
repeat_region	/rpt_family="Alu"	25108. .25208
repeat_region	/rpt_family="MIR"	25485. .25805
repeat_region	/rpt_family="MaLR"	26417. .26463
repeat_region	/rpt_family="ERV1"	26466. .26655
repeat_region	/rpt_family="MER2_type"	26656. .27047
repeat_region	/rpt_family="MaLR"	27048. .27149
repeat_region	/rpt_family="MER2_type"	27246. .27403
repeat_region	/rpt_family="(TA)n"	27309. .27380
repeat_region	/rpt_family="r1"	27403. .27671
repeat_region	/rpt_family="Alu"	27698. .27749
repeat_region	/rpt_family="MER2_type"	27750. .27904
repeat_region	/rpt_family="(TA)n"	27926. .28052
repeat_region	/rpt_family="r2"	28052. .28667
misc_feature	/note="match to EST BF736070 (MID:g12062744)"	28834. .28958
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repeat_region	/rpt_family="Alu"	29727. .30121
repeat_region	/rpt_family="MaLR"	30363. .30543
repeat_region	/rpt_family="MER1_type"	30718. .30919
repeat_region	/rpt_family="MER1_type"	31494. .31783
repeat_region	/rpt_family="Alu"	32028. .32488
repeat_region	/rpt_family="ERV1"	32053. .32080
repeat_region	/rpt_family="(GA)n"	32667. .32787
repeat_region	/rpt_family="MIR"	34079. .34164
repeat_region	/rpt_family="r2"	

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repeat_region      34271..34348
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misc_feature        34409..34703
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repeat_region      35346..35374
                    /rpl_family="(TTTTG)n"
repeat_region      35361..35676
                    /rpl_family="Alu"

Query Match      53.7%; Score 198.2; DB 9; Length 129676;
Best Local Similarity 98.0%; Pred. No. 7.2e-47;
Matches 200; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 166 TGGCGGATGATGATGACGCAAGTCTGTGCATGATCAGCGCCTGTCTCATCCGCTTGC 225
Db 120745 TACAGGATGATGATGACGCAAGTCTGTGCATGATCAGCGCCTGTCTCATCCGCTTGC 120686

QY 226 CGGGTACAGTCTCTTGTGCTGCCAGGAAAGTCACTGTTGATCAGTCTGCTGCA 285
Db 120685 CGGGTACAGTCTCTTGTGCTGCCAGGAAAGTCACTGTTGATCAGTCTGCTGCA 120626

QY 286 CACCCCTCTTGTACGGGCAAGGCCCAAGGAAGTTCGCTCGGCGCTGCAN 345
Db 120625 CACCCCTCTTGTACGGGCAAGGCCCAAGGAAGTTCGCTCGGCGCTGCAG 120566

QY 346 GCCATGCTCCGACCAACATCCT 369
Db 120565 GCCATGCTCCGACCAACATCCT 120542

RESULT 12
AC124493/c 209885 bp DNA linear HTG 05-JUL-2002
LOCUS AC124493
DEFINITION Mus musculus chromosome UNK clone RP23-462P13, WORKING DRAFT
ACCESSION AC124493
VERSION AC124493.2 GI:21699722
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE 1 (bases 1 to 209885)
JOURNAL The sequence of Mus musculus clone
AUTHORS Unpublished
TITLE 2 (bases 1 to 209885)
AUTHORS McPherson,J.D. and Waterston,R.H.
JOURNAL Direct Submission
TITLE Direct Submission
AUTHORS McPherson,J.D. and Waterston,R.H.
JOURNAL Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT On Jul 5, 2002 this sequence version replaced g1:2142614.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Project Information
Center project name: M_BA0462P13

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 208464 bases at least Q40

```

```

Consensus quality: 208911 bases at least Q30
Consensus quality: 209285 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 212112; sum-of-contigs
Quality coverage: 0.00 in Q20 bases; sum-of-contigs
Quality coverage: 11.62 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 11331: contig of 11331 bp in length
* 11332 11431: gap of unknown length
* 11432 28617: contig of 17186 bp in length
* 28618 28717: gap of unknown length
* 28718 49454: contig of 20737 bp in length
* 49455 49554: gap of unknown length
* 49555 107384: contig of 57830 bp in length
* 107385 107484: gap of unknown length
* 107485 209885: contig of 102401 bp in length.
FEATURES
Location/Qualifiers
source 1..209885
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-462P13"
1..11331
/note="assembly_name:Contig8"
11432..28617
/note="assembly_name:Contig9"
28718..49454
/note="assembly_name:Contig10"
49555..107384
/note="assembly_name:Contig11"
107485..209885
/note="assembly_name:Contig12"
BASE COUNT 59789 a 44784 c 46164 g 58745 t 403 others
ORIGIN

Query Match      43.1%; Score 159; DB 2; Length 209885;
Best Local Similarity 87.0%; Pred. No. 2e-35;
Matches 174; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 170 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCCTGTCTCATCCGCGG 229
Db 66382 GGGATCATGTACCGCAAGTCTGTGCATCATCAGCGCCTGTCTCATCCGCGG 66323

QY 230 TACCATGCTCTTGTGCTGCCAGGAAAGTCACTGTTGATCAGTCTGCTGCA 289
Db 66322 TACCATGCTCTTGTGCTGCCAGGAAAGTCACTGTTGATCAGTCTGCTGCA 66263

QY 290 CCTCTTGTACGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCA 349
Db 66262 CCTCTTGTACGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCA 66203

QY 350 TGGCTCCGACCAACATCCT 369
Db 66202 TGGCTCCGACCAACATCCT 66183

RESULT 13
AC010974/c 147131 bp DNA linear PRI 01-MAR-2002
LOCUS AC010974
DEFINITION Homo sapiens BAC clone RP11-159N20 from 2, complete sequence.
ACCESSION AC010974
VERSION AC010974.9 GI:19033964
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

```

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 147131)  
JOURNAL Toward a complete human genome sequence  
MEDLINE Genome Res. 8 (11), 1097-1108 (1998)  
99063792  
PUBMED 9847074

REFERENCE  
AUTHORS 2 (bases 1 to 147131)  
TITLE Vanbrunt, A. and Stromwater, C.  
JOURNAL The sequence of Homo sapiens BAC clone RP11-159N20  
UNPUBLISHED (2001)  
REFERENCE 3 (bases 1 to 147131)  
AUTHORS Waterston, R.H.  
JOURNAL Direct Submission  
Submitted (28-SEP-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
4 (bases 1 to 147131)  
AUTHORS Waterston, R.H.  
JOURNAL Direct Submission  
Submitted (23-MAR-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
5 (bases 1 to 147131)  
AUTHORS Waterston, R.  
JOURNAL Direct Submission  
Submitted (01-MAR-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Mar 1, 2002 this sequence version replaced g1:13435273.

----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc  
Contact: saplensew@wustl.edu  
----- Summary Statistics  
Center project name: H\_NH0159N20  
-----

COMMENT

NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping  
clone sections once, or longer because we provide a small overlap  
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D.  
McPherson, Department of Genetics, Washington University, St. Louis  
MO. For additional information about the map position of this  
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RP11-11 human BAC library was made from the blood of one male  
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,  
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong  
and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the right is RP11-458A7, 200 bp overlap; the  
clone sequenced to the right is RP11-258B17. Actual start of this  
clone is at base position 1 of RP11-159N20; actual end is at base  
position 147131 of RP11-159N20.

# FEATURES

There are polymorphic base differences in the overlap between the  
clone RP11-159N20 and RP11-258B17.

Source	Location/Qualifiers
1. 147131	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="2"
	/map="2"
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	/clone_11b="RP11-11"
	21. 67
repeat_region	/rpt_family="MIR"
repeat_region	118. 1013
misc_feature	/rpt_family="L1"
misc_feature	984. 1176
misc_feature	/note="match to EST BG200048 (NID:g13721735)"
misc_feature	991. 1176
misc_feature	/note="match to EST BG184021 (NID:g13705708)"
misc_feature	991. 1176
misc_feature	/note="match to EST BG187166 (NID:g13708853)"
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repeat_region	1525. 1552
repeat_region	/rpt_family="TTTA)n"
repeat_region	1526. 1814
repeat_region	/rpt_family="Alu"
repeat_region	2299. 2596
repeat_region	/rpt_family="Alu"
repeat_region	4890. 5129
repeat_region	/rpt_family="MALR"
repeat_region	5738. 5757
repeat_region	/rpt_family="(TG)n"
repeat_region	6131. 6178
repeat_region	/rpt_family="GA-rich"
misc_feature	7310. 7364
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repeat_region	7811. 7881
repeat_region	/rpt_family="MIR"
repeat_region	8227. 8260
repeat_region	/rpt_family="(CATTC)n"
repeat_region	8373. 8683
repeat_region	/rpt_family="L1"
misc_feature	8640. 9120
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repeat_region	8776. 8838
repeat_region	/rpt_family="MIR"
misc_feature	8810. 9257
misc_feature	/note="match to EST AA434316 (NID:g2139230) zw24e08.r1"
repeat_region	9348. 9395
repeat_region	/rpt_family="GA-rich"
misc_feature	9731. 9895
misc_feature	/note="match to EST BF347279 (NID:g11294874)"
misc_feature	9743. 9895
misc_feature	/note="match to EST BG184021 (NID:g13705708)"
misc_feature	9743. 9895
misc_feature	/note="match to EST BG187166 (NID:g13708853)"
repeat_region	10053. 10359
repeat_region	/rpt_family="Alu"
repeat_region	12424. 12509
repeat_region	/rpt_family="MIR"
repeat_region	12505. 12671
repeat_region	/rpt_family="MER1_type"
misc_feature	13456. 13776
misc_feature	/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
misc_feature	13854. 13855
misc_feature	/note="match to EST A1239596 (NID:g3834993) qh37b10.x1"
misc_feature	15183. 15321
misc_feature	/note="match to EST BE386060 (NID:g9331425)"
misc_feature	15183. 15321
misc_feature	/note="match to EST BG704350 (NID:g13977603)"
misc_feature	15183. 15321
misc_feature	/note="match to EST BG753617 (NID:g14064270)"

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misc_feature      15184..15320
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misc_feature      15864..18081
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misc_feature      17963..18209
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misc_feature      18637..19184
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misc_feature      18931..19137
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misc_feature      19350..19354
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misc_feature      18938..19409
                   /note="similar to Homo sapiens EST AA779875 (NID:g2839206) af4bD10.s1"
misc_feature      19235..19616
                   /note="match to EST R54748 (NID:g819270) yj75b04.r1"
repeat_region     19406..19426
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misc_feature      19407..19710
                   /note="similar to Bos taurus EST BE750540 (NID:g10164532)"
misc_feature      19458..19795
                   /note="similar to Bos taurus EST BE862268 (NID:g10067956)"
misc_feature      19873..20090
                   /note="match to EST BG200485 (NID:g13722172)"
misc_feature      19926..20089
                   /note="similar to Homo sapiens EST BE963800 (NID:g11767217)"

Query Match      39.5%: Score 145.6; DB 9; Length 147131;
Best Local Similarity 96.7%: Pred.No.1.6e-31;
Matches 148; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 21 TCTTGGCTTCAGAGCTTTGGCGCTGCAATTCACATGCTTACACAGTGTAAGAGAAATTCACAGCTGA 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15333 TCTGCTCGCAGAGCTTTGGCGCTGCAATTCACATGCTTACACAGTGTAAGAGATTCACAGCTGA 15274

Oy 81 ACAACGATGCTCCCTCCCGCAGTTCATTTGTAATTGCAAGCGGTGAACGTTCAAGACATGT 140
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Oy 141 GTCAGAAAGAAAGTATGAGGAGCAAAATGCCGGGA 173
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RESULT 14					
AC110334/c	AC110334	136799 bp	DNA	linear	HTG 13-JUL-2002
LOCUS	Rattus norvegicus clone	36730-140B3, ***	SEQUENCING IN PROGRESS		
DEFINITION	***, 69 unordered pieces.				
ACCESSION	AC110334				
VERSION	AC110334.3	GI:21738206			
KEYWORDS	HTG; HTGS_PHASE1.				

SOURCE ORGANISM	REFERENCE
Norway rat. <i>Rattus norvegicus</i>	1 (bases 1 to 136799)
Eukaryotes: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia, Sclurognathl: Muridae: Murinae: <i>Rattus</i> .	Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C.,
AUTHORS	

Alstrook, S. L., Amarantunge, H. C., Are, J. R., Ayele, M., Banks, T.,  
Barbala, J., Benton, J., Blinage, K., Blankenburg, K., Bonini, D.,  
Bowick, J., Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N. P.,  
Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C.,  
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Chen, G., Chen, R., Chen, Z., Chowdhury, K., Christopoulos, C.,  
Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. P., David, R.,  
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Wozley, K.,  
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 136799)  
AUTHORS Worley, K.C.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 136799)  
Worley, K.C.  
REFERENCE Direct Submission  
AUTHORS Worley, K.C.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 12, 2002 this sequence version replaced gi:18847022.

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information -----  
Center project name: GOLL  
Center clone name: CH230-140B23  
----- Summary Statistics -----  
Sequencing vector: Plasmid:  
Chemistry: Dye-terminator Big Dye: 100k of reads  
Assembly program: Phrap: version 0.990329

Consensus quality: 63796 bases at least Q40  
Consensus quality: 67862 bases at least Q30  
Consensus quality: 71477 bases at least Q20

NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draat\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draat_data.html)).  
NOTE: This is a working draft sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1231: contig of 1231 bp in length  
1232 1331: gap of unknown length  
1332 2411: contig of 1080 bp in length  
2412 2511: gap of unknown length  
2512 3703: contig of 1198 bp in length  
3710 3809: gap of unknown length  
3810 4935: contig of 1126 bp in length  
4936 5035: gap of unknown length  
5036 6214: contig of 1179 bp in length  
6215 6314: gap of unknown length  
6315 7437: contig of 1123 bp in length  
7438 7537: gap of unknown length  
7538 8808: contig of 1271 bp in length  
8809 10058: gap of unknown length  
10059 10158: contig of 1150 bp in length  
10159 11422: gap of unknown length  
11423 11522: contig of 1264 bp in length  
11523 12687: gap of unknown length  
12688 13983: contig of 1165 bp in length  
13984 14083: gap of unknown length  
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15534 15633: gap of unknown length  
15634 16915: contig of 1282 bp in length  
16916 17015: gap of unknown length  
17016 18599: contig of 1584 bp in length  
18600 19997: gap of unknown length  
19998 20097: gap of unknown length  
20098 21362: contig of 1265 bp in length  
21363 21462: gap of unknown length  
21463 22657: contig of 1195 bp in length  
22658 22757: gap of unknown length  
22758 24138: contig of 1381 bp in length  
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29140 29239: gap of unknown length  
29240 30317: contig of 1078 bp in length  
30318 30417: gap of unknown length  
30418 31460: contig of 1043 bp in length  
31461 32719: gap of unknown length  
32720 32819: contig of 1159 bp in length  
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34474 36037: contig of 1564 bp in length  
36038 36137: gap of unknown length  
36138 37200: contig of 1063 bp in length  
37201 38596: gap of unknown length  
38597 40147: contig of 1451 bp in length

40148 40247: gap of unknown length  
40248 41360: contig of 1113 bp in length  
41361 41461: gap of unknown length  
41461 42977: contig of 1517 bp in length  
42977 43078: gap of unknown length  
43078 44720: contig of 1643 bp in length  
44721 44820: gap of unknown length  
44821 46156: contig of 1336 bp in length  
46156 46256: gap of unknown length  
46257 47867: contig of 1611 bp in length  
47868 47967: gap of unknown length  
47968 49429: contig of 1462 bp in length  
49430 49529: gap of unknown length  
49530 50989: contig of 1460 bp in length  
50990 51089: gap of unknown length  
51090 52573: contig of 1484 bp in length  
52574 52673: gap of unknown length  
52674 54837: contig of 2164 bp in length  
54838 54937: gap of unknown length  
54939 56606: contig of 1669 bp in length  
56607 56706: gap of unknown length  
56707 58749: contig of 2043 bp in length  
58750 58849: gap of unknown length  
58850 60835: contig of 1986 bp in length  
60836 60935: gap of unknown length  
60936 62990: contig of 2055 bp in length  
62991 63091: gap of unknown length  
63091 66231: contig of 3141 bp in length  
66232 66331: gap of unknown length  
66332 67598: contig of 1267 bp in length  
67599 67698: gap of unknown length  
67699 69667: contig of 1969 bp in length  
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69768 71637: contig of 1870 bp in length  
71638 71737: gap of unknown length  
71738 73653: contig of 1916 bp in length  
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73754 75227: contig of 1474 bp in length  
75228 75328: gap of unknown length  
75329 76907: contig of 1580 bp in length  
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82121 82220: gap of unknown length  
82221 84767: contig of 2547 bp in length  
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Query Match 21.7% Score 80.2; DB 2; Length 136799;  
Best Local Similarity 87.1%; Pred. No. 2e-12;  
Matches 88; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 166 TGGCGGATCATGTACCGGAGTCTGTGCATCATATGACGCGCTGTATGCTTCG 225  
AC128363/c  
DB 51426 TGCAGGATCATGTATACCGGATCATGTGCATGATGACGACGCTGTATGCTTCG 51367  
QY 226 CGGATACAGTCTGTCTGCTCCCGGAGGAACGATGACG 266  
DB 51366 TGGATACGTCGTCTGTCTGCTCCCGGAGGAACGATGACG 51326

RESULT 15  
AC128363/c  
LOCUS  
DEFINITION  
AC128363 190503 bp DNA linear HTG 19-JUL-2002  
Rattus norvegicus clone CH230-22808, \*\*\* SEQUENCING IN PROGRESS  
AC128363  
AC128363.1 GI:21909012  
VERSION  
KEYWORDS  
HTG: HTGS, PHASE1  
SOURCE  
Rattus norvegicus.  
ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

1 (bases 1 to 190503)

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
JOURNAL

## COMMENT

Munzy, D.M., Adams, C., Adio-Oduola, B., All-oshman, F.R., Allen, C.,  
Albrooks, S.L., Amaralunga, H.C., Are, J.R., Ayele, M., Banks, T.,  
Barbata, J., Benton, J., Blamge, K., Blankenburg, K., Bonni, D.,  
Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,  
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Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
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Weinstock, G. and Gibbs, R.

Unpublished

2 (bases 1 to 190503)

Morley, K.C.

Submitted

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

Project information

Center project name: GZCA

Center clone name: CH230-22808

Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.990329

Consensus quality: 131119 bases at least Q40

Consensus quality: 136808 bases at least Q30

Consensus quality: 141839 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 69 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1002  
1101: gap of unknown length  
1102  
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59756: gap of unknown length  
61354: contig of 1598 bp in length







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:50:02 ; Search time 72.6545 Seconds  
(without alignments)  
11437.514 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369  
Sequence: 1 ggcacatttgcggatgtt.....tggctccgaccacacatct 369

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_101002:\*

1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
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23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	367	99.5	369	22	AAF95007	Human ovarian carc
2	367	99.5	369	24	ABT03274	Human ovarian carc
3	367	99.5	369	24	ABL48956	Human ovarian carc
4	365.4	99.0	1524	24	ABK33543	CDNA encoding huma
5	365.4	99.0	1619	24	ABT03277	Human ovarian carc
6	365.4	99.0	1619	24	ABT03281	Human ovarian carc
7	365.4	99.0	1619	24	ABL40345	Ovarian carcinoma
8	365.4	99.0	1619	24	ABL40349	Ovarian carcinoma
9	365.4	99.0	1890	22	AAF93845	Human CDNA encodin

10	365.4	99.0	1897	24	ABT03284	Human ovarian carc
11	365.4	99.0	1897	24	ABL40352	Ovarian carcinoma
12	352.4	95.5	1953	21	AAF22400	Human secreted pro
13	352.4	95.5	1956	22	AAF64188	Human secreted pro
14	343.4	93.1	396	22	AAF94818	Human ovarian carc
15	343.4	93.1	396	24	ABT03085	Human ovarian carc
16	343.4	93.1	396	24	ABL48768	Ovarian carcinoma
17	341.8	92.6	1010	24	ABT03282	Ovarian carcinoma
18	341.8	92.6	1010	24	ABL40350	Ovarian carcinoma
19	336.4	91.2	2528	22	ABL16690	Human G protein co
20	284	77.0	591	22	AAF94044	Primer specific fo
21	196.8	53.3	480	24	ABT03283	Human ovarian carc
22	196.8	53.3	480	24	ABL40351	Ovarian carcinoma
23	174.2	47.2	1608	24	ABO54231	Human ovarian carc
24	86.4	23.4	430	24	ABL81273	Human ovarian carc
25	36	9.8	44242	23	ABL19930	Drosophila melano
26	35.4	9.6	5811	21	AACT5680	Human OREF ORF1435
27	33.8	9.2	3268	23	AAST7591	DNA encoding novel
28	33.8	9.2	5676	22	AA159341	Human polynucleoti
29	33.8	9.2	4403765	22	AA199683	Mycobacterium tub
30	33.6	9.1	20578	22	ABA16515	Human nervous syst
31	33.2	9.0	2133	22	AAH64972	C glutamic codin
32	33.2	9.0	34980	22	AAH64966	C glutamic codin
33	33	8.9	445	22	AA190253	Human polynucleoti
34	33	8.9	7931	23	ABL25204	Drosophila melano
35	32.2	8.7	479	22	AA126045	Human breast cance
36	32.2	8.7	815	22	AA116843	Human breast cance
37	32.2	8.7	3343	20	AAK87179	Fibroblast growth
38	32.2	8.7	110608	24	ABK83572	Human CDNA differe
39	32	8.7	3496	24	ABK64744	Human benign prost
40	31.8	8.6	759	15	AAQ66584	Sequence of rabbit
41	31.6	8.6	544	22	AAQ60261	Human cancer agent
42	31.6	8.6	658	21	AACT5150	Arabidopsis thalia
43	31.6	8.6	674	21	AACT5371	Arabidopsis thalia
44	31.6	8.6	775	24	ABN99125	Arabidopsis thalia
45	31.6	8.6	924	22	AAK57408	Human Immune/Haema

## ALIGNMENTS

RESULT 1	
ID	AAF95007
AAF95007	standard; DNA; 369 BP.
XX	
AC	AAF95007;
XX	
DT	23-MAY-2001 (first entry)
XX	
DE	Human ovarian cancer associated coding sequence SEQ ID NO: 199.
XX	
KW	Human, ovarian cancer; vaccine; gene therapy; carcinoma; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200118046-A2.
XX	
PD	15-MAR-2001.
XX	
PF	08-SEP-2000; 2000MO-US24827.
XX	
PR	10-SEP-1999; 99US-0394374.
PR	01-MAY-2000; 2000US-0561778.
PR	15-AUG-2000; 2000US-0640173.
PR	07-SEP-2000; 2000US-0656668.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Stolk JA.
XX	
DR	WPI: 2001-211395/21.
XX	
PT	Isolated polypeptides associated with ovarian carcinomas, and the

PT nucleic acids that encode them, useful for the prevention diagnosis and  
 PT treatment of ovarian cancers -  
 XX  
 XX  
 PS Claim 18; Page 189; 189pp; English.

CC The present invention provides a number of coding sequences and proteins,  
 CC the over-expression of which is associated with ovarian carcinoma/cancer.  
 CC These can be used in the diagnosis, treatment and prevention of ovarian  
 CC cancer, optionally by gene therapy or in the form of a vaccine. The  
 CC present sequence is an example of one of these sequences.

XX Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 99.5%; Score 367; DB 22; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-110;  
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTCTTCTTCAGGCTTTGGCGTGCAGAAATCCAGTACCA 60  
 DB 1 GGCACCTTTTGGGATGTTCTTCTTCAGGCTTTGGCGTGCAGAAATCCAGTACCA 60  
 QY 61 GGTGTAAGAAATTCACAGTACGACGCTCTCCCGAGTTCATTTGTGAATTGCAC 120  
 DB 61 GGTGTAAGAAATTCACAGTACGACGCTCTCCCGAGTTCATTTGTGAATTGCAC 120  
 QY 121 GGTGAAGTTCAGACATGTGTGAGAAAGATGATGAGCAAGTGCAGATCATGTA 180  
 DB 121 GGTGAAGTTCAGACATGTGTGAGAAAGATGATGAGCAAGTGCAGATCATGTA 180  
 QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCAGGATACCAATCCTT 240  
 DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCAGGATACCAATCCTT 240  
 QY 241 CTGCTCCCGAGGAACTGAACATGTTGTCATCAGCTGTGTAACCCCTTTGTAA 300  
 DB 241 CTGCTCCCGAGGAACTGAACATGTTGTCATCAGCTGTGTAACCCCTTTGTAA 300  
 QY 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGCCATGGCTCCGAC 360  
 DB 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGCCATGGCTCCGAC 360  
 QY 361 CACCATCTCT 369  
 DB 361 CACCATCTCT 369

## RESULT 2

ABT03274

ID ABT03274 standard; cDNA; 369 BP.

XX ABT03274;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 199.

KM Human: ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
 cytosolic; gene; ss.

XX Homo sapiens.

XX WO200239885-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US45395.

XX 14-NOV-2000; 2000US-0713550.

XX 03-APR-2001; 2001US-0825294.

XX 02-OCT-2001; 2001US-0970966.

XX (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;  
 XX  
 XX WPI; 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Example 1; Page 187; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.

XX Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 99.5%; Score 367; DB 24; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-110;  
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTCTTCTTCAGGCTTTGGCGTGCAGAAATCCAGTACCA 60  
 DB 1 GGCACCTTTTGGGATGTTCTTCTTCAGGCTTTGGCGTGCAGAAATCCAGTACCA 60  
 QY 61 GGTGTAAGAAATTCACAGTACGACGCTCTCCCGAGTTCATTTGTGAATTGCAC 120  
 DB 61 GGTGTAAGAAATTCACAGTACGACGCTCTCCCGAGTTCATTTGTGAATTGCAC 120  
 QY 121 GGTGAAGTTCAGACATGTGTGAGAAAGATGATGAGCAAGTGCAGATCATGTA 180  
 DB 121 GGTGAAGTTCAGACATGTGTGAGAAAGATGATGAGCAAGTGCAGATCATGTA 180  
 QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCAGGATACCAATCCTT 240  
 DB 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCCTTGCAGGATACCAATCCTT 240  
 QY 241 CTGCTCCCGAGGAACTGAACATGTTGTCATCAGCTGTGTAACCCCTTTGTAA 300  
 DB 241 CTGCTCCCGAGGAACTGAACATGTTGTCATCAGCTGTGTAACCCCTTTGTAA 300  
 QY 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGCCATGGCTCCGAC 360  
 DB 301 CGGGCCAAAGGCCCAAGAAAAGGGAAGTTCTGCTCGGCCCTCAGCCATGGCTCCGAC 360  
 QY 361 CACCATCTCT 369  
 DB 361 CACCATCTCT 369

## RESULT 3

ABL48956

ID ABL48956 standard; cDNA; 369 BP.

XX ABL48956;

DT 18-JUN-2002 (first entry)

DE Ovarian carcinoma sequence isolate 57887.

KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALCA/) ALGATE P A.  
 PA (FLIN/) FLING S P.

PI Xu J, Stolk JA, Algate PA, Fling SP;  
 XX  
 DR WPI; 2002-171027/22.

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer.  
 XX  
 PS  
 XX  
 XX

Claim 1a; Page 116; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilized in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The sequences  
 CC given in records ABL48760-ABL48956 represent polynucleotides encoding  
 CC ovarian carcinoma proteins.  
 CC  
 XX  
 XX  
 SQ Sequence 369 BP; 82 A; 109 C; 90 G; 86 T; 2 other;

Query Match 99.5%; Score 367; DB 24; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-110;

Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTCTGCTTNCAGCTTGCCTGCAAAATCAGTGTACCA 60  
 DB 1 GGCACCTTTTGGGATGTTCTGCTTNCAGCTTGCCTGCAAAATCAGTGTACCA 60  
 QY 61 GGTGTGAAGATTCCAGCTGAACAAGACAGCTGCTCCCGAGTTCAATTGATTCAC 120  
 DB 61 GGTGTGAAGATTCCAGCTGAACAAGACAGCTGCTCCCGAGTTCAATTGATTCAC 120  
 QY 121 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180  
 DB 121 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 180  
 QY 181 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 240  
 DB 181 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 240  
 QY 241 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 300  
 DB 241 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 300  
 QY 301 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 360  
 DB 301 GGTGAAGCTTCAAGACATGTTGTGTCAGAAAGATGATGAGCAAGTGGCGGATCATGTA 360  
 QY 361 CACCATCTCT 369  
 DB 361 CACCATCTCT 369

RESULT 4

ABK33543  
 ID ABK33543 standard; cDNA; 1524 BP.

XX AC ABK33543;

XX DT 08-MAY-2002 (first entry)

XX DE cDNA encoding human PRO protein, Seq ID No 15.

XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha; gene; ss.

XX OS Homo sapiens.

XX FM WO200208288-A2.

XX PD 31-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US21066.

XX PR 20-JUL-2000; 2000US-219556P.

XX PR 25-JUL-2000; 2000US-220585P.

XX PR 25-JUL-2000; 2000US-220605P.

XX PR 25-JUL-2000; 2000US-220607P.

XX PR 25-JUL-2000; 2000US-220624P.

XX PR 25-JUL-2000; 2000US-220638P.

XX PR 25-JUL-2000; 2000US-220664P.

XX PR 26-JUL-2000; 2000US-220693P.

XX PR 28-JUL-2000; 2000WO-US20710.

XX PR 23-AUG-2000; 2000WO-US23522.

XX PR 24-AUG-2000; 2000WO-US23328.

XX PR 15-SEP-2000; 2000US-000000P.

XX PR 10-NOV-2000; 2000WO-US30873.

XX PR 28-NOV-2000; 2000US-253646P.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 20-DEC-2000; 2000US-0747259.

XX PR 20-DEC-2000; 2000WO-US34956.

XX PR 28-FEB-2001; 2001WO-US06520.

XX PR 10-MAY-2001; 2001US-0854280.

XX PR 25-MAY-2001; 2001WO-US17092.

XX PA (GERTH ) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 XX DR P-PSDB; AAU83599.

XX WPI; 2002-172001/22.

XX P-PSDB; AAU83599.

XX Claim 2; Figure 15; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,

CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
CC PRO protein coding sequences of the invention.

XX Sequence 1524 BP; 321 A; 433 C; 435 G; 335 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1524;  
Best Local Similarity 99.2%; Pred. No. 1.1e-109;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGGATTTCTTCTTNCAGGCTTGCCTGCAATTCAGTCTACCA 60  
DB 141 GGCACTTTTGGGATTTCTTCTTNCAGGCTTGCCTGCAATTCAGTCTACCA 200  
QY 61 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 120  
DB 201 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 260  
QY 121 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 180  
DB 261 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 320  
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 240  
DB 321 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 380  
QY 241 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 300  
DB 381 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 440  
QY 301 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 360  
DB 441 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 500  
QY 361 CACCATCTT 369  
DB 501 CACCATCTT 509

RESULT 5  
ABT03277

ID ABT03277 standard; cDNA; 1619 BP.

XX ABT03277;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
cytostatic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
XX detecting the presence of ovarian cancer in a patient, and in  
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
PI

XX Claim 2; Page 189-190; 197pp; English.

XX The present invention provides human ovarian cancer associated proteins  
CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
of the invention.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1619;  
Best Local Similarity 99.2%; Pred. No. 1.2e-109;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGGATTTCTTCTTNCAGGCTTGCCTGCAATTCAGTCTACCA 60  
DB 1 GGCACTTTTGGGATTTCTTCTTNCAGGCTTGCCTGCAATTCAGTCTACCA 60  
QY 61 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 120  
DB 121 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 180  
QY 121 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 240  
DB 181 GTGTGAAGATTTCAGCTGAACAACGACTGCTCCCGAGTTCAATTGGAATTGCAC 300  
QY 181 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 240  
DB 241 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 300  
QY 241 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 360  
DB 301 CTGCTCCCGAGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 360  
QY 301 CGGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTGCAGGATCATGCTT 360  
DB 361 CACCATCTT 369  
QY 361 CACCATCTT 369  
DB 361 CACCATCTT 369

RESULT 6  
ABT03281

ID ABT03281 standard; cDNA; 1619 BP.

XX ABT03281;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
cytostatic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
XX detecting the presence of ovarian cancer in a patient, and in  
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
PI

XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 XX  
 PS Claim 2; Page 195; 197pp; English.  
 CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.  
 XX  
 SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1619;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGCGATTGTTCTTTCAGGCTTTCGCTGCAAAATCCAGTCTACCA 60  
 DB 1 GGCACTTTTGGCGATTGTTCTTTCAGGCTTTCGCTGCAAAATCCAGTCTACCA 60  
 QY 61 GTGGAAGAAATTCAGTGAACAGACGCTGCTCCGCCAGTCAATGTAATTGAC 120  
 DB 61 GTGGAAGAAATTCAGTGAACAGACGCTGCTCCGCCAGTCAATGTAATTGAC 120  
 QY 121 GGTGAACGTTCAAGACATGTGTGCAAAAAGATGATGAGCAAAATGCCGGATCATGTA 180  
 DB 121 GGTGAACGTTCAAGACATGTGTGCAAAAAGATGATGAGCAAAATGCCGGATCATGTA 180  
 QY 181 CCGCAATCTCTGTCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCAGTCTT 240  
 DB 181 CCGCAATCTCTGTCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCAGTCTT 240  
 QY 241 CTGCTCCCAAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300  
 DB 241 CTGCTCCCAAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300  
 QY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTGCGCCCTCANGCCATGGCTCCGAC 360  
 DB 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTGCGCCCTCANGCCATGGCTCCGAC 360  
 QY 361 CACCATCT 369  
 DB 361 CACCATCT 369

RESULT 7  
 ABL40345  
 ID ABL40345 standard; cDNA; 1619 BP.  
 XX  
 AC ABL40345;  
 XX  
 DT 28-JUN-2002 (First entry)  
 XX  
 DE Ovarian carcinoma sequence isolate 57887 extended cDNA.  
 XX  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW ss.  
 XX Homo sapiens.  
 XX OS  
 XX PN US2002004491-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.  
 XX  
 XX (XUJ/) XU J.  
 PA (STOLK/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 XX  
 PI XU J, Stolk JA, Algate PA, Fling SP;  
 DR WPI; 2002-171027/22.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer  
 XX  
 PS Claim 1a; Page 119-120; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the extended cDNA sequence of ovarian carcinoma  
 CC isolate 57887 given in record ABL48956.  
 XX  
 SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 99.0%; Score 365.4; DB 24; Length 1619;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACTTTTGGCGATTGTTCTTTCAGGCTTTCGCTGCAAAATCCAGTCTACCA 60  
 DB 1 GGCACTTTTGGCGATTGTTCTTTCAGGCTTTCGCTGCAAAATCCAGTCTACCA 60  
 QY 61 GTGGAAGAAATTCAGTGAACAGACGCTGCTCCGCCAGTCAATGTAATTGAC 120  
 DB 61 GTGGAAGAAATTCAGTGAACAGACGCTGCTCCGCCAGTCAATGTAATTGAC 120  
 QY 121 GGTGAACGTTCAAGACATGTGTGCAAAAAGATGATGAGCAAAATGCCGGATCATGTA 180  
 DB 121 GGTGAACGTTCAAGACATGTGTGCAAAAAGATGATGAGCAAAATGCCGGATCATGTA 180  
 QY 181 CCGCAATCTCTGTCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCAGTCTT 240  
 DB 181 CCGCAATCTCTGTCATCATCAGGCGCTGTCTCATGCTCTGCGGGATCAGTCTT 240  
 QY 241 CTGCTCCCAAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300  
 DB 241 CTGCTCCCAAGGAACTGAATCAGTTTGCATCAGTGTGCAACACCCCTTTGTA 300  
 QY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTGCGCCCTCANGCCATGGCTCCGAC 360  
 DB 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTGCGCCCTCANGCCATGGCTCCGAC 360  
 QY 361 CACCATCT 369  
 DB 361 CACCATCT 369

RESULT 8  
 ABL40349  
 ID ABL40349 standard; cDNA; 1619 BP.  
 XX

AC ABL40349;  
 XX 28-JUN-2002 (first entry)  
 XX Ovarian carcinoma 05915 nucleotide sequence.  
 DE Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 PN US2002004491-A1.  
 PD 10-JAN-2002.  
 XX 03-APR-2001; 2001US-0825294.  
 XX 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656658.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 DR WPI: 2002-171027/22.  
 XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 FT prevention and/or treatment of cancer, especially ovarian cancer.  
 PS Claim 1a; Page 125-126; 131pp; English.  
 XX The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma 05915 nucleotide sequence.  
 CC  
 XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;  
 SQ  
 Query Match 99.0%; Score 365.4; DB 24; Length 1619;  
 Best Local Similarity 99.2%; Pred No. 1.2e-109;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 181 CCGCAAGTCCTGTGCATCATCAGCGGCTGTCTCATGCTCTGCGCGGATACAGTCCTT 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 CTGCTCCCCAGGAAACTGAACCTCAGTTTGCATCAGCTGCTGCAACACCCTCTTTGTA 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 241 CTGCTCCCCAGGAAACTGAACCTCAGTTTGCATCAGCTGCTGCAACACCCTCTTTGTA 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 CGGGCCAAAGGCGCAAGAAAGGGAAGTTTGCCTCGGCGCTCANGCCATGCTCCGCAC 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 301 CGGGCCAAAGGCGCAAGAAAGGGAAGTTTGCCTCGGCGCTCANGCCATGCTCCGCAC 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 361 CACCAATCCT 369  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 361 CACCAATCCT 369  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 9  
 AAF93845  
 ID AAF93845 standard; CDNA; 1890 BP.  
 XX  
 AC AAF93845;  
 XX 23-MAY-2001 (first entry)  
 DE Human CDNA encoding a membrane or secretory protein clone PSEC0181.  
 XX  
 XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW Rheumatoid arthritis; diabetes; ss.  
 OS Homo sapiens.  
 XX Ep1067182-A2.  
 PN 10-JAN-2001.  
 XX 07-JUL-2000; 2000EP-0114090.  
 PF 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-0118775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX (HELI-) HELIX RES INST.  
 PA Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 PI WPI: 2001-093989/11.  
 DR P-PSDB; AAB88418.  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 CC gene therapy or as candidate target molecules in drug development.  
 CC  
 XX Claim 1; SEQ ID 203; 609pp + CD ROM; English.  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by  
 CC AAB88317 - AAB88419. Included in the invention are primers  
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
 CC cDNA sequences of the invention. The invention also includes methods for  
 CC the production of antibodies directed against the proteins, and cDNA  
 CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretory  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies (agonists and antagonists) may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also



CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.

SO Sequence 1890 BP: 419 A; 528 C; 533 G; 410 T; 0 other:

Query Match 99.0%; Score 365.4; DB 22; Length 1890;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGCGGATGTTCTTCTTNCAGGCTTTCGCTGCAATCCAGTGTACCA 60
  |||||||
Db 294 GGCACCTTTTGGCGGATGTTCTTCTTNCAGGCTTTCGCTGCAATCCAGTGTACCA 353
QY 61 GTGTGAAGAAATTCAGCTGGAACAAGACTGCTCCCTCCCGAGTTCAATGGAATTGCAC 120
  |||||||
Db 354 GTGTGAAGAAATTCAGCTGGAACAAGACTGCTCCCTCCCGAGTTCAATGGAATTGCAC 413
  |||||||
QY 121 GGTGAAGTTCACAGCATGTGTCAAGAAAGAGTATGAGCAAAAGTGGCGGATCATGTA 180
  |||||||
Db 414 GGTGAAGTTCACAGCATGTGTCAAGAAAGAGTATGAGCAAAAGTGGCGGATCATGTA 473
  |||||||
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTCCGCGGTACCACTCTT 240
  |||||||
Db 474 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTCCGCGGTACCACTCTT 533
  |||||||
QY 241 CTGCTCCCGAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 300
  |||||||
Db 534 CTGCTCCCGAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 593
  |||||||
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCGCTCGCCCTCAGCCATGCTCCGCAC 360
  |||||||
Db 594 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCGCTCGCCCTCAGCCATGCTCCGCAC 653
  |||||||
QY 361 CACCATCCT 369
  |||||||
Db 654 CACCATCCT 662
  |||||||

```

## RESULT 10

ABT03284  
 ID ABL03284 standard; cDNA; 1897 BP.

AC ABT03284;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PE 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;

DR WPI; 2002-500186/53.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 detecting the presence of ovarian cancer in a patient, and in

PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PS Claim 2; Page 196; 197pp; English.

CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.

SO Sequence 1897 BP: 435 A; 521 C; 532 G; 407 T; 2 other:

Query Match 99.0%; Score 365.4; DB 24; Length 1897;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-109;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GGCACCTTTTGGCGGATGTTCTTCTTNCAGGCTTTCGCTGCAATCCAGTGTACCA 60
  |||||||
Db 280 GGCACCTTTTGGCGGATGTTCTTCTTNCAGGCTTTCGCTGCAATCCAGTGTACCA 339
QY 61 GTGTGAAGAAATTCAGCTGGAACAAGACTGCTCCCTCCCGAGTTCAATGGAATTGCAC 120
  |||||||
Db 340 GTGTGAAGAAATTCAGCTGGAACAAGACTGCTCCCTCCCGAGTTCAATGGAATTGCAC 399
  |||||||
QY 121 GGTGAAGTTCACAGCATGTGTCAAGAAAGAGTATGAGCAAAAGTGGCGGATCATGTA 180
  |||||||
Db 400 GGTGAAGTTCACAGCATGTGTCAAGAAAGAGTATGAGCAAAAGTGGCGGATCATGTA 459
  |||||||
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTCCGCGGTACCACTCTT 240
  |||||||
Db 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCGCTTCCGCGGTACCACTCTT 519
  |||||||
QY 241 CTGCTCCCGAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 300
  |||||||
Db 520 CTGCTCCCGAGGAACTGAATCAGTTTGCATCAGCTGTGCAACACCCCTTTTGTAA 579
  |||||||
QY 301 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCGCTCGCCCTCAGCCATGCTCCGCAC 360
  |||||||
Db 580 CGGGCCCAAGGCCCAAGAAAGGGGAAATTTGCTCGCTCGCCCTCAGCCATGCTCCGCAC 639
  |||||||
QY 361 CACCATCCT 369
  |||||||
Db 640 CACCATCCT 648
  |||||||

```

## RESULT 11

ABL40352  
 ID ABL40352 standard; cDNA; 1897 BP.

AC ABL40352;

DT 28-JUN-2002 (first entry)

DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW ss.

OS Homo sapiens.

PN US2002004491-A1.

PD 10-JAN-2002.

PE 03-APR-2001; 2001US-0825294.

PR 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
 detecting the presence of ovarian cancer in a patient, and in

PR 15-AUG-2000; 2000US-0640173.  
PR 07-SEP-2000; 2000US-0656668.  
PR 14-NOV-2000; 2000US-0713550.  
XX  
PA (XUJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
XX  
PI XU J, STOLK JA, Algate PA, Fling SP;  
XX  
DR WPI: 2002-171027/22.  
XX  
DR P-PSDB: ABB09417.  
XX  
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
XX prevention and/or treatment of cancer, especially ovarian cancer  
XX  
PS Claim 1a; Page 127-128; 131pp; English.  
XX  
XX The invention relates to ovarian tumour polynucleotides and polypeptides  
XX that may be utilised in cancer therapy, for example in a vaccine or  
XX gene therapy. Polypeptides and polynucleotides of the invention are  
XX useful for detecting a cancer in a patient, for stimulating and/or  
XX expanding T-cells specific for a tumour protein, and for inhibiting the  
XX development of a cancer in a patient. They are also useful for  
XX stimulating an immune response in a patient, and for treating a cancer in  
XX a patient and for determining the presence of a cancer in a patient.  
XX The isolated polynucleotides of the invention are useful for their  
XX ability to selectively form duplex molecules with complementary stretches  
XX of the entire desired gene or gene fragments, and for designing and  
XX preparing ribozyme molecules for inhibiting expression of tumour  
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the  
XX invention are also useful in recombinant DNA molecules to direct  
XX expression of a polypeptide in appropriate host cells. The current  
XX sequence represents the ovarian carcinoma O1034C/O591S consensus  
XX  
SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;  
Query Match 99.0%; Score 365.4; DB 24; Length 1897;  
Best Local Similarity 99.2%; Pred. No. 1.2e-109;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
OY 1 GGCACCTTTTGGCGATTTGTTCTTCTTCAGAGGCTTGGCGGCAATCCAGTGTACCA 60  
DB 280 GGCACCTTTTGGCGATTTGTTCTTCTTCAGAGGCTTGGCGGCAATCCAGTGTACCA 339  
OY 61 GTGTGAAGATTTCCAGCTGAACACGACTGCTCTCCCGCCGAGTTGATTTGATTCAC 120  
DB 340 GTGTGAAGATTTCCAGCTGAACACGACTGCTCTCCCGCCGAGTTGATTTGATTCAC 399  
OY 121 GGTGAACCTTCAAGACATGTCTCAGAAAGATGATGAGCAAGATGGCGGATCATGTA 180  
DB 400 GGTGAACCTTCAAGACATGTCTCAGAAAGATGATGAGCAAGATGGCGGATCATGTA 459  
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACAGTCTT 240  
DB 460 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACAGTCTT 519  
OY 241 CTGCTCTCCAGGGAAGCTGACATGTTGATTCAGCTCTGCAACACCCCTTTTGTAA 300  
DB 520 CTGCTCTCCAGGGAAGCTGACATGTTGATTCAGCTCTGCAACACCCCTTTTGTAA 579  
OY 301 CGGGCCAGGCGCCAGAAAGGGAAGTCTGCTCGGCGCTCAGCCATGGCTCCGCAC 360  
DB 580 CGGGCCAGGCGCCAGAAAGGGAAGTCTGCTCGGCGCTCAGCCATGGCTCCGCAC 639  
OY 361 CACCATCTT 369  
DB 640 CACCATCTT 648  
RESULT 12

AAF22400/C  
ID AAF22400 standard; cDNA; 1953 BP.  
XX  
AC AAF22400;  
XX  
DT 26-MAR-2001 (first entry)  
XX  
DE Human secreted protein gene 28 SEQ ID NO:38.  
XX  
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; vitucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;  
KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
KW angiodysplasia; nervous system disorder; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing; skin aging;  
KW food additive; preservative; ss.  
XX  
OS Homo sapiens.  
XX  
FN W0200061629-A1.  
XX  
PD 19-OCT-2000.  
XX  
PE 06-APR-2000; 2000WO-US09071.  
XX  
PR 09-APR-1999; 99US-0128694.  
XX 20-JAN-2000; 2000US-0176931.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX  
PI Ruben SM, Komatsoulis G;  
XX  
DR WPI: 2000-647420/62.  
XX  
DR P-PSDB: AAB63161.  
XX  
PT Isolated nucleic acid molecule encoding a human secreted protein is  
XX used in preventing, treating or ameliorating a medical condition -  
XX  
PS Claim 1; Page 440; 533pp; English.  
XX  
XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134  
XX to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins  
XX and polypeptides homologous to them. Human secreted proteins have  
XX activities based on the tissues and cells the genes are expressed in.  
XX Examples of activities include: immunosuppressive; antiarthritic;  
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
XX cerebroprotective; nootropic; neuroprotective; antibacterial; vitucide;  
XX fungicide; and ophthalmological. The polynucleotides and proteins can be  
XX used to prevent, treat or ameliorate a medical condition in e.g. humans,  
XX mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are  
XX also used in diagnosing a pathological condition or susceptibility to a  
XX pathological condition. Disorders which are diagnosed or treated include  
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
XX disorders e.g. neoplasms of the breast or liver, cardiovascular  
XX disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral  
XX ischaemia, angiodysplasia, nervous system disorders e.g. Alzheimer's  
XX disease, infections caused by bacteria, viruses and fungi and ocular  
XX disorders e.g. corneal infection. The polypeptides can also be used to  
XX aid wound healing and epithelial cell proliferation, to prevent skin  
XX aging due to sunburn, to maintain organs before transplantation, for  
XX supporting cell culture of primary tissues, to regenerate tissues and in  
XX chemotaxis. The polypeptides can also be used as a food additive or  
XX preservative to increase or decrease storage capabilities. AAF22364 to  
XX AAF22372 and AAB63133 represent sequences used in the exemplification of  
XX the present invention.  
SQ Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;  
Query Match 95.5%; Score 352.4; DB 21; Length 1953;  
Best Local Similarity 98.6%; Pred. No. 2.4e-105;

Matches 364; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

OY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTCGCTGCAAAATCCAGTGTACCA 60
    |||||||
DB 1674 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTCGCTGCAAAATCCAGTGTACCA 1615
    |||||||
OY 61 GTGTGAAGATTCAGCTGAACAACGACTGCTCTCCCGAGTTGTAATTCAC 120
    |||||||
DB 1614 GTGTGAAGATTCAGCTGAACAACGACTGCTCTCCCGAGTTGTAATTCAC 1555
    |||||||
OY 121 GGTGAAGCTTCAGACATGTGTGCAAGAAAGTATGAGCAAGTCCGGGATCATGTA 180
    |||||||
DB 1554 GGTGAAGCTTCAGACATGTGTGCAAGAAAGTATGAGCAAGTCCGGGATCATGTA 1495
    |||||||
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTCCGGGATCAGTCTCT 240
    |||||||
DB 1494 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTCCGGGATCAGTCTCT 1435
    |||||||
OY 241 CTGCTCCCGCAGGAACTGAACTGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 300
    |||||||
DB 1434 CTGCTCCCGCAGGAACTGAACTGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 1375
    |||||||
OY 301 CGGCGCAAGGCCCAAGAAAGGGGAAAGTCTGCTCCGCTCCAGCCATGCTCCGAC 360
    |||||||
DB 1374 CGGCGCAAGGCCCAAGAAAGGGGAAAGTCTGCTCCGCTCCAGG-CAAGGCTCCGAC 1316
    |||||||
OY 361 CACCATCTCT 369
    |||||||
DB 1315 CACCATCTCT 1307
    |||||||

```

RESULT 13  
AAf64188/c  
AAf64188 standard; cDNA: 1956 BP.

AC AAF64188;

DT 06-APR-2001 (first entry)

DE Human secreted protein gene 13 SEQ ID NO:23.

Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
antiproliferative; cytoskeletal; cardiant; vasotropic; cerebroprotective;  
neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
ophthalmological; vulnary; autoimmune disease; cardiovascular disorder;  
hyperproliferative disorder; cerebrovascular disorder; wound healing;  
nervous system disorder; ocular disorder; skin aging; chemotaxis;  
food additive; ss.

OS Homo sapiens.

PN WO200077026-A1.

PD 21-DEC-2000.

PE 01-JUN-2000; 2000WO-US14973.

PR 11-JUN-1999; 99US-0138630.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM, Komatsoulis GA;

DR WPI: 2001-071258/08.

DR P-PSDB; AAB75518.

PT Nucleic acid molecules encoding human secreted proteins, used in  
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
PT Parkinson's diseases and cancers -  
PS Claim 1; Page 443-444; 542pp; English.

CC Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide  
CC sequences AAF64175 - AAF64224. The specification includes amino acid  
CC sequences AAB75555 - AAB75606 which represent fragments of the human  
CC secreted proteins, and protein sequences with which they share homology.  
CC The proteins and polynucleotides, their agonists and antagonists have  
CC activities dependent on the tissues and cells in which they are  
CC expressed, examples of these activities include; immunosuppressive;  
CC antithratic; antirheumatic; antiproliferative; cytoskeletal; cardiant;  
CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
CC virucide; fungicide; ophthalmological; and vulnary. The proteins,  
CC polynucleotides, agonists and antagonists can be used to treat or detect  
CC or diagnose various diseases and disorders including, autoimmune  
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders  
CC e.g. neoplasia of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angioneuromatosis, nervous system disorders e.g. Alzheimer's disease,  
CC infections caused by bacteria, viruses and fungi and ocular disorders  
CC e.g. corneal infection. The polypeptides can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin aging due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. Included in the invention are  
CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which  
CC are used in the isolation, identification and characterisation of the  
CC proteins of the invention.

Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;

Query Match 95.5%; Score 352.4; DB 22; Length 1956;  
Best Local Similarity 98.6%; Pred. No. 2,4e-105;  
Matches 364; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

OY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTCGCTGCAAAATCCAGTGTACCA 60
    |||||||
DB 1674 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTCGCTGCAAAATCCAGTGTACCA 1615
    |||||||
OY 61 GTGTGAAGATTCAGCTGAACAACGACTGCTCTCCCGAGTTGTAATTCAC 120
    |||||||
DB 1614 GTGTGAAGATTCAGCTGAACAACGACTGCTCTCCCGAGTTGTAATTCAC 1555
    |||||||
OY 121 GGTGAAGCTTCAGACATGTGTGCAAGAAAGTATGAGCAAGTCCGGGATCATGTA 180
    |||||||
DB 1554 GGTGAAGCTTCAGACATGTGTGCAAGAAAGTATGAGCAAGTCCGGGATCATGTA 1495
    |||||||
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTCCGGGATCAGTCTCT 240
    |||||||
DB 1494 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATGCTCCGGGATCAGTCTCT 1435
    |||||||
OY 241 CTGCTCCCGCAGGAACTGAACTGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 300
    |||||||
DB 1434 CTGCTCCCGCAGGAACTGAACTGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 1375
    |||||||
OY 301 CGGCGCAAGGCCCAAGAAAGGGGAAAGTCTGCTCCGCTCCAGCCATGCTCCGAC 360
    |||||||
DB 1374 CGGCGCAAGGCCCAAGAAAGGGGAAAGTCTGCTCCGCTCCAGG-CAAGGCTCCGAC 1316
    |||||||
OY 361 CACCATCTCT 369
    |||||||
DB 1315 CACCATCTCT 1307
    |||||||

```

RESULT 14  
AAf94818  
ID AAF94818 standard; cDNA: 396 BP.

AC AAF94818;

DT 23-MAY-2001 (first entry)

DE Human ovarian cancer associated coding sequence SEQ ID NO: 9.

XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.

```

XX OS Homo sapiens.
XX PN WO200118046-A2.
XX PD 15-MAR-2001.
XX PF 08-SEP-2000; 2000WO-US24827.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Stolk JA;
XX DR WPI; 2001-211395/21.
XX PT Isolated polypeptides associated with ovarian carcinomas, and the
XX PT nucleic acids that encode them, useful for the prevention diagnosis and
XX PT treatment of ovarian cancers -
XX PS Claim 5; Page 119; 189pp; English.
XX CC The present invention provides a number of coding sequences and proteins,
XX CC the over-expression of which is associated with ovarian carcinoma/cancer.
XX CC These can be used in the diagnosis, treatment and prevention of ovarian
XX CC cancer, optionally by gene therapy or in the form of a vaccine. The
XX CC present sequence is an example of one of these sequences.
XX SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match          93.1%; Score 343.4; DB 22; Length 396;
Best Local Similarity 96.8%; Pred. No. 1.1e-102;
Matches 359; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

OY 1 GGCACCTTTTGGCGATGTTCTTCTTCAGAGCTTTGCGGTGCAAAATCCAGTGTACCA 60
DB 11 GGCACCTTTTGGCGATGTTCTTCTTCAGAGCTTTGCGGTGCAAAATCCAGTGTACCA 70
OY 61 GTGTGAAGAATTCCAGCTGAACACAGACTGCTCTCCGCCGAGTTCAATTGTAATTGCAC 120
DB 71 GTGTGAAGAATTCCAGCTGAACACAGACTGCTCTCCGCCGAGTTCAATTGTAATTGCAC 130
OY 121 GGTGAACGTTCAAGCATGTGTGCAGAAAGAAAGTATGAGCAAAAGTCCGGGATCATGTA 180
DB 131 GGTGAACGTTCAAGCATGTGTGCAGAAAGAAAGTATGAGCAAAAGTCCGGGATCATGTA 190
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGC CGGGTACAGTCTT 240
DB 191 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGC CGGGTACAGTCTT 250
OY 241 CTGCTCCCGAGGAAAGTGAACCTCAGTTTGCATCAGCTGTGCAACACCCCTCTTTGTA 300
DB 251 CTGCTCCCGAGGAAAGTGAACCTCAGTTTGCATCAGCTGTGCAACACCCCTCTTTGTA 310
OY 301 CGGGCCAAAGGCGCAAGAAAAGGGGAA--GTTCGTGCTCGGCCCTCANGCCATGGCTCCGC 358
DB 311 CGGGCCAAAGGCGCAAGAAAAGGGGAAAGTTCTGNCTCGGCCCTCAGGCGAGGCTCCGC 370
OY 359 ACCACCATCTCT 369
DB 371 ACCACCATCTCT 381

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DT 05-SEP-2002 (first entry)
XX DE Human ovarian carcinoma associated coding sequence spq ID NO: 9.
XX KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX KW cytosolic; gene; ss.
XX OS Homo sapiens.
XX PN WO200239885-A2.
XX PD 23-MAY-2002.
XX PF 13-NOV-2001; 2001WO-US45395.
XX PR 14-NOV-2000; 2000US-0713550.
XX PR 03-APR-2001; 2001US-0825294.
XX PR 02-OCT-2001; 2001US-0970966.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX DR WPI; 2002-500186/53.
XX PT Novel ovarian cancer polypeptide and polynucleotide, useful for
XX PT detecting the presence of ovarian cancer in a patient, and in
XX PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX PS Example 1; Page 116; 197pp; English.
XX CC The present invention provides human ovarian cancer associated proteins
XX CC and coding sequences. The sequences can be used in the diagnosis and
XX CC treatment of ovarian cancers. The present sequence is a coding sequence
XX CC of the invention.
XX SQ Sequence 396 BP; 90 A; 117 C; 95 G; 92 T; 2 other;

Query Match          93.1%; Score 343.4; DB 24; Length 396;
Best Local Similarity 96.8%; Pred. No. 1.1e-102;
Matches 359; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

OY 1 GGCACCTTTTGGCGATGTTCTTCTTCAGAGCTTTGCGGTGCAAAATCCAGTGTACCA 60
DB 11 GGCACCTTTTGGCGATGTTCTTCTTCAGAGCTTTGCGGTGCAAAATCCAGTGTACCA 70
OY 61 GTGTGAAGAATTCCAGCTGAACACAGACTGCTCTCCGCCGAGTTCAATTGTAATTGCAC 120
DB 71 GTGTGAAGAATTCCAGCTGAACACAGACTGCTCTCCGCCGAGTTCAATTGTAATTGCAC 130
OY 121 GGTGAACGTTCAAGCATGTGTGCAGAAAGAAAGTATGAGCAAAAGTCCGGGATCATGTA 180
DB 131 GGTGAACGTTCAAGCATGTGTGCAGAAAGAAAGTATGAGCAAAAGTCCGGGATCATGTA 190
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGC CGGGTACAGTCTT 240
DB 191 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGC CGGGTACAGTCTT 250
OY 241 CTGCTCCCGAGGAAAGTGAACCTCAGTTTGCATCAGCTGTGCAACACCCCTCTTTGTA 300
DB 251 CTGCTCCCGAGGAAAGTGAACCTCAGTTTGCATCAGCTGTGCAACACCCCTCTTTGTA 310
OY 301 CGGGCCAAAGGCGCAAGAAAAGGGGAA--GTTCGTGCTCGGCCCTCANGCCATGGCTCCGC 358
DB 311 CGGGCCAAAGGCGCAAGAAAAGGGGAAAGTTCTGNCTCGGCCCTCAGGCGAGGCTCCGC 370
OY 359 ACCACCATCTCT 369
DB 371 ACCACCATCTCT 381

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Fri Nov 8 18:56:48 2002

us-09-970-966-199.std.rng

Page 11

Job time : 78.6545 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:53:42 ; Search time 13.8273 Seconds  
(without alignments)  
8184.096 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggcacatttgcggatgtt.....tgctccgcacacatcct 369

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 443362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2\_6/pdata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/pdata/1/ina/5A.COMB.seq:\*  
4: /cgn2\_6/pdata/1/ina/5B.COMB.seq:\*  
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6: /cgn2\_6/pdata/1/ina/5B.COMB.seq:\*

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.8	9.2	4403765	US-09-103-840A-2	Sequence 2, Appli
2	31.8	8.6	759	US-08-484-126-6	Sequence 6, Appli
3	30.4	8.2	3373	US-08-897-443-2	Sequence 2, Appli
4	30.4	8.2	152331	US-09-128-155-16	Sequence 16, Appli
5	30.4	8.2	176373	US-09-128-155-17	Sequence 17, Appli
6	30.2	8.2	327	US-09-443-184-67	Sequence 67, Appli
7	30	8.1	4154	US-08-131-365B-37	Sequence 37, Appli
8	30	8.1	4154	US-08-668-123-37	Sequence 37, Appli
9	29.6	8.0	2205	US-08-035-392-3	Sequence 3, Appli
10	29.6	8.0	2205	US-08-504-511A-3	Sequence 3, Appli
11	29.2	7.9	1534	US-08-592-126-97	Sequence 97, Appli
12	28.8	7.8	1107	US-08-292-845-5	Sequence 5, Appli
13	28.8	7.8	1107	US-08-252-073A-5	Sequence 5, Appli
14	28.8	7.8	1107	US-08-252-073A-5	Sequence 5, Appli
15	28.8	7.8	4403765	US-09-103-840A-2	Sequence 2, Appli
16	28.8	7.8	4411529	US-09-103-840A-2	Sequence 2, Appli
17	28.6	7.8	637	US-09-280-116-42	Sequence 42, Appli
18	28.4	7.7	500	US-08-998-416-35	Sequence 35, Appli
19	28.2	7.6	2470	US-07-745-206A-14	Sequence 14, Appli
20	28.2	7.6	2470	US-08-311-363-14	Sequence 14, Appli
21	28.2	7.6	5467	US-07-745-206A-12	Sequence 12, Appli
22	28.2	7.6	5467	US-08-311-363-12	Sequence 12, Appli
23	28.2	7.6	6519	US-08-588-985-1	Sequence 1, Appli
24	28.2	7.6	6519	US-08-588-985-1	Sequence 1, Appli
25	28	7.6	570	US-09-095-855-202	Sequence 202, App
26	28	7.6	570	US-09-095-855-202	Sequence 202, App
27	28	7.6	6085	US-09-479-122-8	Sequence 8, Appli

28	27.8	7.5	8060	US-08-766-528-1	Sequence 1, Appl
29	27.6	7.5	343	US-09-423-233-27	Sequence 27, Appl
30	27.6	7.5	344	US-09-423-233-26	Sequence 26, Appl
31	27.6	7.5	3355	US-08-991-944-3	Sequence 3, Appl
32	27.6	7.5	3812	US-09-784-316-1	Sequence 1, Appl
33	27.4	7.4	656	US-09-404-879A-313	Sequence 313, Appl
34	27.4	7.4	3487	US-08-410-540-4	Sequence 4, Appl
35	27.4	7.4	7680	PCT-US95-09819-6	Sequence 6, Appl
36	27.4	7.4	7705	US-08-259-569-16	Sequence 16, Appl
37	27.4	7.4	7705	US-08-826-885-16	Sequence 16, Appl
38	27.4	7.4	7705	545158-2	Patent No. 545158
39	27.4	7.4	7803	US-08-551-356-1	Sequence 1, Appl
40	27.4	7.4	7803	PCT-US93-12687-1	Sequence 1, Appl
41	27.2	7.4	818	US-09-154-083-25	Sequence 25, Appl
42	27.2	7.4	1828	US-08-858-207A-52	Sequence 52, Appl
43	27.2	7.4	2248	US-09-393-554-10	Sequence 10, Appl
44	27.2	7.4	3563	US-09-041-886-20	Sequence 20, Appl
45	27.2	7.4	3596	US-08-779-801-5	Sequence 5, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6284328
;
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
;
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
;
; LENGTH: 4403765
;
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
;
; FEATURE:
;
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
;
; US-09-103-840A-2
;
; Query Match
; Best Local Similarity 9.2%; Score 33.8; DB 4; Length 4403765;
; Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
;
; QY 203 GCGGCTGTCATCGCTGCGGCTACAGTCTTGTGTCCTCCAGGAACTGAAAC 262
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; DB 2688777 GCGGCTTGGGGGGGCGGCAATCGTTGGCCCGGCGCCCTCGAACCAGAA 2688778
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; QY 263 TGAAGTTGATCAGCTGCTGCAACACCCCTTTGTGAAGGGCCAGGCCAAGAAAG 322
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; DB 2688777 CCAGCTCATATGCTGCGATCGGCGCATCACCAGCCGAGACGACGCGATG 2688718
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; QY 323 GGAAGTTCGGCC 335
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; DB 2688717 ATCAGTGAACCT 2688705
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
;
; RESULT 2
; US-08-484-126-6
; Sequence 6, Application US/08484126
; Patent No. 598565
;
; GENERAL INFORMATION:
; APPLICANT: Anderson, W. French
; APPLICANT: Baltrick, Leon F.
```

1 APPLICANT: Mason, James M.  
2 TITLE OF INVENTION: Targetable Vector Particles  
3 NUMBER OF SEQUENCES: 8  
4 CORRESPONDENCE ADDRESS:  
5 ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
6 ADDRESSEE: Cecchi, Stewart & Olstein  
7 STREET: 6 Becker Farm Road  
8 CITY: Roseland  
9 STATE: New Jersey  
10 COUNTRY: USA  
11 ZIP: 07068  
12  
13 COMPUTER READABLE FORM:  
14 MEDIUM TYPE: 3.5 inch diskette  
15 COMPUTER: IBM PS/2  
16 OPERATING SYSTEM: MS-DOS  
17 SOFTWARE: Word Perfect 5.1  
18  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/484,126  
21 FILING DATE: 07-JUN-1995  
22 CLASSIFICATION: 435  
23  
24 PRIOR APPLICATION DATA:  
25 APPLICATION NUMBER: 08/326,347  
26 FILING DATE: 20-OCT-1994  
27 APPLICATION NUMBER: 08/973,307  
28 FILING DATE: 09-NOV-1992  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: Lillie, Raymond J.  
31 REGISTRATION NUMBER: 31,778  
32  
33 REFERENCE/DOCKET NUMBER: 271010-281  
34  
35 TELECOMMUNICATION INFORMATION:  
36 TELEPHONE: 201-994-1700  
37 TELEFAX: 201-994-1744  
38  
39 INFORMATION FOR SEQ ID NO: 6:  
40 SEQUENCE CHARACTERISTICS:  
41 LENGTH: 759 bases  
42 TYPE: nucleic acid  
43 STRANDEDNESS: single  
44 TOPOLOGY: linear  
45  
46 MOLECULE TYPE: genomic DNA  
47 PUBLICATION INFORMATION:  
48 AUTHORS: Ray, et al.  
49  
50 TITLE:  
51 JOURNAL: Biochem. and Biophys. Res. Comm.  
52 VOLUME: 178  
53 ISSUE: NO. 2  
54 PAGES: 507-513  
55 DATE: 1991  
56  
57 US-08-484-126-6

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Query Match          8.6%; Score 31.8; DB 2, Length 759;
Best Local Similarity 50.7%; Pred. No. 0.61;
Matches 75; Conservative 0; Mismatches 73; Indels 0; Gaps 0.

QY      220 CTCTGCGGGAGTACAGTCCTCTGTGCTCCGCCAAGAACTGAATCAGTTGCATCAGCTG 279
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       3   CTCCTCCGTGGCTCCAGCGCTCTGTGTCTACAGCATGAGCCCTCGCCCTGGAGCCCTG 62
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      280 CTGCAACACCCTCTCTTTGTAAAGGGCCCAAGGCCCAAGAAAAGGGAAGTTCGTGCTGGC 339
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       63 CTGACCTCTCTCTCTCTGTGTGATCATCCCCAGGACACAGCCTGTGCCAACCTTCGACCA 122
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      340 CCTCANGCCATGAGTCCGACACCACCATC 367
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      123 CCTATCACCAATGCACCCCTGGACCAAGC 150
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-08-897-443-2/c
: Sequence 2, Application US/08897443
: Patent No. 5981263
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Lal, Preeti
:
```

```

1  APPLICANT: Corley, Neil C.
2  APPLICANT: Shah, Purvi
3  APPLICANT: Kaser, Mathew
4  TITLE OF INVENTION: HUMAN MATRILIN-3
5  NUMBER OF SEQUENCES: 4
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Incyte Pharmaceuticals, Inc.
8  STREET: 3174 Porter Drive
9  CITY: Palo Alto
10 STATE: CA
11 COUNTRY: USA
12 ZIP: 94304
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Diskette
15 COMPUTER: IBM Compatible
16 OPERATING SYSTEM: DOS
17 SOFTWARE: FastSeq for Windows Version 2.0
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/897,443
20 FILING DATE: Filed Herewith
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:
23 FILING DATE:
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Billings, Lucy J.
26 REGISTRATION NUMBER: 36,749
27 REFERENCE/DOCKET NUMBER: PF-0348 US
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 415-855-0555
30 TELEFAX: 415-845-4166
31 INFORMATION FOR SEQ ID NO: 2:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 3373 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 IMMEDIATE SOURCE:
38 LIBRARY: UTRSN0702
39 CLONE: 681719
40 US-08-897-443-2

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Query Match Similarity      8.2%; Score 30.4; DB 2; Length 337;
Best Local Similarity      46.4%; Pred. No. 3.6;
Matches    97; Conservative    0; Mismatches   112; Indels     0; Gaps     0;

QY      161 CAAAGTGGCGGGAATCATVATTACCGCAAGTCGTGCATCATCAGCGCCGTGCTCATCGCC 220
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       638 CCAATGGCAAGATTAGATGATGCCCTGTCCGTGCTTAGCACGCAACCTGGSCACGGAG 579

QY      221 TCTGCGGGGTAACAATCCTTTCTGCTCCCCAGGAAAAGTGAAGTCAATTCATCAACTG 280
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       578 TCTGAGGCTCTCCCATCTGTACAGATCAATTAAGACCCTGGACACATTCCTCCTCAGGGGC 519

QY      281 TGCAACACCCTCTTTTGTAACGGGCGAAGGCCCAAGAAAGSGAAGTTCTGCCCTCGGCC 340
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       518 CGGGCCCCCTCTGCTTGTGAGAGATCGAATGTTCAAGGCAATACTGATGGCCAGCCCGTTC 459

QY      341 CTCANGCCATGGCTCCGCACCAACATCTCT 369
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       458 ATGTGCCCCGTGGACAGATGCCGCACTCT 430


RESULT 4
US-09-128-155-16/c
: Sequence 16, Application US/09128155
: Patent No. 6117654
: GENERAL INFORMATION:
: APPLICANT: Pan, Yang
: TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: 09404/052001
: CURRENT APPLICATION NUMBER: US/09/128.155
: CURRENT FILING DATE: 1998-08-03

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EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 16  
LENGTH: 152331  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(152331)  
OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-16

Query Match 8.2%: Score 30.4; DB 3; Length 152331;  
Best Local Similarity 49.4%: Pred. No. 22;  
Matches 79; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 36 TTGGCTGCAATCCAGTGTACAGTGTGAAGATTCAGCTGCAACGACGCTGCTCT 95  
DB 106016 TTGGGTCGAGTACATTTGGGGATGAGGGAGCTGTAAAGACAGCTTGACCTTTCT 105957  
QY 96 CCCCCAGTTCATTTGATTCGACGCTGAACCTTCAAGACATGTGTGAGAAAGTGA 155  
DB 105956 TCTACCACTACCTGCTCATTTGAATTTTGAAGAAAAAACTCAGAGAGAGAGA 105897

QY 156 TGGAGCAAGTCCGGGATCATGTACCGCAAGTCTCTGTC 195  
DB 105896 AGGAGCAGAGAGAGAGAGATGTATTTAAAGTATTTGC 105857

RESULT 5  
US-09-128-155-17  
Sequence 17, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 176373  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(176373)  
OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-17

Query Match 8.2%: Score 30.4; DB 3; Length 176373;  
Best Local Similarity 49.4%: Pred. No. 23;  
Matches 79; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 36 TTGGCTGCAATCCAGTGTACAGTGTGAAGATTCAGCTGCAACGACGCTGCTCT 95  
DB 77454 TTGGGTCGAGTACATTTGGGGATGAGGGAGCTGTAAAGACAGCTTGACCTTTCT 77513  
QY 96 CCCCCAGTTCATTTGATTCGACGCTGAACCTTCAAGACATGTGTGAGAAAGTGA 155  
DB 77514 TCTACCACTACCTGCTCATTTGAATTTTGAAGAAAAAACTCAGAGAGAGAGA 77573  
QY 156 TGGAGCAAGTCCGGGATCATGTACCGCAAGTCTCTGTC 195

DB 77574 AGGAGCAGAGAGAGAGAGATGTATTTAAAGTATTTGC 77613

RESULT 6  
US-09-443-184-67  
Sequence 67, Application US/09443184A  
Patent No. 6372431  
GENERAL INFORMATION:  
APPLICANT: Cunningham, Mary Jane  
APPLICANT: Zweigler, Gary  
APPLICANT: Kaser, Matthew R.  
APPLICANT: Panzer, Scott  
APPLICANT: Seilhammer, Jeffrey J.  
APPLICANT: Yue, Henry  
APPLICANT: Baughn, Mariah  
APPLICANT: Azimzal, Yalda  
APPLICANT: Lai, Preeti  
TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS  
FILE REFERENCE: PC-0007 US  
CURRENT APPLICATION NUMBER: US/09/443,184A  
CURRENT FILING DATE: 1999-11-19  
NUMBER OF SEQ ID NOS: 138  
SOFTWARE: PERL Program  
SEQ ID NO 67  
LENGTH: 327  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. 6372431 701649802H1  
US-09-443-184-67

Query Match 8.2%: Score 30.2; DB 4; Length 327;  
Best Local Similarity 50.0%: Pred. No. 1.4;  
Matches 74; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 150 AACTGATGAGCAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 209  
DB 36 AACTGATGAGCAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATCAGCGGCT 95  
QY 210 GTTCATGCGCTCTGCGGATGACGCTGTGCTCCAGGAGAACTGACTGATT 269  
DB 96 GGCATATGCGGCTCTGCGGATGACGCTGTGCTCCAGGAGAACTGACTGATT 155  
QY 270 GCATGAGTGTGCAACACCCCTTTG 297  
DB 156 CCCTCCCTGCTGTGAGCTCTTTG 183

RESULT 7  
US-08-131-365B-37  
Sequence 37, Application US/08131365B  
Patent No. 5527690  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESS: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.

```

21P: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/131,365B
FILING DATE: 01-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTS:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 4154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 167..3607
US-08-131-365B-37

Query Match 8.1%; Score 30; DB 1; Length 4154;
Best Local Similarity 56.8%; Pred. No. 5.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Oy 262 CTCAGTTGCATGACGCTGCACACACCCCTCTTGTAACGGGCGCACGCCCAAGAAAG 321
    ||||| 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1711 CTCAGATACACACACGCGCTGTACATAGCCCTGGGGCGCAACGTGCTGGCACCGAGACAG 1770
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Oy 322 GGGAAGTTCGCTCGCGCCCTCANGCATGCGCTCC 356
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1771 AGATGGCCCTGCTGGCGCCACGATGGCTGCTGCCCC 1805

RESULT 8
US-08-668-123-37
Sequence 37, Application US/08668123
Patent No. 5891631
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

```

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1 APPLICATION NUMBER: 08/131,365
2 FILING DATE: 01-OCT-1993
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Parker, David L.
5 REGISTRATION NUMBER: 32,165
6 REFERENCE/DOCKET NUMBER: UTSD:372/PAR
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (512) 418-3000
9 TELEFAX: (512) 474-7577
10 INFORMATION FOR SEQ ID NO: 37:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 4154 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: other nucleic acid
17 FEATURE:
18 DESCRIPTION: /desc = "DNA"
19 NAME/KEY: CDS
20 LOCATION: 167..3607
21 US-08-668-123-37
22
23 Query Match 8.1%; Score 30; DB 2; Length 4154;
24 Best Local Similarity 56.8%; Pred. NO. 5.4;
25 Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0.
26
27 QY 262 CTCGATTGTTCATCAGCTCTCGACACCCCTCTTGTACGGGCCAAGCCCAAGAAAG 321
28 | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
29 Db 1711 CTCGATATACCACACGACGCTCTACCATAGCCCTGGGGCAACGTCGTGGGCAGAGCAG 1770
30 | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
31 QY 322 GGGAAGTTCTGCTCGCTCGCCCTTCANGCCATGCTCC 356
32 | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
33 Db 1771 AGATGCCCTTGCTGGCCCACTGCTGCTGCC 1805
34 | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
35
36 RESULT 9
37 US-08-035-392-3/C
38 ; Sequence 3, Application US/08035392
39 ; Patent No. 5484732
40 ; GENERAL INFORMATION:
41 APPLICANT: Rosenfeld, M. G.
42 APPLICANT: Andersen, B.
43 TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
44 TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
45 NUMBER OF SEQUENCES: 4
46 CORRESPONDENCE ADDRESS:
47 ADDRESSEE: Spensley Horn Jubas & Lubitz
48 STREET: 1880 Century Park East - Suite 500
49 CITY: Los Angeles
50 STATE: California
51 COUNTRY: USA
52 ZIP: 90067
53 COMPUTER READABLE FORM:
54 MEDIUM TYPE: Floppy disk
55 COMPUTER: IBM PC compatible
56 OPERATING SYSTEM: PC-DOS/MS-DOS
57 SOFTWARE: Patent Release #1.0, Version #1.25
58 CURRENT APPLICATION DATA:
59 APPLICATION NUMBER: US/08/035,392
60 FILING DATE: 19930322
61 CLASSIFICATION: 435
62 ATTORNEY/AGENT INFORMATION:
63 NAME: Howells, Stacy L.
64 REGISTRATION NUMBER: 34,842
65 REFERENCE/DOCKET NUMBER: PD-2607
66 TELECOMMUNICATION INFORMATION:
67 TELEPHONE: (619) 455-5100
68 TELEFAX: (619) 455-5110
69 INFORMATION FOR SEQ ID NO: 3:
70 SEQUENCE CHARACTERISTICS:
71 LENGTH: 2205 base pairs
72 TYPE: NUCLEIC ACID
73 STRANDEDNESS: single

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TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: Skn-1a  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..1338  
US-08-035-392-3

Query Match 8.0%; Score 29.6; DB 1; Length 2205;  
Best Local Similarity 64.7%; Pred. No. 5.4;  
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 245 TCCCGAGGGAAGTGAAGTGTTCATGAGTGTGCAACACCCCTTTGTAAGGG 304  
DB 92 TCCCGAGTATCTGTGTCATGAGTGTGCAAGTTCACCATCTCCGACGGG 33  
QY 305 CCAAGGCC 312  
DB 32 CCAAGGCC 25

RESULT 10  
US-08-504-511A-3/C

Sequence 3, Application US/08504511A  
Patent No. 5561224

GENERAL INFORMATION:  
APPLICANT: Rosenfield, M. G.

TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION

NUMBER OF SEQUENCES: 8  
OF THE DEVELOPMENT OF SKIN AND HAIR

CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla

STATE: California  
COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/504,511A

FILING DATE: 20-JUL-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.

REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/002002

TELEPHONE: (619) 678-3070  
TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2205 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:

CLONE: Skn-1a  
FEATURE:

NAME/KEY: CDS  
LOCATION: 46..1338  
US-08-504-511A-3

Query Match 8.0%; Score 29.6; DB 1; Length 2205;  
Best Local Similarity 64.7%; Pred. No. 5.4;  
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 245 TCCCGAGGGAAGTGAAGTGTTCATGAGTGTGCAACACCCCTTTGTAAGGG 304  
DB 92 TCCCGAGTATCTGTGTCATGAGTGTGCAAGTTCACCATCTCCGACGGG 33  
QY 305 CCAAGGCC 312  
DB 32 CCAAGGCC 25

RESULT 11  
US-08-592-126-97/C

Sequence 97, Application US/08592126  
Patent No. 5821091

GENERAL INFORMATION:  
APPLICANT: Gregory Dolganov

TITLE OF INVENTION: Transcripts Encoding Immunomodulatory

NUMBER OF SEQUENCES: 151  
POLYPEPTIDES

CORRESPONDENCE ADDRESS:  
ADDRESS: Denlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto

STATE: CA  
COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,126

FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Shultz, Charles K.

REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 4600-0111

TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1534 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Septin-2.seq  
US-08-592-126-97

Query Match 7.9%; Score 29.2; DB 1; Length 1534;  
Best Local Similarity 46.3%; Pred. No. 6.1;  
Matches 94; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 167 GCCGGATCATGTACCCAGTCTGTCATCAGGAGGCTGTCATGCGCTGCGC 226  
DB 1392 GCGTGTGCTCTCTCCAGTCCGCGGCTTTCTCTCACCCTTGCTCTCTCG 1333  
QY 227 GGGTACCAAGTCTTCTGCTCCCGAGGAACTGAAGTGTGATGAGTGTGCAAC 286  
DB 1332 TGGACCGGCTTCAGAGTGTCAAACTTCATGAGAGCTCCCTTCTCTGAGCTCC 1273  
QY 287 ACCCTCTTTGTAAGCGGCGCAAGGCCCAAGAAAGGGAAGTTCGCTCGGCTCGANG 346  
DB 1272 AGCTCTGCTCTCTCTCACTTGTGACAAACATCTGCTCATCTCTCTCTCTGTC 1213  
QY 347 CCATGCGTCCGACACCATCT 369  
DB 1212 AGTCACTTGAAGACTCTCTCT 1190



Search completed: November 7, 2002, 15:58:03  
Job time : 3169.83 secs

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APPLICATION NUMBER: PCT/US93/12074
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,337
FILING DATE: 10-DEC-1992
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Murine
PCT-US93-12074-5

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Query Match
Best Local Similarity 7.8%; Score 28.8; DB 5; Length 1107;
Matches 78; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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QY 68 GAATTCAGTGAACAGAGTCTCTCCCGAGTTGATGTGATGACAGGTGAC 127
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Db 345 GAATACAGGGTGAATAATTACTTCAAGTGAATAGATATTGTGCTGAGATAT 404
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QY 128 GTTCAAGACATGTGTCAAGAAAGAGTGAAGCAAGTCCGGATCATACCGCAG 187
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Db 405 GTTCAAGACATGTGTCAAGAAAGAGTGAAGCAAGTCCGGATCATACCGCAG 187
    ||| | | | | | | | | | | | | | | | | | | | | | | | |

QY 188 TCCGTGATCATGAGCGGCTGTCTCATCCGCTGCGG 227
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Db 465 TATGGCCCCGAGCAGAGAGTACGAATTCTCACTCCAG 504
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RESULT 15
US-09-103-840A-2
: Sequence 2, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-2007.00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 4403765
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: FEATURE:
: OTHER INFORMATION: CDC 1551
: OTHER INFORMATION: "n" bases at various positions throughout the sequence
: OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Query Match
Best Local Similarity 7.8%; Score 28.8; DB 4; Length 4403765;
Matches 42; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 299 AACGGGCGAAGCCCAAGAAAGAGTTCCTGCGCCCTCAGCCGCTCCGC 358
    ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2200565 AAGGGCGAAGCGAATATCAAGCAAGCCCGCGGCTCTCAAGTTCTCG 2200624
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QY 359 ACCAC 363
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Db 2200625 AACAC 2200629
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 13:45:13 ; Search time 16.0364 Seconds  
(without alignments)  
8163.686 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggcacacttttgcgagatgt.....tggctcgcacacacatcct 369

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCPUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	99.5	369	10	US-09-825-294-199
2	365.4	99.0	1619	10	US-09-825-294-205
3	365.4	99.0	1619	10	US-09-825-294-211
4	365.4	99.0	1897	10	US-09-825-294-214
5	343.4	93.1	396	10	US-09-825-294-9
6	341.8	92.6	1010	10	US-09-825-294-212
7	196.8	53.3	480	10	US-09-825-294-212
8	86.4	23.4	430	10	US-09-825-294-212
9	32.6	8.8	407	10	US-09-867-701-4251
10	32.6	8.8	412	10	US-09-960-352-3015
11	32.6	8.8	423	10	US-09-960-352-3015
12	32.6	8.8	458	10	US-09-960-352-9456
13	31.6	8.6	544	10	US-09-834-975-1886
14	31.6	8.6	775	10	US-09-770-445-893
15	31.4	8.5	1656	12	US-10-033-109-13
16	30.6	8.3	7386	10	US-09-764-855-208
17	30.2	8.2	498	10	US-09-783-590-457
18	30.2	8.2	1063	10	US-09-764-898-137
19	29.4	8.0	4780	10	US-09-886-241-1

20	29.2	7.9	484	10	US-09-764-846-66	Sequence 66, App1
21	29.2	7.9	713	10	US-09-764-846-136	Sequence 136, App
22	29.2	7.9	1347	10	US-09-822-830A-187	Sequence 187, App
23	29.2	7.9	1518	9	US-09-934-060A-23	Sequence 23, App1
24	29.2	7.9	1518	9	US-09-934-060A-29	Sequence 29, App1
25	29.2	7.9	1668	9	US-09-934-060A-1	Sequence 5, App1
26	29.2	7.9	2159	9	US-09-934-060A-1	Sequence 1, App1
27	29.2	7.9	2159	9	US-09-934-060A-3	Sequence 3, App1
28	29.2	7.9	4344	10	US-09-880-107-1754	Sequence 1754, Ap
29	29.2	7.9	4870	12	US-10-044-090-121	Sequence 121, App
30	29.2	7.9	373	10	US-09-878-574-964	Sequence 964, App
31	28.8	7.8	296	10	US-09-974-300-6410	Sequence 97, App1
32	28.8	7.8	3449	9	US-09-905-291A-33	Sequence 33, App1
33	28.8	7.8	3449	10	US-09-909-320-33	Sequence 33, App1
34	28.8	7.8	3449	10	US-09-909-088B-33	Sequence 33, App1
35	28.8	7.8	212	10	US-09-864-761-21354	Sequence 21354, A
36	28.6	7.8	377	10	US-09-880-107-1729	Sequence 1729, Ap
37	28.6	7.8	466	10	US-09-864-761-4612	Sequence 4612, Ap
38	28.6	7.8	1995	10	US-09-780-525-1	Sequence 1, App1
39	28.6	7.8	264	10	US-09-923-876-5109	Sequence 5109, App
40	28.4	7.7	415	10	US-09-960-352-14418	Sequence 14418, A
41	28.4	7.7	628	10	US-09-764-853-72	Sequence 72, App1
42	28.4	7.6	404	10	US-09-867-701-5083	Sequence 5083, Ap
43	28.2	7.6	440	10	US-09-783-590-6440	Sequence 6440, Ap
44	28.2	7.6	470	10	US-09-867-701-5284	Sequence 5284, Ap
45	28.2	7.6				

## ALIGNMENTS

RESULT 1  
US-09-825-294-199 Application US/09825294  
; Sequence 199, App  
; Patent No. US200200491A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
; CURRENT FILING DATE: 210121.484C5  
; CURRENT APPLICATION NUMBER: US/09/825,294  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 199  
; LENGTH: 369  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(369)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-199

Query Match 99.5%; Score 367; DB 10; Length 369;  
Best Local Similarity 100.0%; Pred. No. 1.6e-111;  
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATGTTGCTTNCAGCTTGGCGTCAATTCAGTCTACCA 60  
DB 1 GGCACCTTTTGGCGATGTTGCTTNCAGCTTGGCGTCAATTCAGTCTACCA 60  
QY 61 GGTGAAGATTCACGCTGACGACGCTCTCCCGAGATTCATGTAATTCAC 120  
DB 61 GGTGAAGATTCACGCTGACGACGCTCTCCCGAGATTCATGTAATTCAC 120  
QY 121 GGTGAAGCTTCAAGCATGTGTCAGAAAGATGAGCAAGTCCCGGATCATGTA 180  
DB 121 GGTGAAGCTTCAAGCATGTGTCAGAAAGATGAGCAAGTCCCGGATCATGTA 180

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QY 181 CCGCAAGTCCTGTCATCATCAGCGGCGCTGTCATCGGCTGCGGGTACCACTCTT 240
DB 181 CCGCAAGTCCTGTCATCATCAGCGGCGCTGTCATCGGCTGCGGGTACCACTCTT 240
QY 241 CTGCTCCCCAGGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CTGCTCCCCAGGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

RESULT 2
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Steven P.
; TITLE OF INVENTION: THERAPY AND METHODS FOR THE
; TITL OF INVENTION: THERAPY AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205

Query Match 99.0%; Score 365.4; DB 10; Length 1619;
Best Local Similarity 99.2%; Pred. No. 1,1e-110;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCACTTTTGGGATGTTGCTTCTGCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 60
DB 1 GCGCACTTTTGGGATGTTGCTTCTGCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACAGAGCTGCTCCCGGAGTTGATGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGCTGACAGAGCTGCTCCCGGAGTTGATGTAATTCAC 120
QY 121 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
DB 121 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTCATCATCAGCGGCGCTGTCATCGGCTGCGGGTACCACTCTT 240
DB 181 CCGCAAGTCTGTCATCATCAGCGGCGCTGTCATCGGCTGCGGGTACCACTCTT 240
QY 241 CTGCTCCCCAGGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CTGCTCCCCAGGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

RESULT 3
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US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Steven P.
; TITLE OF INVENTION: THERAPY AND METHODS FOR THE
; TITL OF INVENTION: THERAPY AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211

Query Match 99.0%; Score 365.4; DB 10; Length 1619;
Best Local Similarity 99.2%; Pred. No. 1,1e-110;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGCACTTTTGGGATGTTGCTTCTGCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 60
DB 1 GCGCACTTTTGGGATGTTGCTTCTGCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACAGAGCTGCTCCCGGAGTTGATGTAATTCAC 120
DB 61 GTGTGAAGATTCACAGCTGACAGAGCTGCTCCCGGAGTTGATGTAATTCAC 120
QY 121 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
DB 121 GGTGAAGCTTCAAGACATGTCAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTCATCATCAGCGGCGCTGTCATCGGCTGCGGGTACCACTCTT 240
DB 181 CCGCAAGTCTGTCATCATCAGCGGCGCTGTCATCGGCTGCGGGTACCACTCTT 240
QY 241 CTGCTCCCCAGGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CTGCTCCCCAGGGAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CCGGCGCAAGGCGCAAGAAAGGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CACCATCTCT 369
DB 361 CACCATCTCT 369

RESULT 4
US-09-825-294-214
; Sequence 214, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Steven P.
; TITLE OF INVENTION: THERAPY AND METHODS FOR THE
; TITL OF INVENTION: THERAPY AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
```



ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1897)  
OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-214

Query Match  
Best Local Similarity 99.0%; Score 365.4; DB 10; Length 1897;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATGTTCTTCTTNCAGCCTTTGCGCTGCAATTCAGTGTACCA 60  
DB 280 GGCACCTTTTGGCGATGTTCTTCTTNCAGCCTTTGCGCTGCAATTCAGTGTACCA 339  
QY 61 GTGTGAAGATTCAGCTGAACAAGCAGCTCTCTCCCGAGTTCAATGGAATTCAC 120  
DB 340 GTGTGAAGATTCAGCTGAACAAGCAGCTCTCTCCCGAGTTCAATGGAATTCAC 399  
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180  
DB 400 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 459  
QY 181 CGCAGATCTGTGATCATCAGCGGCTGTCTCATCGCCTCTCCGGGTACAGTCTT 240  
DB 460 CGCAGATCTGTGATCATCAGCGGCTGTCTCATCGCCTCTCCGGGTACAGTCTT 519  
QY 241 CTGCTCCCGAGGAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 520 CTGCTCCCGAGGAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 579  
QY 301 CGGCGCAAGGCCCAAGAAAGGAGGAGTCTGCTCGGCTTCAGGCTGCTCCGAC 360  
DB 580 CGGCGCAAGGCCCAAGAAAGGAGGAGTCTGCTCGGCTTCAGGCTGCTCCGAC 639  
QY 361 CACCATCT 369  
DB 640 CACCATCT 648

RESULT 5  
US-09-825-294-9  
Sequence 9, Application US/09825294  
Patent No. US2002000491A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 396  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(396)  
OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-9

Query Match  
Best Local Similarity 93.1%; Score 343.4; DB 10; Length 396;  
Matches 359; Conservative 0; Mismatches 10; Indels 2; Gaps 1;  
QY 1 GGCACCTTTTGGCGATGTTCTTCTTNCAGCCTTTGCGCTGCAATTCAGTGTACCA 60  
DB 11 GGCACCTTTTGGCGATGTTCTTCTTNCAGCCTTTGCGCTGCAATTCAGTGTACCA 70

QY 61 GTGTGAAGATTCAGCTGAACAAGCAGCTCTCTCCCGAGTTCAATGGAATTCAC 120  
DB 71 GTGTGAAGATTCAGCTGAACAAGCAGCTCTCTCCCGAGTTCAATGGAATTCAC 130  
QY 121 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180  
DB 131 GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 190  
QY 181 CGCAGATCTGTGATCATCAGCGGCTGTCTCATCGCCTCTCCGGGTACAGTCTT 240  
DB 191 CGCAGATCTGTGATCATCAGCGGCTGTCTCATCGCCTCTCCGGGTACAGTCTT 250  
QY 241 CTGCTCCCGAGGAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 251 CTGCTCCCGAGGAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 310  
QY 301 CGGCGCAAGGCCCAAGAAAGGAGGAGTCTGCTCGGCTTCAGGCTGCTCCGAC 358  
DB 311 CGGCGCAAGGCCCAAGAAAGGAGGAGTCTGCTCGGCTTCAGGCTGCTCCGAC 370  
QY 359 ACCACCATCT 369  
DB 371 ACCACCATCT 381

RESULT 6  
US-09-825-294-212  
Sequence 212, Application US/09825294  
Patent No. US2002000491A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 212  
LENGTH: 1010  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-825-294-212

Query Match  
Best Local Similarity 92.6%; Score 341.8; DB 10; Length 1010;  
Matches 365; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 GGCACCTTTTGGCGATGTTCTTCTTNCAGCCTTTGCGCTGCAATTCAGTGTACCA 59  
DB 227 GGCACCTTTTGGCGATGTTCTTCTTNCAGCCTTTGCGCTGCAATTCAGTGTACCA 286  
QY 60 AGTGAAGATTCAGCTGAACAAGCAGCTCTCTCCCGAGTTCAATGGAATTCAC 119  
DB 287 AGTGAAGATTCAGCTGAACAAGCAGCTCTCTCCCGAGTTCAATGGAATTCAC 346  
QY 120 CGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 179  
DB 347 CGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 406  
QY 180 ACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCCTCTCCGGGTACAGTCTT 239  
DB 407 ACCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCCTCTCCGGGTACAGTCTT 466  
QY 240 TCTGCTCCCGAGGAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 299  
DB 467 TCTGCTCCCGAGGAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 526  
QY 300 A-CGGCGCAAGGCCCAAGAAAGGAGGAGTCTGCTCGGCTTCAGGCTGCTCCGAC 358

Db 527 ACCGGCCCAAGGAGGAGGAGTTCTGCGCCCTCAGGCCAGGCTCCGA 586  
QY 359 ACCACATCT 369  
Db 587 ACCACATCT 597

## RESULT 7

US-09-825-294-213  
Sequence 213, Application US/09825294  
Patent No. US2002004491A1  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Scolk, John A.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT APPLICATION NUMBER: US/09/825,294  
CURRENT FILING DATE: 2001-04-03  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 213  
LENGTH: 480  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-825-294-213

Query Match 53.3%; Score 196.8; DB 10; Length 480;  
Best Local Similarity 98.5%; Pred. No. 2.3e-55;  
Matches 198; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGAAGTTTGGGATTTCTTCTTTCAGGCTTGGCGCAATCCAGTGTACCA 60  
Db 280 GCGAAGTTTGGGATTTCTTCTTTCAGGCTTGGCGCAATCCAGTGTACCA 339  
QY 61 GTGTGAAGATTCAGTGAACAACGACTGCTCTCCCGAGTTCATTTGATTCAC 120  
Db 340 GTGTGAAGATTCAGTGAACAACGACTGCTCTCCCGAGTTCATTTGATTCAC 399

QY 121 GGTGAAGTTCAGACATGTGTGAGAAAGATGAGCAAGTCCCGGATTCATGTA 180  
Db 400 GGTGAAGTTCAGACATGTGTGAGAAAGATGAGCAAGTCCCGGATTCATGTA 459  
QY 181 CCGCAAGTCTGTGATCATC 201  
Db 460 CCGCAAGTCTGTGATCATC 480

## RESULT 8

US-09-867-701-4251  
Sequence 4251, Application US/09867701  
Patent No. US2002013237A1  
GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4251  
LENGTH: 430  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-4251

Query Match 23.4%; Score 86.4; DB 10; Length 430;

Best Local Similarity 91.2%; Pred. No. 5.6e-19;  
Matches 114; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

QY 245 TCCGAGGAAAGTGAAGTGTGATCAGCTGTGCAACACCCCTTGTAAAGGG 304  
Db 1 TCCGAGGAAAGTGAAGTGTGATCAGCTGTGCAACACCCCTTGTAAAGGG 60  
QY 305 CCAAGGCCCAAGAAAGGAGTGTGCTGCGCCCTCAGCCATGCTCCGACACC 364  
Db 61 CAAAGG---CAAGAAAGGAGTGTGCTGCGCCCTCAGG-CAGGGCTCCGACACC 116  
QY 365 ATCCT 369  
Db 117 ATCCT 121

## RESULT 9

US-09-960-352-3015  
Sequence 3015, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
TITILE OF INVENTION: MUSCLE AND FAT DEPOSITION  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 3015  
LENGTH: 407  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 13-LIB34-071-Q1-E1-D1  
US-09-960-352-3015

Query Match 8.8%; Score 32.6; DB 10; Length 407;  
Best Local Similarity 51.4%; Pred. No. 0.3;  
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 24 TCGTTCAGGCTTGGCGCTGCAATCCAGTGTACCAAGTGTGAAGATTCAGTGAACA 83  
Db 227 TCGAGCCAGGCTGATGCTTCAAGATCAACCGCTTCATGCAAGATGCGACAGCTAGAAA 286  
QY 84 ACGATGCTCTCCCGCCGAGTTCATTTGAAATGCAAGGATGCAAGCTCAAGACATGTGTC 143  
Db 287 ACCTCTCAACTTCATATNAAGCCATGCTGAGCTAGGCAATGATTCCTGTTGACCTGTTTG 346  
QY 144 AGAAAGAGTATGAGCAAAAGTG 167  
Db 347 AGGCCAAGACATGTTTGAAGTG 370

## RESULT 10

US-09-960-352-13056  
Sequence 13056, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
TITILE OF INVENTION: MUSCLE AND FAT DEPOSITION  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 13056  
LENGTH: 412  
TYPE: DNA

ORGANISM: Bos taurus  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (349),(378)  
OTHER INFORMATION: unsure at all n locations  
OTHER INFORMATION: Clone ID: 56-LIB188-023-Q1-E1-F8  
US-09-960-352-13056

Query Match  
Best Local Similarity 8.8%; Score 32.6; DB 10; Length 412;  
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 24 TCGCTTCAGGCTTGGCGTCGCAATCCAGTGTGAGAAATTCAGCTGAACA 83  
DB 166 TGCAGCCAGGCTCAGTCCCTAAGATCAACCGCTCCATGCAGAACTGGCAGCTAGAAA 225  
QY 84 AGCAGTGCCTCCCTCCCGAGTTGATGTGAAATTCAGCGGTGAACATGTGTC 143  
DB 226 ACCTCTCCAACTTCATCAATGAGCCATGAGTACGAGCATGAATCCGTGACCTGTTTG 285

QY 144 AGAAGAGTGTGAGCAAAAGTG 167  
DB 286 AGGCCAAGCAGCTGTTGAAAGTG 309

RESULT 11  
US-09-960-352-9456  
Sequence 9456, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: MUSCLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 9456  
LENGTH: 423  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 41-LIB188-009-Q1-E1-C10  
US-09-960-352-9456

Query Match  
Best Local Similarity 8.8%; Score 32.6; DB 10; Length 423;  
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 24 TCGCTTCAGGCTTGGCGTCGCAATCCAGTGTGAGAAATTCAGCTGAACA 83  
DB 178 TGCAGCCAGGCTCAGTCCCTAAGATCAACCGCTCCATGCAGAACTGGCAGCTAGAAA 237  
QY 84 AGCAGTGCCTCCCTCCCGAGTTGATGTGAAATTCAGCGGTGAACATGTGTC 143  
DB 238 ACCTCTCCAACTTCATCAATGAGCCATGAGTACGAGCATGAATCCGTGACCTGTTTG 297

QY 144 AGAAGAGTGTGAGCAAAAGTG 167  
DB 298 AGGCCAAGCAGCTGTTGAAAGTG 321

RESULT 12

US-09-960-352-1886  
Sequence 1886, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21(10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 1886  
LENGTH: 458  
TYPE: DNA  
ORGANISM: Bos taurus  
OTHER INFORMATION: Clone ID: 09-LIB188-017-Q1-E1-C9  
US-09-960-352-1886

Query Match  
Best Local Similarity 8.8%; Score 32.6; DB 10; Length 458;  
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 24 TCGCTTCAGGCTTGGCGTCGCAATCCAGTGTGAGAAATTCAGCTGAACA 83  
DB 182 TGCAGCCAGGCTCAGTCCCTAAGATCAACCGCTCCATGCAGAACTGGCAGCTAGAAA 241  
QY 84 AGCAGTGCCTCCCTCCCGAGTTGATGTGAAATTCAGCGGTGAACATGTGTC 143  
DB 242 ACCTCTCCAACTTCATCAATGAGCCATGAGTACGAGCATGAATCCGTGACCTGTTTG 301

QY 144 AGAAGAGTGTGAGCAAAAGTG 167  
DB 302 AGGCCAAGCAGCTGTTGAAAGTG 325

RESULT 13

US-09-834-975-262  
Sequence 262, Application US/09834975  
Patent No. US20020110815A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Brown, Jeffrey  
APPLICANT: Bolt, Andrew  
APPLICANT: Van Huffel, Christophe  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS  
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
FILE REFERENCE: MRI-016B  
CURRENT APPLICATION NUMBER: US/09/834,975  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/197,538  
PRIOR FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 1046  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 262  
LENGTH: 544  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)...(544)  
OTHER INFORMATION: n = A,T,C or G  
US-09-834-975-262

Query Match  
Best Local Similarity 8.6%; Score 31.6; DB 10; Length 544;  
Matches 85; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 115 TTGCAAGGTCGAGCTTTCAGACATGTCTAGAAAGATGAGCAAAAGTCCCGGAT 174  
DB 84 TTGCATGGTNCCTTTTCAACTCTAGTGGCCACAGAGNACCTTNNAAATTTATCCCAAAAT 143  
QY 175 CATGTACCGCAAGTCCCTGTGATCATCAGCGGCTGTCTCATGCGCTCGGGTACCA 234  
DB 144 TGCATCAACATGTGTTTNNAGATNNAACTGTGATTTTTCGCTATGNGGCTACTT 203  
QY 235 GTTCCTTCGCTCCCAAGGAAATGACATGATTTTCATCATGCTGTGCAACACCCCTCT 294

Db 204 TCAGTTTGTCTTNAATNACATTTTNGACTTTTAAAGAGCCTTCATTTGGCCCTTNT 263

QY 295 TTGTACCG 303

Db 264 TTTTAAAG 272

RESULT 14  
US-09-770-445-893

; Sequence 893, Application US/09770445

; Patent No. US20020023281A1

; GENERAL INFORMATION:

; APPLICANT: Gorlach, Jörn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Krickler, Maja

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurlan, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09/770,445

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,472

; NUMBER OF SEQ ID NOS: 999

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 893

; LENGTH: 775

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-770-445-893

Query Match 8.6%; Score 31.6; DB 10; Length 775;  
Best Local Similarity 56.9%; Pred. No. 0.87;  
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 89 TGCCTCCCTCCCGAGTTCATTTGTAATTCAGCGTGAAGCTCAGACATGTGCAGAA 148

Db 349 TTCTCCTTCGACGATTTCTTGGCGAAGCCACGCTACATGTGAAGAAGCTATTGGAATG 408

QY 149 GAAGTAGAGCAAAAGTCCCGGATCATGTACCGCAAGTCC 190

Db 409 GGAGTGAGAGGAAGGAGCGGAGCTAAGCCACCAACCAAGTAC 450

RESULT 15  
US-10-033-109-13

; Sequence 13, Application US/10033109

; Patent No. US20020142390A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.

; APPLICANT: Rafalski, J. Antoni

; TITLE OF INVENTION: Nitrogen Transport Metabolism

; FILE REFERENCE: BB-1210

; CURRENT APPLICATION NUMBER: US/10/033,109

; PRIOR FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27

201

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248

; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 1656

; TYPE: DNA

; ORGANISM: Trifolium aestivum

US-10-033-109-13

Query Match 8.5%; Score 31.4; DB 12; Length 1656;  
Best Local Similarity 54.9%; Pred. No. 1.5;  
Matches 62; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 206 GCGTGTCTCATGCGCTTGGCGGTACAGGCTCTGTGCTCCCAAGGAAGTCA 265

Db 645 GCGTGTCTCTTCACTGGGCGCTCATCGACTGCGGCGGTACGTATCCACTTCCC 704

QY 266 GTTTCATCAGCTGCTGCACACCCCTTTGTACGGGCGCAAGCCCAAGAA 318

Db 705 GCGGCGTGGCGGCTTACCGCGGTACTGGTGGGCGCAAGCAAGAA 757

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Job time: 19.0364 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 : Search time 826.855 Seconds  
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Perfect score: 369  
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Gapop 10.0, Gapext 1.0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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25: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
34: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
35: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
36: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
37: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
39: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
40: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US0509\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	367	99.5	369	1	PCT-US01-45395-199	Sequence 199, App	
2	367	99.5	369	25	US-09-656-668-199	Sequence 199, App	
3	367	99.5	369	28	US-09-713-550-199	Sequence 199, App	
4	367	99.5	369	31	US-09-825-294-199	Sequence 199, App	
5	367	99.5	369	36	US-09-970-966-199	Sequence 199, App	
6	367	99.5	369	42	US-10-212-677-199	Sequence 199, App	
7	365.4	99.0	1524	40	US-10-119-480-15	Sequence 15, App	
8	365.4	99.0	1524	42	US-10-216-160-15	Sequence 15, App	
9	365.4	99.0	1524	42	US-10-216-160-15	Sequence 15, App	
10	365.4	99.0	1524	42	US-10-216-162-15	Sequence 15, App	
11	365.4	99.0	1524	42	US-10-216-163-15	Sequence 15, App	
12	365.4	99.0	1524	42	US-10-216-164-15	Sequence 15, App	
13	365.4	99.0	1524	42	US-10-216-165-15	Sequence 15, App	
14	365.4	99.0	1524	42	US-10-216-166-15	Sequence 15, App	
15	365.4	99.0	1524	42	US-10-216-167-15	Sequence 15, App	
16	365.4	99.0	1524	42	US-10-216-168-15	Sequence 15, App	
17	365.4	99.0	1524	42	US-10-218-612-15	Sequence 15, App	
18	365.4	99.0	1524	42	US-10-218-631-15	Sequence 15, App	
19	365.4	99.0	1524	42	US-10-218-765-15	Sequence 15, App	
20	365.4	99.0	1524	42	US-10-218-764-15	Sequence 15, App	
21	365.4	99.0	1524	42	US-10-218-849-15	Sequence 15, App	

```
22 365.4 99.0 1524 42 US-10-218-930-15 Sequence 15, Appl
23 365.4 99.0 1524 42 US-10-218-956-15 Sequence 15, Appl
24 365.4 99.0 1524 42 US-10-219-003-15 Sequence 15, Appl
25 365.4 99.0 1524 42 US-10-219-010-15 Sequence 15, Appl
26 365.4 99.0 1524 42 US-10-219-060-15 Sequence 15, Appl
27 365.4 99.0 1524 42 US-10-219-061-15 Sequence 15, Appl
28 365.4 99.0 1524 42 US-10-219-062-15 Sequence 15, Appl
29 365.4 99.0 1524 42 US-10-219-063-15 Sequence 15, Appl
30 365.4 99.0 1524 42 US-10-219-064-15 Sequence 15, Appl
31 365.4 99.0 1524 42 US-10-219-065-15 Sequence 15, Appl
32 365.4 99.0 1524 42 US-10-219-066-15 Sequence 15, Appl
33 365.4 99.0 1524 42 US-10-219-067-15 Sequence 15, Appl
34 365.4 99.0 1524 42 US-10-219-068-15 Sequence 15, Appl
35 365.4 99.0 1524 42 US-10-219-069-15 Sequence 15, Appl
36 365.4 99.0 1524 42 US-10-219-070-15 Sequence 15, Appl
37 365.4 99.0 1524 42 US-10-219-071-15 Sequence 15, Appl
38 365.4 99.0 1524 42 US-10-219-072-15 Sequence 15, Appl
39 365.4 99.0 1524 42 US-10-219-073-15 Sequence 15, Appl
40 365.4 99.0 1524 42 US-10-219-074-15 Sequence 15, Appl
41 365.4 99.0 1524 42 US-10-219-075-15 Sequence 15, Appl
42 365.4 99.0 1524 42 US-10-219-077-15 Sequence 15, Appl
43 365.4 99.0 1524 42 US-10-219-150-15 Sequence 15, Appl
44 365.4 99.0 1524 42 US-10-219-464-15 Sequence 15, Appl
45 365.4 99.0 1524 42 US-10-219-465-15 Sequence 15, Appl
```

## ALIGNMENTS

```
RESULT 1
PCT-US01-45395-199
: Sequence 199, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolck, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: CURRENT FILING DATE: 2001-11-13
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 29, 345
: OTHER INFORMATION: n - A,T,C or G
PCT-US01-45395-199
```

```
Query Match 99.5%; Score 367; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 6, Be-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
DB 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACGCTGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
DB 61 GTGTGAAGATTCACAGCTGACGCTGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
QY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
DB 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACCATGCTT 240
```

```
DB 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACCATGCTT 240
QY 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGCTGCTGCAAAACCCCTTTTGA 300
DB 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGCTGCTGCAAAACCCCTTTTGA 300
QY 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCATGCTCCGAC 360
QY 361 CACCATCT 369
DB 361 CACCATCT 369
```

```
RESULT 2
US-09-656-668-199
: Sequence 199, Application US/09656668
: GENERAL INFORMATION:
: APPLICANT: Stolck, John A.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
: FILE OF INVENTION: METHODS OF USE THEREFOR
: CURRENT FILING DATE: 2000-09-07
: CURRENT APPLICATION NUMBER: US/09/656,668
: NUMBER OF SEQ ID NOS: 199
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)...(369)
: OTHER INFORMATION: n - A,T,C or G
US-09-656-668-199
```

```
Query Match 99.5%; Score 367; DB 25; Length 369;
Best Local Similarity 100.0%; Pred. No. 6, Be-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
DB 1 GGCACCTTTTGGGATGTTCTTTCAGAGCTTTGGGCTGCAAAATCCAGTCTACCA 60
QY 61 GTGTGAAGATTCACAGCTGACGCTGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
DB 61 GTGTGAAGATTCACAGCTGACGCTGCTCCCTCCCGAGTTCATTTGTAATTGCAC 120
QY 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
DB 121 GGTGAAGCTTCAAGACATGTGTGAGAAAGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACCATGCTT 240
DB 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCTTGGCGGATACCATGCTT 240
QY 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGCTGCTGCAAAACCCCTTTTGA 300
DB 241 CTGCTCCCGAGGAAACAGTCACTGATTCATGCTGCTGCAAAACCCCTTTTGA 300
QY 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCATGCTCCGAC 360
DB 301 CGGGCCAAAGGCGCCCAAGAAAGGGAAGTTCGCTCGGCGCTCAGGCCATGCTCCGAC 360
QY 361 CACCATCT 369
DB 361 CACCATCT 369
```

RESULT 3

```

US-09-713-550-199
: Sequence 199, Application US/09713550
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C4
: CURRENT APPLICATION NUMBER: US/09/713,550
: CURRENT FILING DATE: 2000-11-14
: NUMBER OF SEQ ID NOS: 205
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(369)
: OTHER INFORMATION: n = A,T,C or G
US-09-713-550-199

```

```

Query Match          99.5%: Score 367: DB 28: Length 369:
Best Local Similarity 100.0%: Pred. No. 6.8e-99:
Matches 369: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

OY 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATCCAGTCTACCA 60
    |||
DB 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATCCAGTCTACCA 60
OY 61 GTGTGAAGATTCACAGTCAAGCAAGCAAGTCTCTCCCGGATTCATTTGTAATGAC 120
    |||
DB 61 GTGTGAAGATTCACAGTCAAGCAAGCAAGTCTCTCCCGGATTCATTTGTAATGAC 120
OY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
    |||
DB 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATTCGCTTGGCGGATACAGTCTT 240
    |||
DB 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATTCGCTTGGCGGATACAGTCTT 240
OY 241 CTGCTCCCGGAGGAAAGTCAAGTCTGATCATGCTGCAACACCCCTCTTTGTA 300
    |||
DB 241 CTGCTCCCGGAGGAAAGTCAAGTCTGATCATGCTGCAACACCCCTCTTTGTA 300
OY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCTTCANGCATTGGCTCCGAC 360
    |||
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCTTCANGCATTGGCTCCGAC 360
OY 361 CACCATCTCT 369
    |||
DB 361 CACCATCTCT 369

```

```

RESULT 4
US-09-825-294-199
: Sequence 199, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA

```

```

: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(369)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

```

```

Query Match          99.5%: Score 367: DB 31: Length 369:
Best Local Similarity 100.0%: Pred. No. 6.8e-99:
Matches 369: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

OY 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATCCAGTCTACCA 60
    |||
DB 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATCCAGTCTACCA 60
OY 61 GTGTGAAGATTCACAGTCAAGCAAGCAAGTCTCTCCCGGATTCATTTGTAATGAC 120
    |||
DB 61 GTGTGAAGATTCACAGTCAAGCAAGCAAGTCTCTCCCGGATTCATTTGTAATGAC 120
OY 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
    |||
DB 121 GGTGAAGCTTCAAGACATGTGTCAAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180
OY 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATTCGCTTCCCGGATACAGTCTT 240
    |||
DB 181 CCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATTCGCTTCCCGGATACAGTCTT 240
OY 241 CTGCTCCCGGAGGAAAGTCAAGTCAAGTCTGATCATGCTGCAACACCCCTCTTTGTA 300
    |||
DB 241 CTGCTCCCGGAGGAAAGTCAAGTCAAGTCTGATCATGCTGCAACACCCCTCTTTGTA 300
OY 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCTTCANGCATTGGCTCCGAC 360
    |||
DB 301 CGGGCCAAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCTTCANGCATTGGCTCCGAC 360
OY 361 CACCATCTCT 369
    |||
DB 361 CACCATCTCT 369

```

```

RESULT 5
US-09-970-966-199
: Sequence 199, Application US/09970966
: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesch, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C6
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 199
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 29, 345
: OTHER INFORMATION: n = A,T,C or G
US-09-970-966-199

```

```

Query Match          99.5%: Score 367: DB 36: Length 369:
Best Local Similarity 100.0%: Pred. No. 6.8e-99:
Matches 369: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

OY 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATCCAGTCTACCA 60
    |||
DB 1 GGCACCTTTTGGGATTTGTTCTTTCCTTNCAGGCTTTGGCTGCAATCCAGTCTACCA 60

```

```

QY 61 GTGTGAAGAAATTCAGCTGTAACACGACGCTCTCCCGAGATTGATGTAATGGAC 120
    |||||||
Db 61 GTGTGAAGAAATTCAGCTGTAACACGACGCTCTCCCGAGATTGATGTAATGGAC 120
QY 121 GGTGAAGCTTAAAGCATGTGTGCAAGAAAGTGTGAGCAAAATGCCGGGATCATGTA 180
    |||||||
Db 121 GGTGAAGCTTAAAGCATGTGTGCAAGAAAGTGTGAGCAAAATGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGCGGGTACCAAGTCTT 240
    |||||||
Db 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGCGGGTACCAAGTCTT 240
QY 241 CTGCTCCCGAGGAAAGTGAACCTGATGATGATGATGATGATGATGATGATGATG 300
    |||||||
Db 241 CTGCTCCCGAGGAAAGTGAACCTGATGATGATGATGATGATGATGATGATGATG 300
QY 301 CGGGCCCAAGGCCCCAAGAAAGGGGAGTTGCTCGGCTCTGAGCCATGCTCCGAC 360
    |||||||
Db 301 CGGGCCCAAGGCCCCAAGAAAGGGGAGTTGCTCGGCTCTGAGCCATGCTCCGAC 360
QY 361 CACCATCTCT 369
    |||||||
Db 361 CACCATCTCT 369

```

## RESULT 6

```

US-10-212-677-199
; Sequence 199, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 29, 345
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-199

```

```

Query Match          99.5%; Score 367; DB 42; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.8e-99;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGGCGTGAATCCATGCTACCA 60
    |||||||
Db 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGGCGTGAATCCATGCTACCA 60
QY 61 GTGTGAAGAAATTCAGCTGTAACACGACGCTCTCCCGAGATTGATGTAATGGAC 120
    |||||||
Db 61 GTGTGAAGAAATTCAGCTGTAACACGACGCTCTCTCCCGAGATTGATGTAATGGAC 120
QY 121 GGTGAAGCTTAAAGCATGTGTGCAAGAAAGTGTGAGCAAAATGCCGGGATCATGTA 180
    |||||||
Db 121 GGTGAAGCTTAAAGCATGTGTGCAAGAAAGTGTGAGCAAAATGCCGGGATCATGTA 180
QY 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGCGGGTACCAAGTCTT 240
    |||||||
Db 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGCGGGTACCAAGTCTT 240
QY 241 CTGCTCCCGAGGAAAGTGAACCTGATGATGATGATGATGATGATGATGATGATG 300
    |||||||

```

```

Db 241 CTGCTCCCGAGGAAAGTGAACCTGATGATGATGATGATGATGATGATGATGATG 300
    |||||||
QY 301 CGGGCCCAAGGCCCCAAGAAAGGGGAGTTGCTCGGCTCTGAGCCATGCTCCGAC 360
    |||||||
Db 301 CGGGCCCAAGGCCCCAAGAAAGGGGAGTTGCTCGGCTCTGAGCCATGCTCCGAC 360
QY 361 CACCATCTCT 369
    |||||||
Db 361 CACCATCTCT 369

```

## RESULT 7

```

US-10-119-480-15
; Sequence 15, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See file wrapper or Palm
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-119-480-15

```

```

Query Match          99.0%; Score 365.4; DB 40; Length 1524;
Best Local Similarity 99.2%; Pred. No. 3.3e-98;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGGCGTGAATCCATGCTACCA 60
    |||||||
Db 141 GGCACATTTTGGGATTTGTTCTTNCAGGCTTTGGCGTGAATCCATGCTACCA 200
QY 61 GTGTGAAGAAATTCAGCTGTAACACGACGCTCTCCCGAGATTGATGTAATGGAC 120
    |||||||
Db 201 GTGTGAAGAAATTCAGCTGTAACACGACGCTCTCTCCCGAGATTGATGTAATGGAC 260
QY 121 GGTGAAGCTTAAAGCATGTGTGCAAGAAAGTGTGAGCAAAATGCCGGGATCATGTA 180
    |||||||
Db 261 GGTGAAGCTTAAAGCATGTGTGCAAGAAAGTGTGAGCAAAATGCCGGGATCATGTA 320
QY 181 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGCGGGTACCAAGTCTT 240
    |||||||
Db 321 CCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTGCGGGTACCAAGTCTT 380
QY 241 CTGCTCCCGAGGAAAGTGAACCTGATGATGATGATGATGATGATGATGATGATG 300
    |||||||
Db 381 CTGCTCCCGAGGAAAGTGAACCTGATGATGATGATGATGATGATGATGATGATG 440
QY 301 CGGGCCCAAGGCCCCAAGAAAGGGGAGTTGCTCGGCTCTGAGCCATGCTCCGAC 360
    |||||||
Db 441 CGGGCCCAAGGCCCCAAGAAAGGGGAGTTGCTCGGCTCTGAGCCATGCTCCGAC 500
QY 361 CACCATCTCT 369
    |||||||
Db 501 CACCATCTCT 509

```

## RESULT 8

```
US-10-216-159A-15
```



```

; Sequence 15, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC6
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-216-159A-15

Query Match          99.0%; Score 365.4; DB 42; Length 1524;
Best Local Similarity 99.2%; Pred. No. 3.3e-98;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGATGTTGCTTTCAGGCTTTCGCAATCCAGTGTGCA 60
DB 141 GGCACATTTTGGGATGTTGCTTTCAGGCTTTCGCAATCCAGTGTGCA 200
QY 61 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 120
DB 201 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 260
QY 121 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 180
DB 261 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 320
QY 181 CGGCAAGTCTGTGATCATATCAGGCGCTGTCTATCGCTCTGCGGGATACAGTCTCT 240
DB 321 CGGCAAGTCTGTGATCATATCAGGCGCTGTCTATCGCTCTGCGGGATACAGTCTCT 380
QY 241 CTGCTCCCAAGGAACTGAATCAGTTGATCAGTGTGCAACACCCCTTTGTAA 300
DB 381 CTGCTCCCAAGGAACTGAATCAGTTGATCAGTGTGCAACACCCCTTTGTAA 440
QY 301 CGGCGCAAGGCGCCAAAGAAAGGGAGTTGCTCGGCGCTCANGCCATGGCTCCGAC 360
DB 441 CGGCGCAAGGCGCCAAAGAAAGGGAGTTGCTCGGCGCTCANGCCATGGCTCCGAC 500

```

```

QY 361 CACCATCCT 369
DB 501 CACCATCCT 509

RESULT 9
US-10-216-160-15
; Sequence 15, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC8
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/10/216,160
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-216-160-15

Query Match          99.0%; Score 365.4; DB 42; Length 1524;
Best Local Similarity 99.2%; Pred. No. 3.3e-98;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACATTTTGGGATGTTGCTTTCAGGCTTTCGCAATCCAGTGTGCA 60
DB 141 GGCACATTTTGGGATGTTGCTTTCAGGCTTTCGCAATCCAGTGTGCA 200
QY 61 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 120
DB 201 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 260
QY 121 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 180
DB 261 GTGTGAAGATTCAGTGTGCAAGACGATGCTCTCCCGAGTTCATTTGAATTGCAC 320
QY 181 CGGCAAGTCTGTGATCATATCAGGCGCTGTCTATCGCTCTGCGGGATACAGTCTCT 240
DB 321 CGGCAAGTCTGTGATCATATCAGGCGCTGTCTATCGCTCTGCGGGATACAGTCTCT 380
QY 241 CTGCTCCCAAGGAACTGAATCAGTTGATCAGTGTGCAACACCCCTTTGTAA 300
DB 381 CTGCTCCCAAGGAACTGAATCAGTTGATCAGTGTGCAACACCCCTTTGTAA 440
QY 301 CGGCGCAAGGCGCCAAAGAAAGGGAGTTGCTCGGCGCTCANGCCATGGCTCCGAC 360
DB 441 CGGCGCAAGGCGCCAAAGAAAGGGAGTTGCTCGGCGCTCANGCCATGGCTCCGAC 500

```

```

RESULT 10
US-10-216-162-15
; Sequence 15, Application US/10216162
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

```

```

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC2
CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 60/069873
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 60/078910
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 60/079728
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-216-162-15

```

```

Query Match          99.0%; Score 365.4; DB 42; Length 1524;
Best Local Similarity 99.2%; Pred. No. 3.3e-98;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGCACCTTTTGGGATTTGCTTCTTCAGGCTTTGGCTTCCAAATCCAGTGTACCA 60
DB 141 GGCACCTTTTGGGATTTGCTTCTTCAGGCTTTGGCTTCCAAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGACAGACGACGCTCCCGAGTTCATTTGTAATGGAC 120
DB 201 GTGTGAAGATTCAGCTGACAGACGACGCTCCCGAGTTCATTTGTAATGGAC 120
QY 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
DB 261 GGTGAACGTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
QY 261 GGTGAACGTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTGATCATGACGCGCTGTCTCATCGCTTCCGGGTACCACTCTT 240
DB 321 CCGCAAGTCTGTGATCATGACGCGCTGTCTCATCGCTTCCGGGTACCACTCTT 240
QY 321 CCGCAAGTCTGTGATCATGACGCGCTGTCTCATCGCTTCCGGGTACCACTCTT 240
QY 241 CTGCTCCCCAGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 300
DB 381 CTGCTCCCCAGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 CGGGCCAGGCGCAAGAAAGGGAAGTTCCTCGGCGCTCANGCCATGAGCTCCGAC 360
DB 441 CGGGCCAGGCGCAAGAAAGGGAAGTTCCTCGGCGCTCANGCCATGAGCTCCGAC 360
QY 361 CACCATCT 369
DB 501 CACCATCT 509

```

```

RESULT 11
US-10-216-163-15
; Sequence 15, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC3
CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 60/069873
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 60/078910
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-216-163-15

```

```

Query Match          99.0%; Score 365.4; DB 42; Length 1524;
Best Local Similarity 99.2%; Pred. No. 3.3e-98;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGCACCTTTTGGGATTTGCTTCTTCAGGCTTTGGCTTCCAAATCCAGTGTACCA 60
DB 141 GGCACCTTTTGGGATTTGCTTCTTCAGGCTTTGGCTTCCAAATCCAGTGTACCA 60
QY 61 GTGTGAAGATTCAGCTGACAGACGACGCTCCCGAGTTCATTTGTAATGGAC 120
DB 201 GTGTGAAGATTCAGCTGACAGACGACGCTCCCGAGTTCATTTGTAATGGAC 120
QY 121 GGTGAACGTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
DB 261 GGTGAACGTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
QY 261 GGTGAACGTTCAAGCATGTGTCAAGAAAGATGATGAGCAAAAGTCCGGATCATGTA 180
QY 181 CCGCAAGTCTGTGATCATGACGCGCTGTCTCATCGCTTCCGGGTACCACTCTT 240
DB 321 CCGCAAGTCTGTGATCATGACGCGCTGTCTCATCGCTTCCGGGTACCACTCTT 240
QY 321 CCGCAAGTCTGTGATCATGACGCGCTGTCTCATCGCTTCCGGGTACCACTCTT 240
QY 241 CTGCTCCCCAGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 300
DB 381 CTGCTCCCCAGGAAAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 300

```

QY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTCGGCCCTCANGCCATGGCTCCGCAC 360  
 DB 441 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTCGGCCCTCANGCCATGGCTCCGCAC 500  
 QY 361 CACCATCCT 369  
 DB 501 CACCATCCT 509

RESULT 12

US-10-216-164-15  
 ; Sequence 15, Application US/10216164  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Geriltsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530P1C5  
 ; CURRENT APPLICATION NUMBER: US/10/216,164  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 15  
 ; LENGTH: 1524  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-216-164-15

Query Match 99.0%; Score 365.4; DB 42; Length 1524;  
 Best Local Similarity 99.2%; Pred. No. 3.3e-98;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGAATCTTTTGGGATGTTGCTTTCAGAGCTTTGCGCTGCAAAATCCAGTGTACCA 60  
 DB 141 GCGAATCTTTTGGGATGTTGCTTTCAGAGCTTTGCGCTGCAAAATCCAGTGTACCA 200  
 QY 61 GTGTGAAGATTCAGCTGTAACAGAGCTGCTCCCGCAGTTTCATGTGATTCGAC 120  
 DB 201 GTGTGAAGATTCAGCTGTAACAGAGCTGCTCCCGCAGTTTCATGTGATTCGAC 260  
 QY 121 GGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAGCAAGTCCCGGATCATGTA 180  
 DB 261 GGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGAGCAAGTCCCGGATCATGTA 320

QY 181 CCGCAATGCTGTGATCATATCAGGCGCTGTCTCATCGCCTTGCGGGTACCAATCTCT 240  
 DB 321 CCGCAATGCTGTGATCATATCAGGCGCTGTCTCATCGCCTTGCGGGTACCAATCTCT 380  
 QY 241 CTGCTCCCGAGGGAAGTAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 300  
 DB 381 CTGCTCCCGAGGGAAGTAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 440  
 QY 301 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTCGGCCCTCANGCCATGGCTCCGCAC 360  
 DB 441 CGGGCCAGGCCCCAAGAAAGGGAAGTTGCTCGGCCCTCANGCCATGGCTCCGCAC 500  
 QY 361 CACCATCCT 369  
 DB 501 CACCATCCT 509

RESULT 13

US-10-216-165-15  
 ; Sequence 15, Application US/10216165  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Geriltsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530P1C7  
 ; CURRENT APPLICATION NUMBER: US/10/216,165  
 ; PRIOR FILING DATE: 2002-08-09  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 15  
 ; LENGTH: 1524  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-216-165-15

Query Match 99.0%; Score 365.4; DB 42; Length 1524;  
 Best Local Similarity 99.2%; Pred. No. 3.3e-98;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGAATCTTTTGGGATGTTGCTTTCAGAGCTTTGCGCTGCAAAATCCAGTGTACCA 60  
 DB 141 GCGAATCTTTTGGGATGTTGCTTTCAGAGCTTTGCGCTGCAAAATCCAGTGTACCA 200

Oy	61	GTGTGAACAATTCCAGCTGAACACAGACTGCTCTCCCGGAGTTCATTGTGAATTGCAC	120
Db	201	GTGTGAACAATTCCAGCTGAACACAGACTGCTCTCCCGGAGTTCATTGTGAATTGCAC	260
Oy	121	GGTGACGTTCAAGCATGTGTCTCAGAAAGAAGTATGGAGCAAAAGTCCGGGATCATGTA	180
Db	261	GGTGACGTTCAAGCATGTGTCTCAGAAAGAAGTATGGAGCAAAAGTCCGGGATCATGTA	320
Oy	181	CCGCAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTCTGCGCGGTACCAAGTCTT	240
Db	321	CCGCAGTCTGTGCATCATCAGCGGCGCTGTCTCATGCGCTCTGCGCGGTACCAAGTCTT	380
Oy	241	CTGCTCCCCCAGGAAACTGAACCTAGTTTGATTCAGCTGTGCAACACCCCTCTTTGTAA	300
Db	381	CTGCTCCCCCAGGAAACTGAACCTAGTTTGATTCAGCTGTGCAACACCCCTCTTTGTAA	440
Oy	301	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTCTGCGCTCGGCCCTCANGCATAGGCTCCGCAC	360
Db	441	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTCTGCGCTCGGCCCTCANGCATAGGCTCCGCAC	500
Oy	361	CACCATTCCT	369
Db	501	CACCATTCCT	509

```

RESULT 14
US-10-216-166-15
; Sequence 15, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEICACIDS
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C9
; CURRENT APPLICATION NUMBER: US/10/216,166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-166-15

```

Query Match	99.08%	Score 365.4	DB 42	Length 1524
Best Local Similarity	99.28%	Pred. No. 3,3e-98		
Matches 366	Conservative 0	Mismatches 3	Indels 0	Gaps
QY	1	GGCAACATTTTGGCGATTGTTCTTGGCTTTCAGCGCTTTGGCGCTGCAAAATCCAGTGTACCA	60	
Db	141	GGCAACATTTTGGCGATTGTTCTTGGCTTTCAGCGCTTTGGCGCTGCAAAATCCAGTGTACCA	200	
QY	61	GTGTGAACAATTTCCAGCTGAGCAACGACTGCTCTCCGCCGAGTTCATTGTGAATTGCAC	120	
Db	201	GTGTGAACAATTTCCAGCTGAGCAACGACTGCTCTCCGCCGAGTTCATTGTGAATTGCAC	260	
QY	121	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCCGGATCATGTA	180	
Db	261	GGTGAACGTTCAAGACATGTGTCAAGAAAGATGATGAGCAAAAGTCCCGGATCATGTA	320	
QY	181	CCGCAAGTCGTGTGATCATAGGGGCGCTGTCTATGGCCGTGCGGGTACAGATCCTT	240	
Db	321	CCGCAAGTCGTGTGATCATAGGGGCGCTGTCTATGGCCGTGCGGGTACAGATCCTT	380	
QY	241	CTGCTCCCCAGGGAACCTGAACCTAGTTTGATCAGCTGTCTGCAACACCCCTCTTTGTAA	300	
Db	381	CTGCTCCCCAGGGAACCTGAACCTAGTTTGATCAGCTGTCTGCAACACCCCTCTTTGTAA	440	
QY	301	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTCTTGCTCGGCCCTCANGCCATAGCTCCGCAC	360	
Db	441	CGGGCCAAAGGCCCAAGAAAAGGGGAAGTTCTTGCTCGGCCCTCANGCCATAGCTCCGCAC	500	
QY	361	CACCATTCCT 369		
Db	501	CACCATTCCT 509		

```

RESULT 15
US-10-216-167-15
/ Sequence 15, Application US/10216167
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gutney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Matanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
/ FILE REFERENCE: P3530P1C4
/ CURRENT APPLICATION NUMBER: US/10/216,167
/ CURRENT FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/065549
/ PRIOR FILING DATE: 1997-10-26
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/

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; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 15  
 ; LENGTH: 1524  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-216-167-15

Query Match 99.0%; Score 365.4; DB 42; Length 1524;  
 Best Local Similarity 99.2%; Pred. No. 3.3e-98;  
 Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGGATGTTCTTCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 60  
 DB 141 GGCACCTTTTGGGATGTTCTTCTTNCAGGCTTGGCTGCAATCCAGTCTACCA 200  
 QY 61 GTGTGAAGATTCAGCTGAACAGAGACTGCTCTCCCGAGTTCAATTGATGCAC 120  
 DB 201 GTGTGAAGATTCAGCTGAACAGAGACTGCTCTCCCGAGTTCAATTGATGCAC 260  
 QY 121 GTGAAGATTCAGACATGTCAGAAAGATGATGAGCAAGTCCGGGATCATGTA 180  
 DB 261 GTGAAGATTCAGACATGTCAGAAAGATGATGAGCAAGTCCGGGATCATGTA 320  
 QY 181 CCGCAAGTCTGTGATCATCAGGCGCTGTCTATGCTCTGCGGGTACAGTCTT 240  
 DB 321 CCGCAAGTCTGTGATCATCAGGCGCTGTCTATGCTCTGCGGGTACAGTCTT 380  
 QY 241 CTGCTCCCGAGGAACTGAATCTGATGATGATGATGATGATGATGATGATG 300  
 DB 381 CTGCTCCCGAGGAACTGAATCTGATGATGATGATGATGATGATGATGATG 440  
 QY 301 CCGGCGAAGGCGCCAGAAAGGGAAGTCTGCTGCGCCCTCANGCCATGCTCCGAC 360  
 DB 441 CCGGCGAAGGCGCCAGAAAGGGAAGTCTGCTGCGCCCTCANGCCATGCTCCGAC 500  
 QY 361 CACCATCTCT 369  
 DB 501 CACCATCTCT 509

Search completed: November 7, 2002, 17:54:11  
 Job time : 850.855 secs



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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 10.3091 Seconds  
(without alignments)  
3937.596 Million cell updates/sec

Title: US-09-970-966-199

Perfect score: 369

Sequence: 1 ggaacattttgcggatgtt.....tgctccgacacacatcct 369

Scoring table: IDENTITY\_NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
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2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365.4	99.0	1524	6 US-10-230-437-15	Sequence 15, App1
2	31.4	8.5	4321	6 US-10-085-198-105	Sequence 105, App
3	31.4	8.5	7097	6 US-10-085-198-107	Sequence 107, App
4	30.8	8.3	1860	6 US-10-266-829-18	Sequence 18, App1
5	29.4	8.0	1372	6 US-10-281-024-16	Sequence 16, App1
6	28.8	7.8	3449	6 US-10-131-813A-293	Sequence 293, App
7	28.8	7.8	3449	6 US-10-131-819A-293	Sequence 293, App
8	28.8	7.8	3449	6 US-10-131-823A-293	Sequence 293, App
9	28.8	7.8	3449	6 US-10-131-824A-293	Sequence 293, App
10	28.8	7.8	3449	6 US-10-131-826A-293	Sequence 293, App
11	28.8	7.8	3449	6 US-10-131-829A-293	Sequence 293, App
12	28.8	7.8	3449	6 US-10-125-926A-293	Sequence 293, App
13	28.8	7.8	3449	6 US-10-127-829A-293	Sequence 293, App
14	28.8	7.8	3449	6 US-10-127-831A-293	Sequence 293, App
15	28.8	7.8	3449	6 US-10-127-835A-293	Sequence 293, App
16	28.8	7.8	3449	6 US-10-127-837A-293	Sequence 293, App
17	28.8	7.8	3449	6 US-10-127-842A-293	Sequence 293, App
18	28.8	7.8	3449	6 US-10-127-850A-293	Sequence 293, App
19	28.8	7.8	3449	6 US-10-127-901A-293	Sequence 293, App
20	28.8	7.8	3449	6 US-10-128-689A-293	Sequence 293, App
21	28.8	7.8	3449	6 US-10-131-830A-293	Sequence 293, App
22	28.8	7.8	3449	6 US-10-131-833A-293	Sequence 293, App
23	28.8	7.8	3449	6 US-10-131-837A-293	Sequence 293, App
24	28.8	7.8	3449	6 US-10-125-830A-293	Sequence 293, App
25	28.8	7.8	3449	6 US-10-127-825A-293	Sequence 293, App
26	28.8	7.8	3449	6 US-10-127-838B-293	Sequence 293, App

C 27	28.8	7.8	3449	6 US-10-127-843A-293	Sequence 293, App
C 28	28.8	7.8	3449	6 US-10-127-849A-293	Sequence 293, App
C 29	28.8	7.8	3449	6 US-10-128-684A-293	Sequence 293, App
C 30	28.8	7.8	3449	6 US-10-128-685A-293	Sequence 293, App
C 31	28.8	7.8	3449	6 US-10-128-686A-293	Sequence 293, App
C 32	28.8	7.8	3449	6 US-10-128-690A-293	Sequence 293, App
C 33	28.8	7.8	3449	6 US-10-128-693A-293	Sequence 293, App
C 34	28.8	7.8	3449	6 US-10-131-821A-293	Sequence 293, App
C 35	28.8	7.8	3449	6 US-10-131-836A-293	Sequence 293, App
C 36	28.8	7.8	3449	6 US-10-137-872A-293	Sequence 293, App
C 37	28.8	7.8	3449	6 US-10-137-873A-293	Sequence 293, App
C 38	28.2	7.6	470	6 US-10-240-423-128	Sequence 128, App
C 39	28	7.6	413	5 US-09-513-999C-2172	Sequence 2172, App
C 40	28	7.6	6085	5 US-09-484-743-8	Sequence 8, App1
C 41	28	7.6	6085	5 US-09-484-331-8	Sequence 8, App1
C 42	28	7.6	6085	5 US-09-455-659A-8	Sequence 8, App1
C 43	27.6	7.5	385	5 US-09-620-607B-20	Sequence 20, App1
C 44	27.6	7.5	450	5 US-09-513-999C-2171	Sequence 2171, App
C 45	27.4	7.4	6227	6 US-10-240-425-364	Sequence 364, App

## ALIGNMENTS

RESULT 1  
US-10-230-437-15  
; Sequence 15, Application US/10230437  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerltsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P350P1094  
; CURRENT FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 15  
; LENGTH: 1524  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; US-10-230-437-15  
Query Match 99.0%; Score 365.4; DB 6; Length 1524;

Best Local Similarity 99.2%; Pred. No. 6,7e-109;  
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGCACCTTTTGGGAGATGTTCTTCCTTNCAGAGCTTTGGCGTGCAGATCTGACCA 60
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Db 141 GGCACCTTTTGGGAGATGTTCTTCCTTNCAGAGCTTTGGCGTGCAGATCTGACCA 200
QY 61 GTGTGAAGATTCAGTCAAGCAAGCACTCTCTCCCGAGTTCATTTGATTTGAC 120
    |||
Db 201 GTGTGAAGATTCAGTCAAGCAAGCACTCTCTCCCGAGTTCATTTGATTTGAC 260
QY 121 GTGTGAAGATTCAGTCAAGCAAGCACTCTCTCCCGAGTTCATTTGATTTGAC 180
    |||
Db 261 GTGTGAAGATTCAGTCAAGCAAGCACTCTCTCCCGAGTTCATTTGATTTGAC 320
QY 181 CGCGAAGTCTGTGCATCATCAGCGGCTCTCTCATCGCTTCGCGGATACAGTCTT 240
    |||
Db 321 CGCGAAGTCTGTGCATCATCAGCGGCTCTCTCATCGCTTCGCGGATACAGTCTT 380
QY 241 CTGCTCCCGAGGAACTGACTGATTTGATCATCAGCTGCTGCAACACCCCTTTGTAA 300
    |||
Db 381 CTGCTCCCGAGGAACTGACTGATTTGATCATCAGCTGCTGCAACACCCCTTTGTAA 440
QY 301 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTGAMGCTATGCTCCGAC 360
    |||
Db 441 CGGCGCAAGGCCCCAAGAAAGGGAAGTTCTGCTCGGCGCTGAMGCTATGCTCCGAC 500
QY 361 CACCATCTCT 369
    |||
Db 501 CACCATCTCT 509
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## RESULT 2

US-10-085-198-105  
; Sequence 105, Application US/10085198  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook et al.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-279  
; CURRENT APPLICATION NUMBER: US/10/085,198  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/271,646  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/276,401  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/311,981  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/312,858  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/271,840  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/277,324  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/286,096  
; PRIOR FILING DATE: 2001-04-21  
; PRIOR APPLICATION NUMBER: 60/299,695  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/315,614  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/272,405  
; PRIOR FILING DATE: 2001-02-28  
; Remaining prior Application data removed - See file Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 653  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 105  
; LENGTH: 4321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-198-105

Query Match 8.5%; Score 31.4; DB 6; Length 4321;  
Best Local Similarity 51.4%; Pred. No. 1.2;  
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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QY 232 CCACTCTTCTGCTCCCGAGGAACTGACTGATTTGATCATGCTGCTGCACACCCC 291
    |||
Db 3800 CCACTCTTCTGCTCCCGAGGAACTGACTGATTTGATCATGCTGCTGCACACCCC 3859
QY 292 TCTTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 351
    |||
Db 3860 TCCCGGCTCTGACTCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3919
QY 352 GCTCCGACCAACATCTCT 369
    |||
Db 3920 GCGCGCCGCTGCGCGGCT 3937
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## RESULT 3

US-10-085-198-107  
; Sequence 107, Application US/10085198  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook et al.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-279  
; CURRENT APPLICATION NUMBER: US/10/085,198  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/271,646  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/276,401  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/311,981  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/312,858  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/271,840  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/277,324  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/286,096  
; PRIOR FILING DATE: 2001-04-21  
; PRIOR APPLICATION NUMBER: 60/299,695  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/315,614  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/272,405  
; PRIOR FILING DATE: 2001-02-28  
; Remaining prior Application data removed - See file Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 653  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 107  
; LENGTH: 7097  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-198-107

Query Match 8.5%; Score 31.4; DB 6; Length 7097;  
Best Local Similarity 51.4%; Pred. No. 1.6;  
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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QY 232 CCACTCTTCTGCTCCCGAGGAACTGACTGATTTGATCATGCTGCTGCACACCCC 291
    |||
Db 3556 CCACTCTTCTGCTCCCGAGGAACTGACTGATTTGATCATGCTGCTGCACACCCC 3615
QY 292 TCTTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 351
    |||
Db 3616 TCCCGGCTCTGACTCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3675
QY 352 GCTCCGACCAACATCTCT 369
    |||
Db 3676 GCGCGCCGCTGCGCGGCT 3693
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## RESULT 4

US-10-266-829-18  
; Sequence 18, Application US/10266829  
; GENERAL INFORMATION:









Qy 221 TCTGCCGGGTACACGCTCTTGTCTCCCGAGGAAACTGACATTCATCAGCTGC 280  
Db 727 TCTTGAAGCTCTCCATCTGTACAGATCATATGACCCGCGGACATCTCCCTCAGGGGC 668  
Qy 281 TGCACACCCCTCTTGTGTACAGGGCCCAAGAGAAAAGGGGAAGTTCTGCTCGGCC 340  
Db 667 CGGGCCCCCTCTGTCTGTGAGATGCGATGTTTCAGGGGCATCTGATGCGCCAGCCAGTC 608  
Qy 341 CTCANCCATGGCTCCGACACCATCTCT 369  
Db 607 ATGTGCCCCGTGTGACAGATGCGCATCTCT 579

## RESULT 11

US-10-131-829A-293/C  
Sequence 293, Application US/10131829A

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C138

CURRENT APPLICATION NUMBER: US/10/131,829A

FILE REFERENCE: P3330R1C138

CURRENT FILING DATE: 2002-04-27

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 293

LENGTH: 3449

TYPE: DNA

ORGANISM: Homo Sapien

Query Match 7.8%; Score 28.8; DB 6; Length 3449;

Best Local Similarity 45.9%; Pred. No. 7.5;

Matches 96; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Db 787 CCAATGGCAAGATATGATGATGCCCGGTCCGCTGTAGCAGCCACTCGGCCAGAG 728  
Qy 221 TCTGCCGGGTACACGCTCTTGTCTCCCGAGGAAACTGACATTCATCAGCTGC 280  
Db 727 TCTTGAAGCTCTCCATCTGTACAGATCATATGACCCGCGGACATCTCCCTCAGGGGC 668  
Qy 281 TGCACACCCCTCTTGTGTACAGGGCCCAAGAGAAAAGGGGAAGTTCTGCTCGGCC 340  
Db 667 CGGGCCCCCTCTGTCTGTGAGATGCGATGTTTCAGGGGCATCTGATGCGCCAGCCAGTC 608  
Qy 341 CTCANCCATGGCTCCGACACCATCTCT 369  
Db 607 ATGTGCCCCGTGTGACAGATGCGCATCTCT 579

## RESULT 12

US-10-125-926A-293/C

Sequence 293, Application US/10125926A

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C138

CURRENT APPLICATION NUMBER: US/10/125,926A

FILE REFERENCE: P3330R1C138

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 293

LENGTH: 3449

TYPE: DNA

ORGANISM: Homo Sapien

Query Match 7.8%; Score 28.8; DB 6; Length 3449;

Best Local Similarity 45.9%; Pred. No. 7.5;

Matches 96; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 161 CAAAGTCCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCC 220  
DB 787 CCAATGGCAAGATTAGATGCCGTGTCCGTAGCCACCTCGGCGCAAGGAG 728  
QY 221 TCTGCCGGTACGACGCTTGTGCTCCCGAGGAACGACTGATGCTGCTGAGCTGC 280  
DB 727 TCTGAGGTCTCCATCTGTACGATCATATGACCCGTGGACATTTCTCCCTCAGGGGC 668  
QY 281 TGCACACCCCTCTTTGTAAAGGGCCCAAGGCAAGAAAGGGAAGTTCTGCTCGGCC 340  
DB 667 CGGGCCCCCTCTGCTTGTGAAGATGCATGTTCAGGGCATACTGATGCGCCAGCCAGTC 608  
QY 341 CTCANGCATGCTCCGACCATCATCT 369  
DB 607 ATGTGCGCCGTGGACAGATGCCGATCCT 579

## RESULT 13

US-10-127-829A-293/C  
Sequence 293, Application US/10127829A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C85  
CURRENT APPLICATION NUMBER: US/10/127,829A  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 293  
LENGTH: 3449  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-127-829A-293

Query Match 7.8%; Score 28.8; DB 6; Length 3449;  
Best Local Similarity 45.9%; Pred. No. 7.5;

Matches 96; Conservative 0; Mismatches 113; Indels 0; Gaps 0;  
QY 161 CAAAGTCCCGGATCATGTACCGCAAGTCTGTGCATCATCAGCGGCTGTCTCATCGCC 220  
DB 787 CCAATGGCAAGATTAGATGCCGTGTCCGTAGCCACCTCGGCGCAAGGAG 728  
QY 221 TCTGCCGGTACGACGCTTGTGCTCCCGAGGAACGACTGATGCTGCTGAGCTGC 280  
DB 727 TCTGAGGTCTCCATCTGTACGATCATATGACCCGTGGACATTTCTCCCTCAGGGGC 668  
QY 281 TGCACACCCCTCTTTGTAAAGGGCCCAAGGCAAGAAAGGGAAGTTCTGCTCGGCC 340  
DB 667 CGGGCCCCCTCTGCTTGTGAAGATGCATGTTCAGGGCATACTGATGCGCCAGCCAGTC 608  
QY 341 CTCANGCATGCTCCGACCATCATCT 369  
DB 607 ATGTGCGCCGTGGACAGATGCCGATCCT 579

## RESULT 14

US-10-127-831A-293/C  
Sequence 293, Application US/10127831A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C107  
CURRENT APPLICATION NUMBER: US/10/127,831A  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 293  
LENGTH: 3449  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-127-831A-293



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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 1589.8 Seconds

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Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agttctcttgcagagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: OLIGO\_MUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 10

Total number of hits satisfying chosen parameters: 1389073

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database: GenEmbl:

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rtd:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcg\_hum:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	606	97.0	129676	9	AC079773 Homo sapi
2	555	88.8	826	9	BC011449 Homo sapi
3	555	88.8	1832	9	AK094501 Homo sapi
4	549	87.8	1890	6	AX136281 Sequence
5	393	62.9	1524	6	AX358762 Sequence
6	393	62.9	1524	6	AX362255 Sequence
7	365	58.4	587	6	AX136698 Sequence
8	359	57.4	1362	6	AX319942 Sequence
9	359	57.4	1362	9	AF034633 Homo sapi
10	359	57.4	2528	6	AX319944 Sequence
11	352	56.3	444	6	AX150120 Sequence
12	27	4.3	92874	2	AC112072 Sequence
13	24	3.8	70395	2	AC099884 Mus muscu
14	23	3.7	94718	9	AC026770 Homo sapi
15	23	3.7	167693	2	AC011639 Homo sapi
16	23	3.7	176967	2	AC022742 Homo sapi
17	23	3.7	180837	2	AC022824 Homo sapi
18	23	3.7	184485	2	AC096679 Homo sapi
19	23	3.7	192464	9	AC090971 Homo sapi
20	23	3.7	200145	2	AC126666 Rattus no
21	22	3.5	256	6	AX393645 Sequence
22	22	3.5	1388	8	AT065052 Arabidops
23	22	3.5	1982	8	NTA294474 Nicotiana
24	22	3.5	2666	8	AF035577 Amblyomma
25	22	3.5	3190	3	AB019231 Arabidops
26	22	3.5	43570	8	AB019231 Arabidops
27	22	3.5	86093	2	AC114102 Rattus no
28	22	3.5	90020	8	ATT24H18 Rattus no
29	22	3.5	94029	2	AC117309 Rattus no
30	22	3.5	98506	8	ATT2L20 Arabidops
31	22	3.5	99541	2	AC126575 Rattus no
32	22	3.5	110000	2	AC098517 Rattus no
33	22	3.5	11914	10	AL596180 Mouse DNA
34	22	3.5	11982	2	AC103498 Rattus no
35	22	3.5	115643	2	AC094168 Rattus no
36	22	3.5	126363	2	AC123419 Rattus no
37	22	3.5	138918	9	AL445433 Human DNA
38	22	3.5	158728	2	AC114056 Rattus no
39	22	3.5	160008	2	AC022823 Homo sapi
40	22	3.5	163932	2	AC020693 Homo sapi
41	22	3.5	194402	2	AC096152 Rattus no
42	22	3.5	196863	2	AC107560 Rattus no
43	22	3.5	198843	2	AC102588 Mus muscu
44	22	3.5	206648	2	AC123116 Rattus no
45	22	3.5	209095	2	AC094585 Rattus no

# ALIGNMENTS

RESULT 1  
AC079773/c 129676 bp DNA linear PRI 09-JAN-2002  
DEFINITION Homo sapiens BAC clone Rp11-258B17 from 2, complete sequence.  
AC079773  
AC079773 8 GI:15145561  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 129676)  
AUTHORS Sulston, J.E. and Waterston, R.  
TITLE Toward a complete human genome sequence  
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792  
 PUBMED 9847074  
 REFERENCE 2 (bases 1 to 129676)  
 AUTHORS Shah,N., Meyer,R., Boyer,E. and Dignan,G.  
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 129676)  
 AUTHORS Waterston,R.H.  
 JOURNAL Direct Submission  
 Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 4 (bases 1 to 129676)  
 AUTHORS Waterston,R.H.  
 JOURNAL Direct Submission  
 Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 5 (bases 1 to 129676)  
 AUTHORS Waterston,R.H.  
 JOURNAL Direct Submission  
 Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 COMMENT On Aug 9, 2001 this sequence version replaced gi:14488388.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc  
 Contact: saplens@wustl.wustl.edu  
 ----- Summary Statistics  
 Center project name: H\_NH0258B17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:  
 The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatenos, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://dpcpac.med.buffalo.edu)  
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-1122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

FEATURES  
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 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

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1388..1412
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1397..3331
/rpt_family="L1"
2346..2370
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9444..9466
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11961..11969
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14175..14337
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20170..20305
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25485..25805
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26417..26463
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26466..26655
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                31494..31783
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                32028..32488
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repeat_region /rpt_family="(GA)n"
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repeat_region /rpt_family="MIR"
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repeat_region /rpt_family="L2"
                34271..34348
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                34409..34703
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGACAGAGACGCGCGCGGACGCGAAGACAGACGCGCGCTCCACAAACG 60
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Db 119919 AGTTCTCTTGACAGAGACGCGCGCGGACGCGAAGACAGACGCGCGCTCCACAAACG 119860

QY 61 GCGCGTGTGCGTGTGAGAGTGCATGTAGCGCGCGCTTCTGTTGTTGGCGTGTG 120
    |||||||
Db 119859 GCGCGTGTGCGTGTGAGAGTGCATGTAGCGCGCGCTTCTGTTGTTGGCGTGTG 119800

QY 121 CAGCGACAGGCGGCGACACACCTGTCAGAACACCCCGGAACTGTCGAGAGAC 180
    |||||||
Db 119799 CAGCGACAGGCGGCGACACACCTGTCAGAACACCCCGGAACTGTCGAGAGAC 119740

QY 181 CGGTGACAGAGGCGGTTGATGACCGCGTGTAGAGGTAGAAAAACTCTCCGAGAGGAG 240
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Db 119739 CGGTGACAGAGGCGGTTGATGACCGCGTGTAGAGGTAGAAAAACTCTCCGAGAGGAG 119680

QY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTGGTGGTGGCGCGAGC 300
    |||||||
Db 119679 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGCTGGTGGTGGCGCGAGC 119620

QY 301 CATGATCTCTCCGATCTGTTGGGCATCCAGCATCGGCCCAATGTCAACAAATCAGCCC 360
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Db 119619 CATGATCTCTCCGATCTGTTGGGCATCCAGCATCGGCCCAATGTCAACAAATCAGCCC 119560

QY 361 TGCGGACAGACGAGCAGAGGAGAGACAGAAAAAGAAAAACACACATGAGAACAG 420
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Db 119559 TGCGGACAGACGAGCAGAGGAGAGACAGAAAAAGAAAAACACACATGAGAACAG 119500

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QY 421 TAAATGATTAACCATTAATATTAGCCCTCTGTTCTGTGCTTACTGGCCAGAAAT 480
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QY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAGAGAGAAATT 540
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Db 119439 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCCACAGAGAGAAATT 119380

QY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 600
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Db 119379 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 119320

QY 601 ACAGTG 606
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Db 119319 ACAGTG 119314

RESULT 2
BC011449 826 bp mRNA linear PRI 22-AUG-2001
LOCUS     Homo sapiens, clone IMAGE:4026092, mRNA.
DEFINITION
ACCESSION BC011449
VERSION    BC011449.1 GI:15277472
KEYWORDS   SOURCE
ORGANISM   Homo sapiens.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 826)
REFERENCE 1
AUTHORS   Strausberg,R.
TITLE      Direct Submission
JOURNAL    Submitted (25-JUN-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.ncl.nih.gov
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DP
            CDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbio.org
            contact: amadensystemsbio.org
            Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
            Greene, Mark Kettelman and Anuradha Madan

REMARK
COMMENT    Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 25 Row: n Column: 18
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.

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            /db_xref="taxon:9606"
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            /lab_host="DH10B-R"
            /note="vector: pORF7"

BASE COUNT 237 a 197 c 228 g 164 t
ORIGIN
Query Match    88.8%; Score 555; DB 9; Length 826;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGACGCGCGTGCACAAACG 60
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Db 190 AGTTCTCTTGACAGAGACTGGCGCGGAGCGGAAGACAGACGCGCGTGCACAAACG 249

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QY 61 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGGTGGCGTGTG 120  
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 QY 121 CAGCGACAGCGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180  
 DB 310 CAGCGACAGCGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 369  
 QY 181 CGGTACAGAGCGCGGTGTATGACGAGTGAAGTGAAGAAACGCTCCGAGAGGGGAG 240  
 DB 370 CGGTACAGAGCGCGGTGTATGACGAGTGAAGTGAAGAAACGCTCCGAGAGGGGAG 429  
 QY 241 GAGGATCATGTACGCGCGGAGTAGAGCTCCGAGTGTGCTGGTGGTGGCGCAGC 300  
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 DB 490 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGCGCAATGTACAAATCAGCCC 549  
 QY 361 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 420  
 DB 550 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 609  
 QY 421 TAAATGAATAAACCATTAATATTATTAGCCCTCTGCTGTCTACTGCGCAGGAAT 480  
 DB 610 TAAATGAATAAACCATTAATATTATTAGCCCTCTGCTGTCTACTGCGCAGGAAT 669  
 QY 481 GGTACCAATTTTTCAGTGTGTGACCTTGTGACAGCTCTTTTGGCCAAAGACAGAAATTT 540  
 DB 670 GGTACCAATTTTTCAGTGTGTGACCTTGTGACAGCTCTTTTGGCCAAAGACAGAAATTT 729  
 QY 541 AACACGTTTCAACCCGGGGGAGTGGCTGTGTAAAGAACCATTAATAGCTTTAG 600  
 DB 730 AACACGTTTCAACCCGGGGGAGTGGCTGTGTAAAGAACCATTAATAGCTTTAG 789  
 QY 601 ACAGTG 606  
 DB 790 ACAGTG 795  
 RESULT 3  
 AK094501 1832 bp mRNA linear PRI 15-JUL-2002  
 LOCUS AK094501  
 DEFINITION Homo sapiens cDNA FLJ137182.1 f1s, clone BRALZ2001350, weakly similar to Homo sapiens Gz-selective GTPase-activating protein (GGS20) mRNA.  
 ACCESSION AK094501  
 VERSION AK094501.1 GI:21753575  
 KEYWORDS oligo capping; f1s (full insert sequence).  
 SOURCE Homo sapiens alzheimer cortex cDNA to mRNA, clone\_11b:BRALZ2 clone:BRALZ2001350.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1  
 AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanada, K., Waga, S., Oshima, A., Murakawa, K., Kanehori, K., Takahashi, F., Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K., and Isogai, T.  
 TITLE NED0 human cDNA sequencing project  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1832)  
 AUTHORS Isogai, T. and Yamamoto, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 COMMENT NED0 human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.  
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 BASE COUNT 411 a 501 c 513 g 407 t  
 ORIGIN  
 Query Match 88.8%; Score 555; DB 9; Length 1832;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGTTCTCTTTCAGAGAGTGGCGCGGACGCGGAGACGAGCAGGCGCTGACAAAGCG 60  
 DB 1226 AGTTCTCTTTCAGAGAGTGGCGCGGACGCGGAGACGAGCAGGCGCTGACAAAGCG 1285  
 QY 61 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGGTGGCGTGTG 120  
 DB 1286 GCGCGTGTGCTGTGAGTGGCATGTACGCGCAGGCGCTTCTGCTGGTGGCGTGTG 1345  
 QY 121 CAGCGACAGCGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180  
 DB 1346 CAGCGACAGCGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1405  
 QY 181 CGGTACAGAGCGCGGTGTATGACGAGTGAAGTGAAGAAACGCTCCGAGAGGGGAG 240  
 DB 1406 CGGTACAGAGCGCGGTGTATGACGAGTGAAGTGAAGAAACGCTCCGAGAGGGGAG 1465  
 QY 241 GAGGATCATGTACGCGCGGAGTAGAGCTCTGCTGCTGTGGTGGCGCAGC 300  
 DB 1466 GAGGATCATGTACGCGCGGAGTAGAGCTCTGCTGCTGTGGTGGCGCAGC 1525  
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 DB 1526 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGCGCAATGTACAAATCAGCCC 1585  
 QY 361 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 420  
 DB 1586 TGGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1645  
 QY 421 TAAATGAATAAACCATTAATATTATTAGCCCTCTGCTGTCTACTGCGCAGGAAT 480  
 DB 1646 TAAATGAATAAACCATTAATATTATTAGCCCTCTGCTGTCTACTGCGCAGGAAT 1705  
 QY 481 GGTACCAATTTTTCAGTGTGTGACCTTGTGACAGCTCTTTTGGCCAAAGACAGAAATTT 540  
 DB 1706 GGTACCAATTTTTCAGTGTGTGACCTTGTGACAGCTCTTTTGGCCAAAGACAGAAATTT 1765  
 QY 541 AACACGTTTCAACCCGGGGGAGTGGCTGTGTAAAGAACCATTAATAGCTTTAG 600  
 DB 1766 AACACGTTTCAACCCGGGGGAGTGGCTGTGTAAAGAACCATTAATAGCTTTAG 1825  
 QY 601 ACAGTG 606  
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RESULT 4	AXI36281	1890 bp	DNA	Linear	PAT 30-MAY-2001
LOCUS	AXI36281				
DEFINITION	Sequence 203 from Patent EP1067182.				
ACCESSION	AXI36281				
VERSION	AXI36281.1	GI:14272687			
KEYWORDS					
SOURCE	human.				
ORGANISM	human.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 1890)				
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.				
TITLE	Secretory protein or membrane protein				
JOURNAL	Patent: EP 1067182-A 203 10-JAN-2001;				
FEATURES	Helix Research Institute (UP)				
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CDS	/note="unnamed protein product"				
	/codon_start=1				
	/protein_id="CAC39782.1"				
	/db_xref="GI:14272688"				
	/translation="MWVIGIAATFCGLFLPGLALQIQYOCSEFOLNDCSPEVIT				
	NCITVNDMCKEYMEQISAGIMYRKSCASSAACLISAGYOSPCSPKLNVCISCN				
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BASE COUNT	419 a 528 c 533 g 410 t				
ORIGIN					
Query Match	87.8%; Score 549; DB 6; Length 1890;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches 599; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY	7 CCTTTCAGAGAGACTGGCCCGGAGCGGAGCGAAGACAAACGGCGGCGCT 66				
Db	1290 CCTTTCAGAGAGACTGGCCCGGAGCGGAGCGAAGACAAACGGCGGCGCT 1349				
QY	67 GTCGGTGTGGAGTGGCCGATGACGCGGAGCGGCGCTTCGCTGGTGGCGCTGCAGCGA 126				
Db	1350 GTCGGTGTGGAGTGGCCGATGACGCGGAGCGGCGCTTCGCTGGTGGCGCTGCAGCGA 1409				
QY	127 CAGGCGGAGCAGACAGACACTGCACGAAACACCCCGCGAAGTCTGCGAGACACCGTGA 186				
Db	1410 CAGGCGGAGCAGACAGACACTGCACGAAACACCCCGCGAAGTCTGCGAGACACCGTGA 1469				
QY	187 CAGAGCGCGCTTGATGACACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAGAGAGAT 246				
Db	1470 CAGAGCGCGCTTGATGACACCGAGCTGAGGTAGAAAAAGCTCTCCGAAAGGGAGAGAGAT 1529				
QY	247 CATGTACGCCCGGAAGTGTGAGACCTGTCACATCGGCTGTGGGTTGGCCGAGCCATGAT 306				
Db	1530 CATGTACGCCCGGAAGTGTGAGACCTGTCACATCGGCTGTGGGTTGGCCGAGCCATGAT 1589				
QY	307 CCTCCGAATCTGTGTTGGGCATTCACAGCATAGGCCCAATGTCAACAACATCAGCCCTGGGCA 366				
Db	1590 CCTCCGAATCTGTGTTGGGCATTCACAGCATAGGCCCAATGTCAACAACATCAGCCCTGGGCA 1649				
QY	367 GACACGACAGAGAGAGAGACAGAGAAAAAACAACACACATGAGAAACACAGTAATG 426				
Db	1650 GACACGACAGAGAGAGAGACAGAGAAAAAACAACACACATGAGAAACACAGTAATG 1709				
QY	427 AATAAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGGCCGAGAAATGTATCC 486				
Db	1710 AATAAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGGCCGAGAAATGTATCC 1769				
QY	487 AATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCCACAGCAAGAAATTTAACCT 546				

Db	1770	AAITTTTCAGTGTGACTTGCACACTCTTTTGGCCACAGACAGAAAGAAATTAAACT	1829
Qy	547	GTTTAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAATGCTTTAGACATG	606
Db	1830	GTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAGACATG	1889
RESULT 5			
AX358762			
LOCUS	AX358762	1524 bp	DNA
DEFINITION	Sequence 15 from Patent WO0193983.		linear
ACCESSION	AX358762		
VERSION	AX358762.1	GI:18675282	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,		
	Godwin, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,		
	Matanabe, C.K. and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
	the same		
JOURNAL	Patent: WO 0193983-A 15 13-DEC-2001;		
FEATURES	Genentech Inc. (US)		
source	Location/Qualifiers		
	1..1524		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	321 a 433 c 435 g 335 t		
ORIGIN			
Query Match	62.9%; Score 393; DB 6; Length 1524;		
Best Local Similarity	100.0%; Pred. NO. 1.8e-228;		
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	AGTTCTCCTTCAGAGACTGGCCGGGAGCGGAGCAAGAGCAAGGGCGCTGCACAAACG	60
Db	1132	AGTTCTCCTTCAGAGACTGGCCGGGAGCGGAGCAAGAGCAAGGGCGCTGCACAAACG	1191
Qy	61	GGCGGTGCGGTGTGGAGTGGCATGTACGCGCAGGGCGTTCTGTGTGGCTGCTG	120
Db	1192	GGCGGTGCGGTGTGGAGTGGCATGTACGCGCAGGGCGTTCTGTGTGGCTGCTG	1251
Qy	121	CAGCGACAGGGGCGCAGCAGCACCCTGCACGAACACCCGCGAAATCTCTCGAGAGAC	180
Db	1252	CAGCGACAGGGGCGCAGCAGCACCCTGCACGAACACCCGCGAAATCTCTCGAGAGAC	1311
Qy	181	CGTGTACAGAGACGGGTTGATGACCGAGCTGAGTAAAGAAACGTCCTCGAAGGGAG	240
Db	1312	CGTGTACAGAGACGGGTTGATGACCGAGCTGAGTAAAGAAACGTCCTCGAAGGGAG	1371
Qy	241	GAGGATCATGTAGAGCCCGGAAGTAGACCTGCTCCAGTGGCTTGGGCGGCGAGC	300
Db	1372	GAGGATCATGTAGAGCCCGGAAGTAGACCTGCTCCAGTGGCTTGGGCGGCGAGC	1431
Qy	301	CATGATCTCCGAATCTGTTGGGCGATCCAGCATAGCGGCAATGTCAACAATACGCC	360
Db	1432	CATGATCTCCGAATCTGTTGGGCGATCCAGCATAGCGGCAATGTCAACAATACGCC	1491
Qy	361	TGGGACAGACAGAGAGAGAGAGAGAGAGA 393	
Db	1492	TGGGACAGACAGAGAGAGAGAGAGAGAGA 1524	
RESULT 6			
AX362255			
LOCUS	AX362255	1524 bp	DNA
DEFINITION	Sequence 15 from Patent WO0208288.		linear
ACCESSION	AX362255		
VERSION	AX362255.1	GI:18694585	
KEYWORDS			

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..1524  
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Query Match 62.9%; Score 393; DB 6; Length 1524;  
Best Local Similarity 100.0%; Pred. No. 1.8e-228;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGAGAGAGACTGCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 60  
DB 1132 AGTTCTCTTGAGAGAGACTGCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 1191

QY 61 GGGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120  
DB 1192 GGGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1251

QY 121 CAGCGACAGCGGAG 180  
DB 1252 CAGCGACAGCGGAG 1311

QY 181 CGTGTACAGAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAGGGGAG 240  
DB 1312 CGTGTACAGAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAGGGGAG 1371

QY 241 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
DB 1372 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431

QY 301 CATGATCTCTCCGATCTGTTGGGATCCAGCATACGGCCAAATGTCAACAATCAGCCC 360  
DB 1432 CATGATCTCTCCGATCTGTTGGGATCCAGCATACGGCCAAATGTCAACAATCAGCCC 1491

QY 361 TGGCGACAGACGAG 393  
DB 1492 TGGCGACAGACGAG 1524

RESULT 7  
AX136698/c 587 bp DNA linear PAT 30-MAY-2001  
LOCUS Sequence 620 from Patent EP1067182.  
DEFINITION AX136698  
ACCESSION AX136698  
VERSION AX136698.1 GI:14273102  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ota, T., Isega, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.  
TITLE Secretory protein or membrane protein  
JOURNAL Patent: EP 1067182-A 620 10-JAN-2001;  
Helix Research Institute (JP)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"

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ORIGIN

Query Match 58.4%; Score 365; DB 6; Length 587;  
Best Local Similarity 99.8%; Pred. No. 2.3e-211;  
Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 191 AGCGGTTGATGACCGAG 250  
DB 417 AGCGGTTGATGACCGAG 358

QY 251 TAGCGCCGAGAGTAG 310  
DB 357 TAGCGCCGAGAGTAG 298

QY 311 CGAATCTGTTGGGATCCAGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 370  
DB 297 CGAATCTGTTGGGATCCAGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 238

QY 371 CGAGCAG 430  
DB 237 CGAGCAG 178

QY 431 AAACATTAATAATTTAGCCCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 490  
DB 177 AAACATTAATAATTTAGCCCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 118

QY 491 TTTTCACTGTTGAGCTTGACAGCTTCTTTTCCCAAGCAAGAGAGAGAGAGAGAGAGAGAG 550  
DB 117 TTTTCACTGTTGAGCTTGACAGCTTCTTTTCCCAAGCAAGAGAGAGAGAGAGAGAGAGAG 58

QY 551 CAAACCGGGGGAG 606  
DB 57 CAAACCGGGGGAG 2

RESULT 8  
AX139942/c 1362 bp DNA linear PAT 14-DEC-2001  
LOCUS Sequence 1 from Patent WO0181634.  
DEFINITION AX139942  
ACCESSION AX139942  
VERSION AX139942.1 GI:17901489  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Galvin, K.A. and Rudolph-Owen, L.A.  
TITLE Methods and compositions for the diagnosis and treatment of cardiovascular and tumorigenic disease using 4941  
JOURNAL Millennium Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..1362  
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VTSALVALPLFAMGTEYPLVNVPSHRGLTCRSTRHDEPSTNMSICTLSSRWI  
VFOSSIFGAFVYLVLVLSVAFMCMNMQVLAAPKSKGSLAGSTRPPOLEKSSSEST  
AARQITIEFLIVTLVAVCMNPQIRIMAAKPKHDMTRSYFRAYMILLPSESEFY  
LSSVINPLLYTSOOPFRVEYOVLCRSLQHANHEKRLVYHAHSTDSARFVORPL  
LEASRQSSARTEKIFLSTPSEAEPOKSKSLSELEPNSGAKPANSANENGFOE  
HEV"

BASE COUNT 263 a 435 c 362 g 302 t  
ORIGIN

Query Match 57.4%; Score 359; DB 6; Length 1362;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-207;  
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGAGAGTGGCCGGGAGCGGAGAGCAACGCGCTGCACAAAGCG 60  
 DB 1215 AGTTCTCTTGCAGAGAGAGTGGCCGGGAGCGGAGAGCAACGCGCTGCACAAAGCG 1156  
 QY 61 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 120  
 DB 1155 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 1096  
 QY 121 CAGCGACAGCGCGGAGAGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 180  
 DB 1095 CAGCGACAGCGCGGAGAGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 1036  
 QY 181 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGGAAGAGGAG 240  
 DB 1035 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGGAAGAGGAG 976  
 QY 241 GAGGATCATGTAGCGCGGAGTGGAGCTGTCAGTGGTGGTGGTGGCGGAGC 300  
 DB 975 GAGGATCATGTAGCGCGGAGTGGAGCTGTCAGTGGTGGTGGTGGCGGAGC 916  
 QY 301 CATGATCTCTCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 359  
 DB 915 CATGATCTCTCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 857

RESULT 9  
 AF034633/c 1362 bp mRNA linear PRI 13-JUL-1998  
 LOCUS Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,  
 DEFINITION complete cds.  
 ACCESSION AF034633  
 VERSION AF034633.1 GI:2654160  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1362)  
 AUTHORS McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,  
 Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,L.H.  
 Cloning and characterization of two human G protein-coupled  
 receptor genes (GPR38 and GPR39) related to the growth hormone  
 secretagogue and neurotensin receptors  
 Genomics 46 (3), 426-434 (1997)

JOURNAL 2 (bases 1 to 1362)  
 MEDLINE 98110578  
 PUBMED 9441746  
 REFERENCE 2 (bases 1 to 1362)  
 AUTHORS McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feighner,S.D.,  
 Hreniuk,D.L., Smith,R.G., Van Der Ploeg,L.H.T. and Howard,A.D.  
 Direct Submission  
 JOURNAL Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co.,  
 Inc., PO Box 2000, Rahway, NJ 07065, USA  
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 VTSALVALPLLFAMGTEYPLVNVPSHRGLTCSRSTRHHEQPTSNMSICTNLISMT  
 VFOOSIFGAFVYLVLVLSVAFMCMNMVYLKSSQGSJAGSTRPOLKSESESR  
 ARQCTIIFLRILVTLAVCMNPQIRIAAAPHKIDMTSYFRAYMILPFSETEFY  
 LSSVNLPLTVSSQGFRRVFOVLCRSLQHANHEKRLRYHAHSTDSARVORPL  
 LFASRRSSARTEKIFLSTPSEAEPOKSSLSLESLPEPNSGAKPANSAAENGRQE  
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 BASE COUNT 263 a 435 c 362 g 302 t  
 ORIGIN

Query Match 57.4%; Score 359; DB 9; Length 1362;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-207;  
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGAGTGGCCGGGAGCGGAGAGCAACGCGCTGCACAAAGCG 60  
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 DB 1155 GCGCGTGTGGTGGTGGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 1096  
 QY 121 CAGCGACAGCGCGGAGAGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 180  
 DB 1095 CAGCGACAGCGCGGAGAGAGTGGCATGTAGCGGAGCGCTTCCTCGGTGGTGGCGTGTG 1036  
 QY 181 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGGAAGAGGAG 240  
 DB 1035 CGTGTACAGAGAGCGGCTGTATGACCGAGCTGAGGTAGAAAAAGCTTCGGAAGAGGAG 976  
 QY 241 GAGGATCATGTAGCGCGGAGTGGAGCTGTCAGTGGTGGTGGTGGCGGAGC 300  
 DB 975 GAGGATCATGTAGCGCGGAGTGGAGCTGTCAGTGGTGGTGGTGGCGGAGC 916  
 QY 301 CATGATCTCTCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 359  
 DB 915 CATGATCTCTCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 857

RESULT 10  
 AX319944/c 2528 bp DNA linear PAT 14-DEC-2001  
 LOCUS Sequence 3 from Patent WO0181634.  
 ACCESSION AX319944  
 VERSION AX319944.1 GI:17901491  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Galvin,K.A. and Rudolph-Owen,L.A.  
 TITLE Methods and compositions for the diagnosis and treatment of  
 cardiovascular and tumorigenic disease using 4941  
 Patent: WO 0181634-A 3 01-NOV-2001;  
 JOURNAL Millennium Pharmaceuticals, Inc. (US)  
 FEATURES  
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 /db\_xref="taxon:9606"  
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 SYTISCKLHTLFECSTATLHVTLFSERIATCPHPRIVAVSGPCOVKLLIGFVW  
 VTSALVALPLLFAMGTEYPLVNVPSHRGLTCSRSTRHHEQPTSNMSICTNLISMT"

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 SYTISCKLHTLFECSTATLHVTLFSERIATCPHPRIVAVSGPCOVKLLIGFVW  
 VTSALVALPLLFAMGTEYPLVNVPSHRGLTCSRSTRHHEQPTSNMSICTNLISMT"



TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Weinstock, G. and Gibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 92874)  
Worley, R.C.  
Direct Submission  
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 92874)  
Worley, R.C.  
Direct Submission  
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 13, 2002 this sequence version replaced g1:20303189.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GRJD  
Center clone name: CH230-286021  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 32512 bases at least Q40  
Consensus quality: 34515 bases at least Q30  
Consensus quality: 35930 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 50 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
1057: contig of 1057 bp in length  
1058 1157: gap of unknown length  
1158 2410: contig of 1253 bp in length  
2411 2510: gap of unknown length  
2511 3571: contig of 1061 bp in length  
3572 3672: gap of unknown length  
3672 5359: contig of 1588 bp in length  
5359 5260: gap of unknown length  
5260 6436: contig of 1077 bp in length  
6436 6537: gap of unknown length  
6537 7705: contig of 1169 bp in length  
7705 7806: gap of unknown length  
7806 8911: contig of 1106 bp in length  
8911 9012: gap of unknown length  
9012 10370: contig of 1359 bp in length  
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11915 12014: gap of unknown length  
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13145 13245: gap of unknown length  
13245 14584: contig of 1339 bp in length  
14584 14685: gap of unknown length  
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17756 19240: contig of 1485 bp in length  
19240 19341: gap of unknown length  
19341 20647: contig of 1307 bp in length  
20647 20747: gap of unknown length  
20747 22171: contig of 1424 bp in length  
22171

FEATURES  
source

22272 22272: gap of unknown length  
22272 23762: contig of 1491 bp in length  
23762 23862: gap of unknown length  
23862 25356: contig of 1694 bp in length  
25356 25657: gap of unknown length  
25657 26711: contig of 1055 bp in length  
26711 26811: gap of unknown length  
26811 28747: contig of 1936 bp in length  
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35624 37292: contig of 1668 bp in length  
37292 37392: gap of unknown length  
37392 38486: contig of 1094 bp in length  
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74628 74728: gap of unknown length  
74728 76923: contig of 2194 bp in length  
76923 77023: gap of unknown length  
77023 79345: contig of 2323 bp in length  
79345 79445: gap of unknown length  
79445 82316: contig of 2871 bp in length  
82316 82416: gap of unknown length  
82416 84866: contig of 2450 bp in length  
84866 84967: gap of unknown length  
84967 87959: contig of 2993 bp in length  
87959 88060: gap of unknown length  
88060 92874: contig of 4815 bp in length.  
92874  
Location/Qualifiers  
1..92874  
/organism="Rattus norvegicus"  
/db\_xref="taxon:10116"  
/clone="CH230-286021"

BASE COUNT 23927 a 19653 c 20425 g 23828 t 5041 others  
ORIGIN

Query Match 4.3%; Score 27; DB 2; Length 92874;  
Best Local Similarity 100.0%; Pred. No. 0.00041;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 GAGAGGAGGAGGAGATCATGACGCC 256  
|||||

Db 75643 GAGAGGAGGAGGAGATCATGACGCC 75669

RESULT 13  
AC099984 70395 bp DNA linear HTG 22-NOV-2001  
LOCUS AC099984  
DEFINITION Mus musculus clone RP23-24D9, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC099984  
VERSION AC099984.1 GI:17047350  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Mus musculus.  
ORGANISM Mus musculus.

REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Baran, N., Bastien, V., Boguslavsky, L., Bouckigalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeBartolano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Harford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lemazures, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menusz, L., Milhova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnuppach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

JOURNAL  
TITLE  
REFERENCE  
AUTHORS

Unpublished  
2 (bases 1 to 70395)  
1 (bases 1 to 70395)  
Mus musculus, clone RP23-24D9  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L13721  
Center clone name: 24\_D\_9

NOTE: This record contains 84 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone

\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 734: contig of 734 bp in length  
735 834: gap of 100 bp  
835 1576: contig of 742 bp in length  
1577 1676: gap of 100 bp  
1677 2451: contig of 775 bp in length  
2452 2551: gap of 100 bp  
2552 3284: contig of 733 bp in length  
3285 3384: gap of 100 bp  
3385 4118: contig of 734 bp in length  
4119 4218: gap of 100 bp  
4219 4957: contig of 739 bp in length  
4958 5057: gap of 100 bp  
5058 5810: contig of 753 bp in length  
5811 5910: gap of 100 bp  
5911 6622: contig of 712 bp in length  
6623 6722: gap of 100 bp  
6723 7458: contig of 736 bp in length  
7459 7558: gap of 100 bp  
7559 8357: contig of 799 bp in length  
8358 8457: gap of 100 bp  
8458 9202: contig of 745 bp in length  
9203 9302: gap of 100 bp  
9303 10054: contig of 752 bp in length  
10055 10154: gap of 100 bp  
10155 10911: contig of 757 bp in length  
10912 11011: gap of 100 bp  
11012 11745: contig of 734 bp in length  
11746 11845: gap of 100 bp  
11846 12584: contig of 739 bp in length  
12585 12684: gap of 100 bp  
12685 13430: contig of 746 bp in length  
13431 13530: gap of 100 bp  
13531 14266: contig of 736 bp in length  
14267 14366: gap of 100 bp  
14367 15105: contig of 739 bp in length  
15106 15205: gap of 100 bp  
15206 15932: contig of 727 bp in length  
15933 16032: gap of 100 bp  
16033 16767: contig of 725 bp in length  
16768 16867: gap of 100 bp  
16868 17607: contig of 740 bp in length  
17608 17707: gap of 100 bp  
17708 18512: contig of 805 bp in length  
18513 18612: gap of 100 bp  
18613 19336: contig of 724 bp in length  
19337 19436: gap of 100 bp  
19437 20162: contig of 726 bp in length  
20163 20262: gap of 100 bp  
20263 21001: contig of 739 bp in length  
21002 21101: gap of 100 bp  
21102 21820: contig of 719 bp in length  
21821 21920: gap of 100 bp  
21921 22647: contig of 727 bp in length  
22648 22747: gap of 100 bp  
22748 23424: contig of 677 bp in length  
23425 23524: gap of 100 bp  
23525 24268: contig of 744 bp in length  
24269 24368: gap of 100 bp  
24369 25107: contig of 739 bp in length  
25108 25207: gap of 100 bp  
25208 25956: contig of 749 bp in length  
25957 26056: gap of 100 bp  
26057 26801: contig of 745 bp in length  
26802 26901: gap of 100 bp  
26902 27633: contig of 732 bp in length  
27634 27733: gap of 100 bp  
27734 28467: contig of 734 bp in length  
28468 28567: gap of 100 bp  
28568 29307: contig of 740 bp in length  
29308 29407: gap of 100 bp







REFERENCE 1 (bases 1 to 176967)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Homo sapiens chromosome 15, clone RP11-762A1  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 176967)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bede, F.,  
 Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,  
 Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
 Dearellano, K., Dewar, K., Domino, M., Doyle, M., Feneator, J.,  
 Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,  
 Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
 Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
 Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,  
 Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,  
 McPheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,  
 Plierre, N., Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,  
 Zimmer, A. and Zody, M.

TITLE Direct Submission  
 JOURNAL Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome  
 COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Feb 25, 2001 this sequence version replaced g1:11990718.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: 762\_A1  
 Center clone name: 762\_A1

Summary Statistics  
 Sequencing vector: M13; M77815; 2% of reads  
 Chemistry: Dye-terminator Big Dye; 98% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 176032 bases at least Q40  
 Consensus quality: 176449 bases at least Q30  
 Consensus quality: 176615 bases at least Q20  
 Insert size: 186000; agarose-ff  
 Quality coverage: 9.0 in Q20 bases; agarose-ff  
 Quality coverage: 9.5 in Q20 bases.

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 14400: contig of 14400 bp in length  
 \* 14401 14500: gap of 100 bp  
 \* 14501 61165: contig of 46665 bp in length  
 \* 61166 61265: gap of 100 bp  
 \* 61266 112521: contig of 51256 bp in length  
 \* 112522 112621: gap of 100 bp  
 \* 112622 176967: contig of 64346 bp in length.

FEATURES  
 SOURCE  
 1. 176967  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="15"  
 /map="15"  
 /clone="RP11-762A1"  
 /clone\_1lb="RPCT-11 Human Male BAC"

misc-feature

1. 14400  
 /note="assembly-fragment  
 clone\_end:SP6  
 vector\_side:left"  
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 14501..61165  
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 misc-feature  
 61266..112521  
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 misc-feature  
 112622..176967  
 /note="assembly-fragment  
 clone\_end:T7  
 vector\_side:right"

BASE COUNT 53791 a 35746 c 36226 g 50904 t 300 others

ORIGIN

Query Match 3 7%: Score 23; DB 2: Length 176967;  
 Best Local Similarity 100.0%; Pred. NO. 0.12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GAGACAGACAGAAAAGAAAACA 404

Db 166420 GAGACAGACAGAAAAGAAAACA 166398

RESULT 17  
 AC022824  
 LOCUS

DEFINITION Homo sapiens chromosome 15 clone RP11-81117 map 15, WORKING DRAFT  
 SEQUENCE, 8 unordered pieces.

ACCESSION AC022824.5 GI:22123655

VERSION AC022824.5  
 KEYWORDS HTG: HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULFILLP.  
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 180837)

AUTHORS Birren, B., Nusbaum, C. and Lander, E.

TITLE Homo sapiens chromosome 15, clone RP11-81117

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 180837)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bede, F.,  
 Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,  
 Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
 Dearellano, K., Dewar, K., Domino, M., Doyle, M., Feneator, J.,  
 Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,  
 Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
 Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
 Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,  
 Macdonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,  
 McPheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,  
 Plierre, N., Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,  
 Zimmer, A. and Zody, M.

Direct Submission

Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 180837)

REFERENCE Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

AUTHORS Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Chepel, Y., Collymore, A.,  
 Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,  
 Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,  
 McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,





LOCUS	AC090971/c	192464 bp	DNA	linear	PRI 27-NOV-2001
DEFINITION	Homo sapiens chromosome 15 clone RP11-56B16 map 15q21.3, complete sequence.				
ACCESSION	AC090971				
VERSION	AC090971.3	GI:17105278			
KEYWORDS	HTG.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	MurrayYota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 192464) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dots, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.				
TITLE	Sequencing of human chromosome 15 D15S146-D15S117 region				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 192464) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dots, M., Dichtoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Tralcoff, R. and Hood, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAR-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA				
REFERENCE	3 (bases 1 to 192464) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dots, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.				
AUTHORS	Direct Submission				
TITLE	Submitted (27-NOV-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA				
COMMENT	On Nov 27, 2001 this sequence version replaced gi:13624393. ----- Genome Center Center: Multimegabase Sequencing Center Center code: UMWSC Web site: http://chroma.mbl.washington.edu/msg_www Contact: leorowen@systemsbiology.org ----- Summary Statistics Sequencing vector: pUC18; L08752 Chemistry: Dye-terminator Big Dye; 90% of reads Chemistry: Dye-terminator Big Dye; 10% of reads Assembly program: Phrap; version 0.990399				
FEATURES	Note: Data from overlapping BACs AC026770 [drafting center: UMWSC], AC011639 [drafting center: WMBR], AC016824 [drafting center: GTC], and AC090970 [drafting center: UMWSC] was added for finishing.				
SOURCE	Location/Qualifiers 1..192464 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="15" /map="15q21.3" /clone="RP11-56B16" /clone_lib="RPCI human BAC library 11" /note="Data from overlapping BACs CTD-2308G16, RP11-13H19, RP11-47K1, and CTD-2650P22 was added and the consensus sequence was determined from RP11-56B16 to the extent possible" 1..167631 /note="Overlap with RP11-13H19 AC011639" 1..12888 /note="Overlap with CTD-2308G16 AC026770" 76219..192464 /note="Overlap with CTD-2650P22 AC090970" 80765..192464 /note="Overlap with RP11-47K1 AC016824"				
BASE COUNT	56858 a 39351 c 40295 g 55960 t				
ORIGIN					

	Query Match	Score 23:	DB 9:	Length 192464;
	Best Local Similarity	100.0%	Pred. No. 0.13;	
Matches	23; Conservative	0;	Mismatches	0; Indels
				Gaps 0;
Oy	382 GAGACACAGAAAAAACA	404		
Db	1656 GAGACACAGAAAAAACA	1634		

RESULT	20
AC126666/c	Locus
DEFINITION	AC126666      200145 bp    DNA          linear       HTG-11-JUL-2002 Rattus norvegicus clone CH230-3P12, *** SEQUENCING IN PROGRESS ***, 61 unordered pieces.
ACCESSION	AC126666
VERSION	AC126666.1 GI:21703541
KEYWORDS	HTG; HGMS.PHASE1.
SOURCE	Norway rat. Rattus norvegicus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 200145)
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T., Barbadi,A.J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.J., Bowie,S., Brivet,M., Brown,E., Brown,M., Bryant,N.P., Buhalc,C., Burich,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davey-Carroll,L., Dedrich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Donhaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Easthart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabelis,A., Gau,j., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guvera,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huliy.S., Hume,J., Jackson,L.E., Jacobson,B., Jia,X., Johnson,R., Jolive,S., Jouhad,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,U., Kover,C., Kratochv,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Li,J., Li,z., Licharge,O., Lieu,C., Liu,J., Liu.W., Loulseged,H., Locado,R.J., Lu,X., Lucier,A., Lucier,R., Lune,R., Ma,f., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel.G., Metzker,M., Miner,G., Miner.Z., Mitchell.T., Monabati.K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newton.N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokkenko,S., Ogum,M., Okwuonu.G., Orangunye,N., Oviedo,R., Pace,A., Payton.B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Qules,M., Ren,X., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N., Slisson.I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Swatek,A., Tabop,P., Tamerisa,A., Tamersiz,K., Tang,H., Taney,J., Taylor,C., Taylor,V., Tellford,B., Thomas.N., Thomas,S., Usmani,K., Vasquez,L., Vera.Y., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-More-S., Warren,R., Washington,C., Wallington,S., Williams.G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,y., Wu,Y.F., Zhou,d., Zorrilla,s., Nelson,D., Weinstock,G. and Gibbs.R.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 200145) Worley,K.C. Direct Submission
AUTHORS	Submitted (08-JUL-2002) Human Genome Sequencing Center, Department Of Molecular And Human Genetics, Baylor College Of Medicine, One Baylor Plaza, Houston, TX 77030, USA
JOURNALT	3 (bases 1 to 200145)

**AUTHORS**  
**TITLE** Worley, K.C.  
**JOURNAL** Direct Submission  
 Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
**COMMENT** ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GARR  
 Center clone name: CH230-3p12  
 ----- Summary Statistics  
 Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 141149 bases at least Q40  
 Consensus quality: 153199 bases at least Q30  
 Consensus quality: 163387 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 61 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1  
 1278 1277: contig of 1277 bp in length  
 1378 1377: gap of unknown length  
 2612 2611: contig of 1234 bp in length  
 2712 2711: gap of unknown length  
 3824 3823: contig of 1112 bp in length  
 3924 3923: gap of unknown length  
 5558 5557: contig of 1634 bp in length  
 5658 5657: gap of unknown length  
 6745 6744: contig of 1087 bp in length  
 6845 6844: gap of unknown length  
 9032 9031: contig of 2188 bp in length  
 9132 9131: gap of unknown length  
 9133 9132: contig of 1034 bp in length  
 10166 10165: gap of unknown length  
 10167 10166: gap of unknown length  
 10267 10266: contig of 1950 bp in length  
 12217 12216: gap of unknown length  
 12317 12316: gap of unknown length  
 13659 13658: contig of 1343 bp in length  
 13759 13758: gap of unknown length  
 14883 14882: contig of 1123 bp in length  
 14982 14981: gap of unknown length  
 16043 16042: contig of 1061 bp in length  
 16143 16142: gap of unknown length  
 17419 17418: contig of 1276 bp in length  
 17519 17518: gap of unknown length  
 18666 18665: contig of 1147 bp in length  
 18766 18765: gap of unknown length  
 20244 20243: contig of 1478 bp in length  
 20344 20343: gap of unknown length  
 21981 21980: contig of 1636 bp in length  
 22080 22079: gap of unknown length  
 23559 23558: contig of 1479 bp in length  
 23659 23658: gap of unknown length  
 26064 26063: contig of 2405 bp in length  
 26164 26163: gap of unknown length  
 28332 28331: contig of 2068 bp in length  
 28333 28332: gap of unknown length  
 29791 29790: contig of 1459 bp in length  
 29891 29890: gap of unknown length  
 32062 32061: contig of 2171 bp in length  
 32162 32161: gap of unknown length  
 33492 33491: contig of 1330 bp in length  
 33592 33591: gap of unknown length  
 36632 36631: contig of 3040 bp in length

36633 36732: gap of unknown length  
 36733 38706: contig of 1974 bp in length  
 38707 38806: gap of unknown length  
 38807 41743: contig of 2937 bp in length  
 41744 41843: gap of unknown length  
 41844 43997: contig of 2154 bp in length  
 43998 44097: gap of unknown length  
 44098 46188: contig of 2091 bp in length  
 46189 46288: gap of unknown length  
 46289 47496: contig of 1208 bp in length  
 47497 47596: gap of unknown length  
 47597 50501: contig of 2905 bp in length  
 50502 50601: gap of unknown length  
 50602 52796: contig of 2195 bp in length  
 52797 52896: gap of unknown length  
 52897 54956: contig of 2066 bp in length  
 54957 55056: gap of unknown length  
 55057 57502: contig of 2446 bp in length  
 57503 57602: gap of unknown length  
 57603 60331: contig of 2729 bp in length  
 60332 60431: gap of unknown length  
 60432 64147: contig of 3716 bp in length  
 64148 64247: gap of unknown length  
 64248 67257: contig of 3010 bp in length  
 67258 67357: gap of unknown length  
 67358 70431: contig of 3074 bp in length  
 70432 70531: gap of unknown length  
 70532 73160: contig of 2629 bp in length  
 73161 73260: gap of unknown length  
 73261 76727: contig of 3467 bp in length  
 76728 76827: gap of unknown length  
 76828 79798: contig of 2971 bp in length  
 79799 79898: gap of unknown length  
 79899 83250: contig of 3352 bp in length  
 83251 83350: gap of unknown length  
 83351 87386: contig of 4036 bp in length  
 87387 87486: gap of unknown length  
 87487 92256: contig of 4770 bp in length  
 92257 92356: gap of unknown length  
 92357 95623: contig of 3267 bp in length  
 95624 95723: gap of unknown length  
 95724 100814: contig of 5091 bp in length  
 100815 100914: gap of unknown length  
 100915 103683: contig of 2769 bp in length  
 103684 103784: gap of unknown length  
 103784 107334: contig of 3551 bp in length  
 107335 107434: gap of unknown length  
 107435 112025: contig of 4591 bp in length  
 112026 112125: gap of unknown length  
 112126 115493: contig of 3268 bp in length  
 115494 115493: gap of unknown length  
 115494 120200: contig of 4707 bp in length  
 120201 126100: gap of unknown length  
 126100 126200: gap of unknown length  
 126201 129942: contig of 3742 bp in length  
 129943 130042: gap of unknown length  
 130043 133696: contig of 3654 bp in length  
 133697 133796: gap of unknown length  
 133797 138631: contig of 4835 bp in length  
 138632 138731: gap of unknown length  
 138732 144408: contig of 5677 bp in length  
 144409 144508: gap of unknown length  
 144509 149333: contig of 4825 bp in length  
 149334 149433: gap of unknown length  
 149434 153926: contig of 4483 bp in length

Query Match 3.7%: Score 23; DB 2; Length 200145;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 23; Conservatively 0; Mismatches 0; Indels 0; Gaps 0;  
 0Y 377 GGAGCGAGACGACGAGAAAGAA 399  
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="5"
/clone="RAF105-01-E17(R21170)"
/notes="ecotype: Columbia"

BASE COUNT      541 a      376 c      450 g      615 t

Query Match
Best Local Similarity 100.0%; Score 22; DB 8; Length 1982;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 374 GCAGGAGGAGAGACAGAGAAA 395
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Db 1697 GCAGGAGGAGAGACAGAGAAA 1718

RESULT 24
LOCUS NTA294474 2666 bp mRNA linear PLN 12-APR-2002
DEFINITION Nicotiana tabacum mRNA for SET-domain-containing protein (set1
gene).
ACCESSION AJ294474
VERSION AJ294474.1 GI:15485583
KEYWORDS SET-domain-containing protein; set1 gene.
SOURCE common tobacco.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS Shen, W.H.
TITLE NtSET1, a member of a newly identified subgroup of plant
SET-domain-containing proteins, is chromatin-associated and its
ectopic overexpression inhibits tobacco plant growth
JOURNAL Plant J. 28 (4), 371-383 (2001)
MEDLINE 21605275
PUBMED 11737775

REFERENCE
AUTHORS Shen, W.H.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2000) Shen W.H., Biologie Cellulaire, Institut de
Biologie Molculaire des Plantes, 12 rue du General Zimmer,
Strasbourg 67084, FRANCE

FEATURES
source Location/Qualifiers
1..2666
/organism="Nicotiana tabacum"
/db_xref="taxon:4097"
/clone="P8F83b"
/cell_line="BY2"
/clone_lib="lambda-ZAP"
1..2666
/gene="set1"
/feature="set1"
157..2271
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/function="chromatin modeling"
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/protein_id="CAC67503.1"
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VEDELRRTQIDESRDGSGRBDLAKSNMLMTGVTNQRIGNAPGIEVGL
EFEMELCVGLAAPTMAIDYMSKLTMEDEPLAVISVSGDGGDGLITGGO
GGVORKDQGVDFQKLEKRLALEKSVHRANEVYRIVGCVADVAPGKITYDGLXIO
ESMAEKNGVGVNFKYKILRVGQPEAEVYMSIOQKCVASRVVILPDLTSGAS
OPVCLVNDVDEKPAFTYITPSLAKSKFVWPRSPSCHVGGCQPGDSNCACIOSN
GGFLPYSGLVILSTKITLHEGSAACSPNCRNRSQGPAPARLDFVTKNKGWGLR
SWDPLRGGFICEVAGVIDAQNSDNDITFPAIRIYALEERDNDERSKVPFPLV
ISAKNGNISIRMHNSCPNVYMWLVVROSNNEDATYHIAFFAIRHIPQDELFDYGM

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```

DRADHRKKCLCGSLNCRGYFY"

BASE COUNT      739 a      477 c      659 g      790 t      1 others

Query Match
Best Local Similarity 100.0%; Score 22; DB 8; Length 2666;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNAAAAAAAAAAAAAAAAA 625
|||||
Db 2632 GTGNAAAAAAAAAAAAAAAAA 2653

RESULT 25
LOCUS AF035577 3190 bp mRNA linear INV 05-MAY-2000
DEFINITION Amblyomma americanum retinoid X receptor (RXR1) mRNA, complete cds.
ACCESSION AF035577
VERSION AF035577.1 GI:3098333
KEYWORDS
SOURCE Amblyomma americanum.
ORGANISM Amblyomma americanum
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Amblyomma.
1 (bases 1 to 3190)
Guo, X., Xu, Q., Harmon, M.A., Jin, X., Laudet, V., Mangelsdorf, D.J. and
Palmer, M.J.
Isolation of two functional retinoid X receptor subtypes from the
Ixodid tick, Amblyomma americanum (L.)
Mol. Cell. Endocrinol. 139 (1-2), 45-60 (1998)
9705073

REFERENCE
AUTHORS Palmer, M.J., Guo, X. and Xu, Q.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1997) Entomology, Oklahoma State University, 127
Noble Research Center, Stillwater, OK 74078, USA

FEATURES
source Location/Qualifiers
1..3190
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91..1293
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/db_xref="GI:3098334"
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ADSEVESTSGGAPPEPMPLERLIEALRVSQGTSESAQODPPVSSICQADAROLHO
LVQWAKHLPHEEELPLEDRMVLKAGWELLTAASHSRVSVDGIVLATGLVQRRS
AHGAGVGAIIPDRLTELVAKMKREKMDRTLEGLCLAVLVFNPEAKGLRCPSCGPGGE
SVSALEEHCRQOQPPQGRFPAKMLRLRLPALRSTIGKLEHLFFFKLIGPTIDNFFLS
MLEAPSDP"

BASE COUNT      800 a      723 c      785 g      881 t      1 others

Query Match
Best Local Similarity 100.0%; Score 22; DB 3; Length 3190;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNAAAAAAAAAAAAAAAAA 625
|||||
Db 3169 GTGNAAAAAAAAAAAAAAAAA 3190

RESULT 26
LOCUS AB019231 4370 bp DNA linear PLN 27-DEC-2000
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone:MG03.

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ACCESSION AB019231 BA000015  
 VERSION AB019231.1 GI:3869070  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (strain:Colombia) DNA, clone\_11b:Mitsui P1 clone:MG03.  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (sites)  
 Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H. and Tabata, S.  
 Arabidopsis thaliana chromosome 5. X. Structural analysis of the regions of 3,076,755 bp covered by sixty P1 and TAC clones  
 DNA Res. 7 (1), 31-63 (2000)  
 20811125  
 2 (bases 1 to 43570)  
 Nakamura, Y.  
 Direct Submission  
 Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamura@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)  
 Address for correspondence: kaos@kazusa.or.jp  
 For the latest information on annotation of this clone, please see [http://www.kazusa.or.jp/kaos/cgi-bin/agd\\_graph.cgi?c=MG03](http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MG03)  
 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.  
 The software programs used to predict genes include: Gral1 (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Gral1-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://gremlini1.zool.iastate.edu/cgi-bin/sp.cgi>).  
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.  
 The 5' clone is MMN10 and the 3' clone is F15112.  
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 /strain="Colombia"  
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 /note="gene\_id:MG03.1  
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 /protein\_id="BA96932.1"  
 /db\_xref="GI:8777342"  
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/evidence=not\_experimental  
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 /db\_xref="GI:8777343"  
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 SORITCKKCYGLNGVYKIAOAGISISDRSKIHGEIDCEKSAISRYKSTAAIN  
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 NENDTLRLKQIILGNASLKHILSOPSSPKPMQVYVQVAVRYINSEVRCQNP  
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 AGLDKASLEAEITGILNTIREATGKCMGSLHRNSPLMSGSGSPINISQVA  
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 VKNLSILKTRIKLNDIRYLDGTIDIPVDKSRARHNLNLNVLNIPNITVIGITV  
 ERVVAEDMKSKOIKDGTWKVLEVEGNLAVMGTPINGRTTSTNNVSVSTLGI  
 EAARTTIIDETIGVNGMSIDIRHMLLADVMTYRGEVIGIORTGIQKMDKSLMG  
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 VLMVSDLLKRTIGENVYKILALIKVSAISDEVMSCLEHLEAVSEDEEYVVT  
 CLEHLHLDDSTLILQVSSOPSSSRTPRDDIYFTTLQVIOAKDKKAREKRL  
 IFKILREADVDVSDTLVGLCHRLTSLVLDLSTYTLQMDPKDRKADNGLNREA  
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 RLIVRETRFALVTLWLEALYDDEFGMMRLSRSIDRLVDEGLSQTLLTSLRQOV  
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 ILFAAGSSALAIKSMGRTALSAARNGAEVYKALVAVEPDAFTDKKGGCPFLMA  
 VQGSDIDVYVELMKGRSSLNNAKSGNTALHVAATPKKIKIYELLDDNNPSPTKA

CDS  
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 23411..23561,23892..24051))  
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 /evidence=not\_experimental  
 /product="serine/threonine protein kinase-like"  
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 /db\_xref="GI:8777347"

CDS  
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 AHARVOGILTLPTVLDNMTLRIRAVGAEGLVYHOGYAIHRDJKVENILDKDVF  
 PTLMDGPATKIVNSDGYERLREFRGTGCIAPADEFAIVSRKSDYSYCVLL  
 VLLTRKAKADLARPAKAEKLTMLMFWTRLEAPMTVDVALCNKISIEGLNRLQTA  
 RNCINPQALERPAMDVEETMREAAFPVKEPELVERISTK"  
 complement(join(25224..25460,25563..25996,26073..26262,  
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CDS  
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 IYEFMANGLEHRIEAFKTVGSPRKGTLPLRVLDWYTRMILAVGAAGLYLHEE  
 LKIVNRVAGNILLDADEFKLTDEGLATKIVEDENGVEQOORITPMKASMGYIAE  
 GISMLVSTKTDVYSAGALVLTGTRKPEFSDNPAGKKNLTWMLFVMPRIEDAPVK  
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 RRSAST"  
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 GAVDFLVKIRKNEKLMQHWARRCHSSGSGESGIDHKSKSVKPESTGSENDASI  
 SDHARNSSGSGLSNDGSDSGSTQSSWTNRADTKTSTSPNOFPDAPNKGTYE  
 NCGAHVNRLEAEDEKQIGTSGTQMSMSKKAEEPGDLEKKNKYSVALERNNDPIL

Query Match 3.5%: Score 22; DB 8; Length 43570;

Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 426 GAATAAACCATAAATATTTA 447  
 Db 33922 GAATAAACCATAAATATTTA 33901

RESULT 27  
 AC114102 86093 bp DNA linear HTG 13-JUL-2002  
 LOCUS AC114102  
 DEFINITION Rattus norvegicus clone CH230-70H23, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\* 56 unordered pieces.  
 ACCESSION AC114102  
 VERSION AC114102.2 GI:21732042  
 KEYWORDS HTG; HTGS; PHASE1.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

# REFERENCE

## AUTHORS

- Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 86093)  
 Murny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,  
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 Weinstein, G., and Glibbs, R.  
 Direct Submission  
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 Worley, K.C.  
 Direct Submission  
 Submitted (07-MAR-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 86093)  
 Worley, K.C.  
 Direct Submission  
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 11, 2002 this sequence version replaced gi:19224429.  
 ----- Genome Center -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
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 Center clone name: CH230-70H23  
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 Sequencing vector: Plasmid:  
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 Consensus quality: 11488 bases at least Q30  
 Consensus quality: 12089 bases at least Q20

# COMMENT

## JOURNAL

## AUTHORS

## TITLE

## JOURNAL

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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 56 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
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 \* This record will be updated with the finished sequence  
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 Bevan, M., Robben, J., Grymonprez, B., Volckaert, G., Bancroft, I.,  
 Mewes, H.W., Rudd, J., Lemcke, K. and Mayer, K.F.X.  
 JOURNAL  
 REFERENCE  
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AUTHORS EU Arabidopsis sequencing project.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckewits.biochem.mpg.de,mayer@mips.biochem.mpg.de,project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bsrc.ac.uk

COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

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AC117309
VERSION 1
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SOURCE Norway rat.
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REFERENCE 1 (bases 1 to 94029)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
          Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,
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Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 94029)
Worley,K.C.
Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 94029)
Worley,K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20162656.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GTRW
Center clone name: CH230-49C23
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 46565 bases at least Q40
Consensus quality: 49416 bases at least Q30
Consensus quality: 51546 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1035: contig of 1035 bp in length
* 1036 1135: gap of unknown length
* 1136 2169: contig of 1034 bp in length

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* 2170 2269: gap of unknown length
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* 4694 4793: gap of unknown length
* 4794 5880: contig of 1087 bp in length
* 5881 5980: gap of unknown length
* 5981 7412: contig of 1432 bp in length
* 7413 7512: gap of unknown length
* 7513 8599: contig of 1087 bp in length
* 8600 10028: gap of unknown length
* 10029 10128: contig of 1329 bp in length
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* 11470 11470: contig of 1342 bp in length
* 11471 11570: gap of unknown length
* 11571 13101: contig of 1531 bp in length
* 13102 13201: gap of unknown length
* 13202 14815: contig of 1614 bp in length
* 14816 14915: gap of unknown length
* 14916 16276: contig of 1361 bp in length
* 16277 16376: gap of unknown length
* 16377 17491: contig of 1115 bp in length
* 17492 17591: gap of unknown length
* 17592 19229: contig of 1638 bp in length
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* 23519 23618: gap of unknown length
* 23619 24641: contig of 1023 bp in length
* 24642 24741: gap of unknown length
* 24742 25989: contig of 1248 bp in length
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* 27577 27676: gap of unknown length
* 27677 29077: contig of 1401 bp in length
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* 32524 32623: gap of unknown length
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* 39487 39586: gap of unknown length
* 39587 41095: contig of 1509 bp in length
* 41096 41195: gap of unknown length
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* 43877 43976: gap of unknown length
* 43977 45933: contig of 1957 bp in length
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* 48595 50676: contig of 2082 bp in length
* 50677 50776: gap of unknown length
* 50777 52256: contig of 1480 bp in length
* 52257 52356: gap of unknown length
* 52357 53735: contig of 1379 bp in length
* 53736 53835: gap of unknown length
* 53836 56056: contig of 2221 bp in length
* 56057 56157: gap of unknown length
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* 60298 60397: gap of unknown length

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* 62001 62100: gap of unknown length
* 62101 63819: contig of 1719 bp in length
* 63820 63919: gap of unknown length
* 63920 65809: contig of 1890 bp in length
* 65810 65909: gap of unknown length
* 65910 69086: contig of 3177 bp in length
* 69087 69186: gap of unknown length
* 69187 70950: contig of 1764 bp in length
* 70951 71051: gap of unknown length
* 71051 73409: contig of 2359 bp in length
* 73410 73509: gap of unknown length
* 73510 77602: contig of 4093 bp in length
* 77603 77702: gap of unknown length
* 77703 80954: contig of 3252 bp in length
* 80955 81055: gap of unknown length
* 81055 84839: contig of 3785 bp in length
* 84840 84939: gap of unknown length
* 84940 88896: contig of 3957 bp in length
* 88897 88996: gap of unknown length
* 88997 92149: contig of 3153 bp in length
* 92150 92249: gap of unknown length
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    /clone="CH230-49C23"

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Query Match
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 372 GAGCAGAGGAGAGACAGACA 393
Db 21467 GAGCAGAGGAGAGACAGACA 21446

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RESULT 30
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DEFINITION Arabidopsis thaliana DNA chromosome 5, BAC clone T2L20 (ESSA
PROJECT).
ACCESSION AL592312
VERSION AL592312.1 GI:14586356
KEYWORDS
SOURCE
ORGANISM
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  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  1 (bases 1 to 98506)
  Beyer, M., Murphy, G., Ridley, P., Hudson, S., Bancroft, I., Mewes, H.W.,
  Rudd, S., Schoof, H. and Mayer, K.F.X.
  Unpublished
  2 (bases 1 to 98506)
  EU Arabidopsis sequencing project.
  Direct Submission
  Submitted (28-JUN-2001) IBI/MIPS, National Research Center for
  Environment and Health, Ingolstaedter Landstr. 1, 85758 Neuherberg,
  FRG, E-mail: schoofsf.de, kmayergsf.de
  Project Coordinator: Mike
  Innes Centre, Colney Lane, NR4 7UD Norwich, UK, E-mail:
  michael.bevan@bsrc.ac.uk

```

## COMMENT

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

## FEATURES

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      /variety="Columbia"

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PIR:S01642"
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RLSVASEGLKRSKELTSSRMAIVSKAFYHLRRONERKRLTHREGAKACTLGALY
AFVPGDCFADIKEDLPLQHPSAIKNIILTKLQRPMPPLGSESEPEFDSVLPED
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19296..19499,19593..19719,19915..20147))
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COSSSHMTREMRVLVELRSALASFILQLYVELDKRGEDLVKIPKALPILLAVINL
FSNLGFSFSLHAYRECDSSVDCSYPMPLVFDRLPEVNEGSGOWTDCDELDAINLYK
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VEOPLISIRDELTFERRKRGVMEIEVQVLTQDSLRMLRNCEQATRRKVPNMSD
QEMLEVYNNRYEKELVPHINHLGELARGLLQVOKLKLIDLETAMLELOILRANET
NFATIALPAFELISVMLFVLRWLKDSKAOGRGRARJHRLVVEIKRIMQVOS
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* 14423 15968: contig of 1546 bp in length
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* 16069 17508: contig of 1440 bp in length
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* 17609 18750: contig of 1142 bp in length
* 18751 18850: gap of unknown length
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* 20241 21555: contig of 1315 bp in length
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* 21656 23881: contig of 2226 bp in length
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* 25374 25474: gap of unknown length
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* 31902 33033: contig of 1132 bp in length
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* 33134 34401: contig of 1268 bp in length
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* 34502 35650: contig of 1149 bp in length
* 35651 35751: gap of unknown length
* 35751 37568: contig of 1818 bp in length
* 37569 39838: contig of 2170 bp in length
* 39839 42459: contig of 2521 bp in length
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* 56292 59810: contig of 3519 bp in length
* 59811 59910: gap of unknown length
* 59911 62030: contig of 2120 bp in length
* 62031 62130: gap of unknown length
* 62131 64127: contig of 1997 bp in length
* 64128 64227: gap of unknown length
* 64228 66921: contig of 2694 bp in length
* 66922 67021: gap of unknown length
* 67022 69333: contig of 2212 bp in length
* 69334 69333: gap of unknown length
* 69334 72107: contig of 2774 bp in length
* 72108 72207: gap of unknown length
* 72208 74866: contig of 2659 bp in length
* 74867 74966: gap of unknown length
* 74967 77985: contig of 3019 bp in length
* 77986 78085: gap of unknown length
* 78086 80387: contig of 2301 bp in length
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Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 6525 TTTTCCACACAGCAGACAGAA 6546
QY 516 TTTTCCACACAGCAGACAGAA 537
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RESULT 32
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Sequence split into 4 fragments LOCUS AC098517 Accession AC098517
Fragment Name Begin End
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AC098517_2 200001 310000
AC098517_3 300001 384467

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LOCUS AC098517 Rattus norvegicus clone CH230-684A, *** SEQUENCING IN PROGRESS ***
DEFINITION Rattus norvegicus clone CH230-684A, *** SEQUENCING IN PROGRESS ***
VERSION AC098517.5 GI:21729566
KEYWORDS HTG; HTGS; PHASEL.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 384467)

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REFERENCE
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., All-oman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
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Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frintz,P.,
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
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Miner,G., Miner,Z., Mitchell,T., Mohabab,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Nwokenkwo,S., Oguh,M., Nguyen,N.,
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\* 65778 65877: gap of unknown length  
 \* 65878 67075: contig of 1198 bp in length  
 \* 67076 67175: gap of unknown length  
 \* 67176 69030: contig of 1855 bp in length  
 \* 69031 69130: gap of unknown length  
 \* 69131 70706: contig of 1576 bp in length  
 \* 70707 70806: gap of unknown length

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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 60522 GTGNNAAAAAAAAAAAAAA 60543

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 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 111914)  
 TROMANS, A.  
 Direct Submission  
 Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clones@wtsanger.ac.uk  
 humbry@sanger.ac.uk  
 On Apr 10, 2002 this sequence version replaced gi:19068255.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em., EMBL; SW,  
 SWISSPROT; Tr., TrEMBL; Wp., WormPeP; Information on the WormPeP  
 database can be found at  
 http://www.sanger.ac.uk/Projects/C-elegans/wormpep RP23-24338 is  
 from the RPI-23 Mouse PAC Library  
 constructed by the group of Pieter de Jong.  
 For further details see http://www.chori.org/dacpac/home.htm  
 VECTOR: pBAC3.6.

## FEATURES

SOURCE location/Qualifiers

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 /db\_xref="taxon:10090"  
 /chromosome="11"  
 /clone="RP23-24338"  
 /clone\_id="RPI-23"  
 BASE COUNT 29940 a 27406 c 26381 g 28187 t  
 ORIGIN

Query Match 3.5%; Score 22; DB 10; Length 111914;  
 Best Local Similarity 100.0%; Pired. No. 0.49;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 385 AGACAGAGAAAAAGAAAAACACA 406

Db 97095 AGACAGAGAAAAAGAAAAACACA 97116  
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 LOCUS Rattus norvegicus clone CH230-31p10, \*\*\* SEQUENCING IN PROGRESS  
 DEFINITION  
 ACCESSION AC103498.3 GI:21728661  
 VERSION AC103498.3  
 KEYWORDS HTG; HTGS\_PHASE1.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 114382)  
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
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 Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,  
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 Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinsón, R., Wang, O.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
 Williams, G., Williamson, A., Wleccyk, R., Woodson, C., Worley, K.,  
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
 Weinstein, G. and Gibbs, R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 114382)  
 Worley, K.C.  
 Direct Submission  
 Submitted (25-NOV-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 114382)  
 Worley, K.C.  
 Direct Submission  
 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 11, 2002 this sequence version replaced gi:117973362.

## REFERENCE

## AUTHORS

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center Project name: GHTP
Center Clone name: CH230-31P10
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 34683 bases at least Q40
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* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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4799 5881: contig of 1084 bp in length
5882 7043: contig of 1062 bp in length
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* 62322 62421: gap of unknown length
* 62422 63629: contig of 1208 bp in length
* 63630 63729: gap of unknown length
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Best Local Similarity 100.0%: Pred. No. 0.49;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNNAAAAAAAAAAAAAAAAAAAA 625  
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Db 23893 GTGNNAAAAAAAAAAAAAAAAAAAA 23914

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 1 (bases 1 to 115643)  
 REFERENCE  
 AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., All-oman, F.R., Allen, C., Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Ayala, M., Banks, T., Barbato, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Bivlev, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinn, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J., Guevara, M., Gunatane, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratoch, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Liew, C., Liu, J., Liu, W., Loussegod, H., Lozardo, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkwo, S., Oguh, M., Okunolu, G., Orangunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherger, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Nelson, D., Weinstein, G., and Gibbs, R.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 115643)  
 AUTHORS Worley, K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 115643)  
 REFERENCE  
 AUTHORS Worley, K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Jul 6, 2002 this sequence version replaced gi:17940880.  
 COMMENT  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GACW

Center clone name: CH230-2A19  
 ----- Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 32912 bases at least Q40  
 Consensus quality: 35872 bases at least Q30  
 Consensus quality: 38377 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a "working draft" sequence. It currently  
 \* consists of 76 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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 \* 1142: gap of unknown length  
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 \* 3565: gap of 1050 bp in length  
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 \* 4715: gap of unknown length  
 \* 4814: gap of 1225 bp in length  
 \* 6039: contig of 1225 bp in length  
 \* 6040: gap of unknown length  
 \* 6140: gap of 1063 bp in length  
 \* 7202: contig of 1063 bp in length  
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 \* 7302: gap of 1202 bp in length  
 \* 8504: contig of 1202 bp in length  
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 \* 8604: gap of 1119 bp in length  
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 \* 9824: gap of 1034 bp in length  
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 \* 10857: gap of unknown length  
 \* 10858: gap of 1190 bp in length  
 \* 10958: contig of 1190 bp in length  
 \* 12147: gap of unknown length  
 \* 12148: gap of 1045 bp in length  
 \* 13248: contig of 1045 bp in length  
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 \* 13392: gap of 1162 bp in length  
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 \* 14555: gap of unknown length  
 \* 14654: gap of 1141 bp in length  
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 \* 15796: gap of unknown length  
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 \* 15895: gap of 1089 bp in length  
 \* 16984: gap of unknown length  
 \* 17085: gap of 1040 bp in length  
 \* 18124: contig of 1040 bp in length  
 \* 18125: gap of unknown length  
 \* 18224: gap of 1120 bp in length  
 \* 18225: gap of unknown length  
 \* 19344: contig of 1120 bp in length  
 \* 19345: gap of unknown length  
 \* 19445: gap of 1209 bp in length  
 \* 20653: contig of 1209 bp in length  
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 \* 21854: contig of 1101 bp in length  
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 \* 21954: gap of 1180 bp in length  
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 \* 23135: gap of unknown length  
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 \* 24464: contig of 1230 bp in length  
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 \* 33614: gap of unknown length

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* 37977 38076: gap of unknown length
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* 40515 41828: contig of 1314 bp in length
* 41829 41928: gap of unknown length
* 41929 43037: contig of 1109 bp in length
* 43038 43137: gap of unknown length
* 43138 44396: contig of 1259 bp in length
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* 46019 46118: gap of unknown length
* 46119 47247: contig of 1129 bp in length
* 47248 47347: gap of unknown length
* 47348 48380: contig of 1033 bp in length
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* 49649 49748: gap of 1168 bp in length
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* 56848 58321: contig of 1474 bp in length
* 58322 58421: gap of unknown length
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* 59975 61027: contig of 1053 bp in length
* 61028 61127: gap of unknown length
* 61128 62295: contig of 1168 bp in length
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* 63807 65223: contig of 1417 bp in length
* 65224 65323: gap of unknown length
* 65324 66551: contig of 1328 bp in length
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* 66752 68012: contig of 1261 bp in length
* 68013 68112: gap of unknown length
* 68113 69345: contig of 1133 bp in length
* 69346 71454: gap of unknown length
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Query Match 3.5%; Score 22; DB 2; Length 115643;  
 Best Local Similarity 100.0%; Pred. No. 0.49;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 604 GTGNAAAAAAAAAAAAAA 625  
 Db 19119 GTGNAAAAAAAAAAAAAA 19098

RESULT 36  
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 LOCUS AC123419 126363 bp DNA linear HTG 23-JUL-2002  
 DEFINITION Rattus norvegicus clone CH230-248113, \*\*\* SEQUENCING IN PROGRESS  
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 VERSION AC123419.2 GI:21902987  
 KEYWORDS HTG: HTGS, PHASEL  
 SOURCE Rattus norvegicus.  
 ORGANISM Rattus norvegicus

# REFERENCE AUTHORS

- 1 (bases 1 to 126363)  
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-oshan,F.R., Allen,C., Alsbrooks,S.L., Amarantune,H.C., Are,J.R., Ayele,M., Banks,T., Barbarella,J., Benton,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,E., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Louised,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabac,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okunnu,G., Orgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojudoxan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshari,N., Sisson,I., Sodergren,E., Sonaite,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleczek,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G., and Gibbs,R.
- Unpublished  
 Direct Submission  
 2 (bases 1 to 126363)  
 Worley,K.C.  
 Direct Submission  
 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Jul 18, 2002 this sequence version replaced gi:21240349.
- REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 Project Information  
 Center project name: GYDX  
 Center clone name: CH230-248113  
 Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap version 0.990329  
 Consensus quality: 85769 bases at least Q40  
 Consensus quality: 89524 bases at least Q30

Consensus quality: 91611 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 43 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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 \* 5918 6919: contig of 1002 bp in length  
 \* 6920 7019: gap of unknown length  
 \* 7020 8031: contig of 1012 bp in length  
 \* 8032 8131: gap of unknown length  
 \* 8132 9676: contig of 1545 bp in length  
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 \* 12880 12979: gap of unknown length  
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 \* 14378 14477: gap of unknown length  
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 \* 17399 17498: gap of unknown length  
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 \* 18640 18739: gap of unknown length  
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 \* 19761 19860: gap of unknown length  
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 \* 21196 21295: gap of unknown length  
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 \* 25365 25464: gap of unknown length  
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 \* 34903 35002: gap of unknown length  
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 \* 36618 36717: gap of unknown length  
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 \* 48612 48711: gap of unknown length  
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 \* 51643 54649: contig of 3008 bp in length  
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## FEATURES

source

BASE COUNT 34487 a 24052 c 23828 g 37023 t 6973 others

## ORIGIN

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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 ACAGCAGAGAGAGATTAAACA 544  
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## RESULT 37

AL445433

## LOCUS

DEFINITION Human DNA sequence from clone Rpl1-234N17 on chromosome 1, complete

## ACCESSION

VERSION AL445433

## KEYWORDS

SOURCE HTG.

## ORGANISM

human.

## REFERENCE

AUTHORS Barlow,K.

## TITLE

JOURNAL

## COMMENT

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 \* 56890 60517: contig of 3628 bp in length  
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 \* 75363 75462: gap of unknown length  
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 \* 88024 88123: gap of unknown length  
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 AL445433.14 GI:13751981  
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 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 138918)  
 Barlow,K.  
 Direct Submission  
 Submitted (20-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequests@sanger.ac.uk  
 On Apr 22, 2001 this sequence version replaced gi:12329466.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following





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36368 GAAGAACACGATGAGAACAC 36389

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VERSION AC114056.3 GI:22218410
KEYWORDS HTG: HTGS. PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 158728)
Muzny, D., Marle, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angilano, D.,
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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Kowals, C., Kraft, C., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
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Lorensheima, L., Louised, H., Lozado, R., Lu, J., Lu, X., Ma, O.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Mallory, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M., McNeill, T., Meene, E., Milsosavljevic, A.,
Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Morris, S., Muidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Naoxelen, O., Okunio, G.,
Olariunsaogun, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfankuch, C., Plopper, F., Polinder, A.,
Popovic, D., Primus, E., Pu, L., L., Pazo, M., Qilroz, J., Rachlin, E.,
Reuter, K., Regier, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,
Reuter, M., Richards, S., Riggs, F., Rives, C., Rodery, T., Rojas, A.,
Rose, G., Rose, R., Ruiz, S., Sanders, W., Saverly, G., Scherer, S.,
Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
Sisson, I., Sitter, C., D., Smaj, D., Sneed, A., Sodergren, E.,
Song, X., Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A.,
Stratek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseña, D.,
Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleciyk, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D., R.,
Holt, R., A., Smith, H., O., Weinstock, G., and Glibbs, R., A.,
Direct Submission
Unpublished
2 (bases 1 to 158728)
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 158728)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 14, 2002 this sequence version replaced gi:21731615.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKW
Center clone name: CH230-19217
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 92840 bases at least Q40
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Consensus quality: 105423 bases at least Q20
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* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraftdata.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 80 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1218: contig of 1218 bp in length
* 1219 1318: gap of unknown length
* 1319 2614: contig of 1296 bp in length
* 2615 2714: gap of unknown length
* 2715 3714: contig of 1000 bp in length
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REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.	
TITLE	(bases 1 to 160008)	
JOURNAL	Homo sapiens chromosome 1, clone RP11-76A15	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 160008) Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckert,Y.R., Bedalov,F., Boguski,W.K.Y.L., Boukhalter,B., Brown,A., Burkett,G., Castle,A., Choepel,V., Colangelo,M., Collins,S., Collumore,A., Cooke,P., Dearthellano,K., Dewar,K., Domito,M., Doyle,M., Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardina,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Kerasats,A., Klein,T., Landers,T., Lehoczy,J., Levine,R., Lien,C., Liu,G., Locke,K., Macdonald,P., Marguis,N., McEwan,P., McGuirk,A., McKernan,K., McNeeters,R., Melchior,J., Meneus,L.P., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K., Pierre,N.N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye-S., Theodore,J., Tirelli,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
REFERENCE	3 (bases 1 to 160008)	
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beka.F., Bousgalter,L., Boukhalter.B., Brown.A., Burckett.G., Campiolano,A., Castle,A., Choepel.V., Colangelo.M., Collins.S., Collimore,A., Cooke.P., Dearthellano,K., Dewar,K., Diaz.J.S., Dodge,S., Domito,M., Doyle,M., Ferreira,P., Fitzhugh.W., Gage.D., Galagan,J., Gardyna,S., Glnde,S., Guyotte,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,	



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AUTHORS Birren, B., Linton, L., Nusbaum, C., and Lander, E.
          Homo sapiens chromosome 6, clone RP11-574H19
          Unpublished
JOURNAL 2 (bases 1 to 163932)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
          Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
          Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
          Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
          Deatellano, K., Dewar, K., Domino, M., Doyle, M., Feresstor, J.,
          Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
          Gardyna, S., Grant, G., Hagos, B., Hearford, A., Horton, L.,
          Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
          Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K.,
          Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
          McPheeters, R., Meldrim, J., Menus, L., Morrow, J., Naylor, J.,
          Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
          Piere, N., Pisanli, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
          Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
          Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
          Titrrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
          Zimmer, A. and Zody, M.
          Direct Submission
TITLE Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 163932)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
          Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
          Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
          Campopiano, A., Castle, A., Choepe, Y., Colangelo, M., Collins, S.,
          Collymore, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S.,
          Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W.,
          Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
          Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L.,
          Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
          Klein, J., Labocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
          Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
          McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
          Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mienna, V., Morrow, J.,
          Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
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          Testaye, S., Theodore, J., Titrrell, A., Travers, M., Triggillo, J.,
          Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
          Young, G., Zainoun, J., Zimmer, A. and Zody, M.
          Direct Submission
TITLE Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE On Mar 16, 2000 this sequence version replaced g1:6730833.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          Genome Center
COMMENT Center: Whitehead Institute/ MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence_submissions@genome.wi.mit.edu
          Project Information
          Center project name: L5272
          Center clone name: 574_H19
          Summary Statistics
          Sequencing vector: M13; M7815; 100% of reads
          Chemistry: Dye-terminator Big Dye; 100% of reads
          Assembly program: Phrap; version 0.960731
          Consensus quality: 159231 bases at least Q40
          Consensus quality: 161639 bases at least Q30
          Consensus quality: 162468 bases at least Q20
          Insert size: 160000; agarose-fp
          Insert size: 163332; sum-of-ctrls
          Quality coverage: 5.4 in Q20 bases; agarose-fp
          Quality coverage: 5.2 in Q20 bases; sum-of-ctrls
          NOTE: This is a 'working draft' sequence. It currently
          * consists of 8 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          1 2756: contig of 2756 bp in length
          * 2757 2856: gap of 100 bp
          * 2857 7124: contig of 4266 bp in length
          * 7125 7224: gap of 100 bp
          * 7225 14958: contig of 7734 bp in length
          * 14959 15058: gap of 100 bp
          * 15059 21054: contig of 5996 bp in length
          * 21055 21154: gap of 100 bp
          * 21155 31520: contig of 10366 bp in length
          * 31521 31620: gap of 100 bp
          * 31621 58637: contig of 27017 bp in length
          * 58638 58737: gap of 100 bp
          * 58738 110374: contig of 51637 bp in length
          * 110375 110474: gap of 100 bp
          * 110475 163932: contig of 53458 bp in length.
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          /chromosome="6"
          /map="6"
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          /clone_id="RP11 Human Male BAC"
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          clone_end:77
          vector_side:right"
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          /note="assembly-fragment"
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          /note="assembly-fragment"
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                  21155..31520
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                  vector_side:left"
misc_feature      58738..110374
                  /note="assembly_fragment"
misc_feature      110475..163932
                  /note="assembly_fragment"
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ORIGIN
Query Match      3.5%: Score 22; DB 2; Length 163932;
Best Local Similarity 100.0%; Prid. NO. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 397 GAAACACACACATGAGAACAC 418
Db 124291 GAAACACACACATGAGAACAC 124312

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RESULT 41
AC096152/c
LOCUS
DEFINITION      Rattus norvegicus clone CH230-10H22, *** SEQUENCING IN PROGRESS
VERSION          AC096152.4 GI:21723293
KEYWORDS
SOURCE           Norway rat.
ORGANISM        Rattus norvegicus
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
                1 (bases 1 to 194402)
Munry,D.M., Adams,C., Adlo-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Blimage,K., Blankenburg,K., Bonini,D.,
Bouck,J., Bowle,S., Bivela,M., Brown,E., Brown,M., Bryant,N.P.,
Bunyah,C., Burch,P., Burkett,C., Butrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Devalla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Eathart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,U., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Huljic,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S.,
Karlsoson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,D., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickets,R., Primus,E., Pu,L.L., Ruiz,S., Savely,G.,
Rives,M., Rojas,A., RojudoKan,I., Rolfe,M., Ruiz,S., Savely,G.,
Scherrer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,T.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

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REFERENCE
AUTHORS
TITLE
JOURNAL

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COMMENT

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Mang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs.R.
Direct Submission
Unpublished
2 (bases 1 to 194402)
Worley,K.C.
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 194402)
Worley,K.C.
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:117943838.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GENS
Center clone name: CH230-10H22
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 127428 bases at least Q40
Consensus quality: 136154 bases at least Q30
Consensus quality: 142855 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1394: contig of 1394 bp in length
1395
1494: gap of unknown length
1495
2724: contig of 1230 bp in length
2725
2824: gap of unknown length
2825
4385: contig of 1561 bp in length
4386
4485: gap of unknown length
4486
5770: contig of 1285 bp in length
5771
5870: gap of unknown length
5871
7046: contig of 1176 bp in length
7047
7146: gap of unknown length
7147
8157: contig of 1011 bp in length
8158
8257: gap of unknown length
8258
9501: contig of 1244 bp in length
9502
9601: gap of unknown length
9601
10892: contig of 1291 bp in length
10893
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12125: contig of 1133 bp in length
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13786: gap of unknown length
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14899: contig of 1113 bp in length
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* 31007 31106: gap of unknown length
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* 59523 61124: contig of 1602 bp in length
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* 61225 63082: contig of 1858 bp in length
* 63083 63182: gap of unknown length
* 63183 63422: contig of 2240 bp in length
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* 67344 67443: gap of unknown length
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* 83574 85680: contig of 2107 bp in length
* 85681 85780: gap of unknown length
* 85781 88048: contig of 2268 bp in length
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* 90892 90991: gap of unknown length
* 90992 94419: contig of 3428 bp in length

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Rattus norvegicus clone CH230-101c21, *** SEQUENCING IN PROGRESS
AC107560.3 GI:21731887
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 196863)
REFERENCE
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C.,
Albrooks,S.L., Amaraltinge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimarge,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Boyle,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
David,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichteage,O., Lieu,C., Liu,J., Liu,W., Louised,H.,
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Moser,M., Neal,D., Newton,J., Newton,S., Oguh,M., Okunoye,N.,
Nguyen,N., Nickerson,E., Nwokweno,S., Oguh,M., Okunoye,N.,
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Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ruiz,S., Savery,G.,
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Sutton,A., Swalek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telirod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,J., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
TITLE
JOURNAL
REFERENCE
Direct Submission
Unpublished
2 (bases 1 to 196863)

```

AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Worley, R.C.  
Direct Submission  
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 196863)  
Worley, R.C.  
Direct Submission  
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 11, 2002 this sequence version replaced g1:18846298.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GLED  
Center clone name: CH230-101C21  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 153108 bases at least Q40  
Consensus quality: 159647 bases at least Q30  
Consensus quality: 166406 bases at least Q20

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 62 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1583: contig of 1583 bp in length  
1584 1683: gap of unknown length  
1684 3141: contig of 1458 bp in length  
3142 3241: gap of unknown length  
3242 4603: contig of 1362 bp in length  
4604 4703: gap of unknown length  
4704 5942: contig of 1239 bp in length  
5943 6042: gap of unknown length  
6043 7195: contig of 1154 bp in length  
7197 7296: gap of unknown length  
7297 8768: contig of 1472 bp in length  
8769 10096: gap of unknown length  
10097 10196: gap of unknown length  
10197 11583: contig of 1387 bp in length  
11584 11683: gap of unknown length  
11684 13846: contig of 2163 bp in length  
13847 13946: gap of unknown length  
13948 15263: contig of 1317 bp in length  
15264 15363: gap of unknown length  
15364 17140: contig of 1777 bp in length  
17141 17240: gap of unknown length  
17241 18396: contig of 1156 bp in length  
18397 18496: gap of unknown length  
18497 20297: contig of 1801 bp in length  
20298 20397: gap of unknown length  
20399 21828: contig of 1431 bp in length  
21829 21928: gap of unknown length  
21929 23391: contig of 1463 bp in length  
23392 23491: gap of unknown length  
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66188 68851: contig of 2664 bp in length  
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72846 72945: contig of 3894 bp in length  
72946 76703: gap of unknown length  
76704 76804: contig of 3758 bp in length  
76805 79385: gap of unknown length  
79386 79485: contig of 2582 bp in length  
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82330 84638: contig of 2744 bp in length  
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97657 97756: gap of unknown length  
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 Birren,B., Nusbaum,C. and Lander,E.  
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 JOURNAL Unpublished  
 AUTHORS 2 (bases 1 to 198843)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B.,  
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 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 198843)  
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Allen,A., Allen,N., Anderson,S.,  
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouckgalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,  
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 Zembek,L., Zimmer,A. and Zody,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

On Aug 21, 2002 this sequence version replaced gi:17061674.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L19066  
 Center clone name: 334.D.14  
 ----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 191519 bases at least Q40  
 Consensus quality: 194846 bases at least Q30  
 Consensus quality: 195925 bases at least Q20  
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 Insert size: 196443; sum-of-contigs  
 Quality coverage: 5.8 in Q20 bases; agarose-fp  
 Quality coverage: 5.8 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 25 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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 4661 4760: gap of 100 bp  
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 6543 8314: contig of 1772 bp in length  
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 8415 10954: contig of 2540 bp in length  
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 53157 53256: gap of 100 bp  
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 63273 63372: gap of 100 bp  
 63373 73192: contig of 9820 bp in length  
 73193 73292: gap of 100 bp  
 73293 86006: contig of 12714 bp in length  
 86007 86106: gap of 100 bp  
 86107 99113: contig of 13007 bp in length  
 99114 99213: gap of 100 bp  
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 135935 151141: contig of 15207 bp in length

\* 151142 151241: gap of 100 bp  
 \* 151242 162188: contig of 10947 bp in length  
 \* 162189 162288: gap of 100 bp  
 \* 162289 176380: contig of 14092 bp in length  
 \* 176381 176480: gap of 100 bp  
 \* 176481 187921: contig of 11441 bp in length  
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## FEATURES

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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 412 AGAACACAGTAAATGAATMAAA 433  
 Db 122888 AGAACACAGTAAATGAATMAAA 122867

RESULT 44  
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 DEFINITION  
 Rattus norvegicus clone CH230-68C1, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 94 unordered pieces.  
 AC123116  
 AC123116.2 GI:21671831  
 HTG; HTGS-PHASE1.  
 SOURCE  
 ORGANISM  
 Norway rat.  
 Rattus norvegicus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

## REFERENCE

## AUTHORS

1 (bases 1 to 206648)  
 Muzny,D.,Marle, Metzker,M.,Lee, Abramson,S., Adams,C., Alder,J.,  
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
 Bismato,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,  
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  
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 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,  
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 Direct Submission  
 TITLE  
 JOURNAL  
 REFERENCE  
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 Worley,K.C.  
 Direct Submission  
 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 206648)

AUTHORS Rat Genome Sequencing Consortium.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-AUG-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 COMMENT On Jul 2, 2002 this sequence version replaced gi:21239864.

----- Genome Center

Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GLJLV  
 Center Clone name: CH230-68C1

----- Summary Statistics

Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
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 Consensus quality: 143073 bases at least Q30  
 Consensus quality: 149355 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 94 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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 DB 27826 GTGNNAAAAAAAAAAAAAAAAAAAA 27847

RESULT 45  
 AC094585 209095 bp DNA linear HMG 10-JUL-2002  
 LOCUS Rattus norvegicus clone CH230-4B10, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 DEFINITION 50 unordered pieces.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISMAC094585  
AC094585.3 GI:21716318  
HTG: HTGS\_PHASE1.  
Norway rat.  
Rattus norvegicusEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.REFERENCE  
AUTHORS

1 (bases 1 to 209095)

Mazny,D.M., Adams,C., Adio-Oduola,B., Ali-oshman,F.R., Allen,C.,  
Alsbrook,S.L., Amaralung,H.C., Are,J.R., Ayale,M., Banks,T.,  
Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonni,D.,  
Bouch,J., Bowe,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P.,  
Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Devilla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,  
Douthaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Edinhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escoto,M.,  
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P.,  
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,  
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,  
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,  
Honsl,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Kretovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
Li,J., Li,Z., Licherage,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,  
Locado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,  
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,  
Miner,G., Miner,Z., Mitchell,T., Monabot,K., Morgan,M., Morris,S.,  
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
Nguyen,N., Nickerson,E., Nwokenwo,S., Ogun,M., Okunolu,G.,  
Orgunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,  
Peters,L., Pickens,R., Primus,E., Pu,L.L., Qules,M., Ren,Y.,  
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,  
Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,  
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,  
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,  
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,O.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,  
Williams,G., Williamson,A., Wlecczyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zortilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNALUnpublished  
2 (bases 1 to 209095)Worley,K.C.  
Direct Submission  
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 209095)REFERENCE  
AUTHORS  
TITLE  
JOURNALWorley,K.C.  
Direct Submission  
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 9, 2002 this sequence version replaced g1:17941347.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GAYO

Center clone name: CH230-4B10

----- Summary Statistics

Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap, version 0.990329  
Consensus quality: 167289 bases at least Q40  
Consensus quality: 173510 bases at least Q30  
Consensus quality: 178689 bases at least Q20\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a "working draft" sequence. It currently  
\* consists of 50 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1	1112: contig of 1112 bp in length
1113	1212: gap of unknown length
1213	2236: contig of 1024 bp in length
2237	2336: gap of unknown length
2337	3580: contig of 1244 bp in length
3581	3680: gap of unknown length
3681	4766: contig of 1086 bp in length
4767	4866: gap of unknown length
4867	6218: contig of 1352 bp in length
6219	6318: gap of unknown length
6319	7371: contig of 1053 bp in length
7372	7471: gap of unknown length
7472	8840: contig of 1369 bp in length
8841	8940: gap of unknown length
8941	10775: contig of 1835 bp in length
10776	10875: gap of unknown length
10876	11921: contig of 1046 bp in length
11922	12021: gap of unknown length
12022	13777: contig of 1756 bp in length
13778	13877: gap of unknown length
13878	15074: contig of 1197 bp in length
15075	15174: gap of unknown length
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17380	17479: gap of unknown length
17480	19141: contig of 1662 bp in length
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22077	22176: gap of unknown length
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24974	26892: contig of 1919 bp in length
26893	26992: gap of unknown length
26993	29416: contig of 2424 bp in length
29417	29516: gap of unknown length
29517	31342: contig of 1826 bp in length
31343	31442: gap of unknown length
31443	34482: contig of 3040 bp in length
34483	34582: gap of unknown length
34583	37422: contig of 2840 bp in length
37423	37522: gap of unknown length
37523	39813: contig of 2291 bp in length
39814	39913: gap of unknown length
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42854	42953: gap of unknown length
42954	45285: contig of 2332 bp in length
45286	45385: gap of unknown length
45386	47238: contig of 1833 bp in length
47239	47338: gap of unknown length
47339	49742: contig of 2404 bp in length
49743	49842: gap of unknown length
49843	53151: contig of 3309 bp in length
53152	53251: gap of unknown length
53252	57575: contig of 4334 bp in length
57576	57676: gap of unknown length
57676	61427: contig of 3752 bp in length
61428	61527: gap of unknown length

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* 65269 65368: gap of unknown length
* 65369 65358: contig of 3990 bp in length
* 65359 65458: gap of unknown length
* 65459 73738: contig of 4280 bp in length
* 73739 73838: gap of unknown length
* 73839 76862: contig of 3144 bp in length
* 76863 77082: gap of unknown length
* 77083 82330: contig of 5248 bp in length
* 82331 82430: gap of unknown length
* 82431 86139: contig of 3709 bp in length
* 86140 86239: gap of unknown length
* 86240 90925: contig of 4686 bp in length
* 90926 91025: gap of unknown length
* 91026 96815: contig of 5790 bp in length
* 96816 96915: gap of unknown length
* 96916 103229: contig of 6314 bp in length
* 103230 103329: gap of unknown length
* 103330 108061: contig of 4732 bp in length
* 108062 108161: gap of unknown length
* 108162 115067: contig of 6906 bp in length
* 115068 115167: gap of unknown length
* 115168 122612: contig of 7445 bp in length
* 122613 122712: gap of unknown length
* 122713 131195: contig of 8483 bp in length
* 131196 131295: gap of unknown length
* 131296 138832: contig of 7537 bp in length
* 138833 138932: gap of unknown length
* 138933 146861: contig of 7929 bp in length
* 146862 146961: gap of unknown length
* 146962 156062: contig of 9101 bp in length
* 156063 156162: gap of unknown length
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* 170910 171009: gap of unknown length
* 171010 180780: contig of 9771 bp in length
* 180781 180880: gap of unknown length
* 180881 191473: contig of 10593 bp in length
* 191474 191573: gap of unknown length
* 191574 200286: contig of 8723 bp in length
* 200287 200386: gap of unknown length
* 200387 200909: contig of 8699 bp in length
* 200910 200995: Location/Qualifiers
  1.209095
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    /clone="CH230-4B10"
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BASE COUNT 57040 a 44873 c 45519 g 56094 t 5569 others
ORIGIN
```

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Query Match 3.5%: Score 22; DB 2; Length 209095;
Beet Local Similarity 100.0%; Pred.No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 604 GTGNAAAAAAAAAAAAAAAAAA 625
DB 354 GTGNAAAAAAAAAAAAAAAAAA 375
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Search completed: November 7, 2002, 22:21:03  
Job time : 3364.8 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 ; Search time 494.345 Seconds  
(without alignments)  
12088.985 Million cell updates/sec

Title: US-09-970-966-199  
Perfect score: 369  
Sequence: 1 ggcacatttgcgagtglt.....tggctccgcacacacatcct 369

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hci:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hci:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
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25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_tod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365.4	99.0	704	13	BI919074 603180881
2	363.8	98.6	987	14	BO668420 AGENCOURT
3	360.6	97.7	747	13	BI917149 603181571
4	354.4	96.0	707	12	BG753617 602732803
5	354.4	96.0	707	13	BI913989 603180565
6	353.4	95.8	920	9	AL538562 AL538562

7	352.8	95.6	698	13	BI554034
8	343.4	93.1	690	12	BI669845
9	341.8	92.6	1010	12	BF345141
10	336.4	91.2	593	10	BE386060
11	331	89.7	704	13	BI823714
12	328.6	89.1	705	12	BG753353
13	321.6	87.2	850	12	BE736301
14	321.4	87.1	340	14	HO6756
15	314.4	85.2	654	12	BE746601
16	306.8	83.1	576	14	BO342438
17	305.6	82.8	948	14	BO882838
18	304.2	82.4	795	9	AU080197
19	292	79.1	571	14	BM709964
20	285.4	77.3	573	10	BE395206
21	282	76.4	768	9	AU080744
22	281.4	76.3	664	10	BB552617
23	279.4	75.7	1490	11	AK012406
24	274.4	74.4	570	13	BI831919
25	266.6	72.2	383	9	AI614768
26	266.6	72.2	754	9	AU067460
27	256.4	69.5	352	9	AA349894
28	255.8	68.0	890	10	AW954549
29	250.8	68.0	878	12	BF125425
30	241	65.3	878	12	BF125664
31	229.4	62.2	775	9	AU035640
32	227.8	61.7	673	10	BB644064
33	227.8	61.7	806	12	BG704350
34	222.2	60.2	784	9	AU050830
35	215.8	58.5	311	10	AW417548
36	212.2	57.5	688	13	BI344761
37	203.6	55.2	395	14	R20352
38	203.6	55.2	429	14	H17189
39	198.2	53.7	522	9	AI767459
40	198.2	53.7	541	14	BM974798
41	198.2	53.7	651	14	AV717094
42	198.2	53.7	652	14	BM980701
43	198.2	53.7	738	14	BM981455
44	197.8	53.6	1272	14	BQ224442
45	196.8	53.3	480	10	BE336607

## ALIGNMENTS

RESULT 1  
LOCUS BI919074 704 bp mRNA linear EST 16-OCT-2001  
DEFINITION BI919074 603180881F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5244956 5',  
mRNA sequence.

ACCESSION BI919074  
VERSION BI919074.1 GI:16200128  
KEYWORDS  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 704)

NIH-MGC <http://mhc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLM1618 row: a column: 21

High quality sequence start: 4

High quality sequence stop: 702.

## FEATURES

Location/Qualifiers

source

1. 704

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5244956"

/clone\_lib="NIH\_MGC\_121"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH\_MGC library."

BASE COUNT 132 a 237 c 204 g 131 t

ORIGIN

Query Match 99.08; Score 365.4; DB 13; Length 704;

Best Local Similarity 99.28; Pred. No. 8.1e-103;

Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGCACACTTTTGGCGATGTTCTTGCTTNCAGGCTTGGCGTGCACAAATCCAGTCTACCA 60

318 GGCACACTTTTGGCGATGTTCTTGCTTNCAGGCTTGGCGTGCACAAATCCAGTCTACCA 377

61 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCCGAGTTTCATTTGAATTCGAC 120

378 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCCGAGTTTCATTTGAATTCGAC 437

121 GGTGAAGTTCAACACATGCTGCAGAAAGAGTATGATGAGCAAGTGGCGGATCATGTA 180

438 GTGAAGCTTCAACACATGCTGCAGAAAGAGTATGATGAGCAAGTGGCGGATCATGTA 497

181 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 240

498 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 557

241 CTGCTCCCGAGGAAATGTAACATGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 300

558 CTGCTCCCGAGGAAATGTAACATGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 617

301 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCAATGCGTCCGAC 360

618 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCAATGCGTCCGAC 677

361 CACCATCT 369

678 CACCATCT 686

RESULT 2

B0668420 987 bp mRNA linear EST 15-JUL-2002

LOCUS B0668420

DEFINITION AGENCOURT\_8301981 NIH\_MGC\_102 Homo sapiens CDNA clone IMAGE:6275121

ACCESSION B0668420

VERSION B0668420.1 GI:21778667

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

FEATURES

source

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LCM2457 row: m column: 10

High quality sequence stop: 583.

Location/Qualifiers

1. 987

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:6275121"

/clone\_lib="NIH\_MGC\_102"

/tissue\_type="epidermoid carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: salivary gland; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 196 a 314 c 285 g 191 t

ORIGIN

Query Match 98.68; Score 363.8; DB 14; Length 987;

Best Local Similarity 98.98; Pred. No. 3.2e-102;

Matches 365; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GGCACACTTTTGGCGATGTTCTTGCTTNCAGGCTTGGCGTGCACAAATCCAGTCTACCA 60

272 GGCACACTTTTGGCGATGTTCTTGCTTNCAGGCTTGGCGTGCACAAATCCAGTCTACCA 331

61 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCCGAGTTTCATTTGAATTCGAC 120

332 GTGTGAAGAAATTCAGCTGAACAACGACTGCTCCCTCCCGAGTTTCATTTGAATTCGAC 391

121 GGTGAAGTTCAACACATGCTGCAGAAAGAGTATGATGAGCAAGTGGCGGATCATGTA 180

392 GTGAAGCTTCAACACATGCTGCAGAAAGAGTATGATGAGCAAGTGGCGGATCATGTA 451

181 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 240

452 CCGCAAGTCTGTGCATCATCAGGCGCTGCTCATGCGCTTCGCGGATACAGTCTT 511

241 CTGCTCCCGAGGAAATGTAACATGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 300

512 CTGCTCCCGAGGAAATGTAACATGATTTGCATCAGCTGTGCAACACCCCTTTGTAA 571

301 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCAATGCGTCCGAC 360

572 CCGGCGCAAGGCCCAAGAAAGGGAAGTTCTGCTCGGCCCTCAGGCAATGCGTCCGAC 631

361 CACCATCT 369

632 CACCATCT 640

RESULT 3

B1917149 747 bp mRNA linear EST 16-OCT-2001

LOCUS B1917149

DEFINITION 603181571F1 NIH\_MGC\_121 Homo sapiens CDNA clone IMAGE:5245648 5',

ACCESSION B1917149

VERSION B1917149.1 GI:16181111

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)



JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaapb-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM1619 row: n column: 17  
 High quality sequence stop: 737.

FEATURES  
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 Location/Qualifiers  
 /organism="Homo sapiens"  
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 /clone="IMAGE:5245648"  
 /clone\_lib="NIH\_MGC\_121"  
 /lab\_host="DH10B"  
 /note="Organ: Brain; Vector: pCMV-Sport6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3  
 fetal brains, female age 20 weeks, female age 24 weeks,  
 and male age 26 weeks. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb, insert size range  
 0.7-3.5 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 017. Note:  
 this is a NIH\_MGC Library."

BASE COUNT 140 a 245 c 216 g 146 t  
 ORIGIN

Query Match 97.7%; Score 360.6; DB 13; Length 747;  
 Best Local Similarity 98.4%; Pred. No. 2,7e-101;  
 Matches 363; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTGAATCCAGTGTACCA 60  
 DB 325 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTGAATCCAGTGTACCA 384  
 QY 61 GTGTGAAGATTCCAGTGAACAAGCAGCTGCTCCCGAGTTCATTTGGAATTGAC 120  
 DB 385 GTGTGAAGATTCCAGTGAACAAGCAGCTGCTCCCGAGTTCATTTGGAATTGAC 444  
 QY 121 GGTGAAGTTCAAGACATGTGTGAGAAGAAGTATGAGCAAGTGGCGGATCATGTA 180  
 DB 445 GGTGAAGTTCAAGACATGTGTGAGAAGAAGTATGAGCAAGTGGCGGATCATGTA 504  
 QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 240  
 DB 505 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 564  
 QY 241 CTGTCTCCCGGGAAGTGAACATGATTTGATGATGATGATGATGATGATGATGAT 300  
 DB 565 CTGTCTCCCGGGAAGTGAACATGATTTGATGATGATGATGATGATGATGATGAT 624  
 QY 301 CCGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTTCANCCATGGCTCCGAC 360  
 DB 625 CCGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTTCANCCATGGCTCCGAC 684  
 QY 361 CACCATCTT 369  
 DB 685 CACCATCTT 693

RESULT 4  
 BG753617 670 bp mRNA EST 15-MAY-2001  
 LOCUS BG753617  
 DEFINITION 602732803f1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:4876392 5',  
 mRNA sequence.  
 ACCESSION BG753617  
 VERSION BG753617.1 GI:14064270  
 KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS NIH-MGC http://imgc.mcl.nih.gov/  
 TITLE 1 (bases 1 to 670)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaapb-r@mail.nih.gov  
 Tissue Procurement: ATCC

cdna Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM1759 row: e column: 01  
 High quality sequence stop: 585.

FEATURES  
 source  
 1. 670  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4876392"  
 /clone\_lib="NIH\_MGC\_43"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; Vector: pCMV-Sport6; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

BASE COUNT 144 a 198 c 165 g 163 t  
 ORIGIN

Query Match 96.0%; Score 354.4; DB 12; Length 670;  
 Best Local Similarity 98.9%; Pred. No. 2,1e-99;  
 Matches 366; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTGAATCCAGTGTACCA 60  
 DB 32 GGCACCTTTTGGCGATGTTCTTGCCTTNCAGGCTTGGCGTGAATCCAGTGTACCA 91  
 QY 61 GTGTGAAGATTCCAGTGAACAAGCAGCTGCTCCCGAGTTCATTTGGAATTGAC 120  
 DB 92 GTGTGAAGATTCCAGTGAACAAGCAGCTGCTCCCGAGTTCATTTGGAATTGAC 151  
 QY 121 GGTGAAGTTCAAGACATGTGTGAGAAGAAGTATGAGCAAGTGGCGGATCATGTA 180  
 DB 152 GGTGAAGTTCAAGACATGTGTGAGAAGAAGTATGAGCAAGTGGCGGATCATGTA 211  
 QY 181 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 240  
 DB 212 CCGCAAGTCTGTGATCATCAGCGGCTGTCTCATCGCTCTCCGGGTACAGTCTT 271  
 QY 241 CTGTCTCCCGGGAAGTGAACATGATTTGATGATGATGATGATGATGATGATGAT 299  
 DB 272 CTGTCTCCCGGGAAGTGAACATGATTTGATGATGATGATGATGATGATGATGAT 331  
 QY 300 ACGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTTCANCCATGGCTCCGCA 359  
 DB 332 ACGGCAAGGCGCCCAAGAAAGGGGAAGTTCCTCGGCGCTTCANCCATGGCTCCGCA 391  
 QY 360 CACCATCTT 369  
 DB 392 CACCATCTT 401

RESULT 5  
 B1913989

LOCUS B1913989 707 bp mRNA linear EST 16-OCT-2001  
 DEFINITION 603180565F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5244569 5',  
 mRNA sequence.  
 ACCESSION B1913989  
 VERSION B1913989.1 GI:16178286  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 707)  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LLM11617 row: a column: 18  
 High quality sequence stop: 698.

FEATURES  
 source  
 1..707  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="5244569"  
 /clone\_lib="NIH\_MGC\_121"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: PCMV-SPORT6; Site: 1; NotI;  
 site: 2: EcoRV (destroyed); RNA source anonymous pool of 3  
 fetal brains, female age 20 weeks, female age 24 weeks,  
 and male age 26 weeks. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb. Insert size range  
 0.7-3.5 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 017. Note:  
 this is a NIH\_MGC Library."

BASE COUNT 133 a 233 c 209 g 132 t  
 ORIGIN

Query Match 96.0%; Score 354.4; DB 13; Length 707;  
 Best Local Similarity 98.9%; Pred. No. 2.2e-99;  
 Matches 366; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 60  
 |||||||  
 DB 286 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 345  
 |||||||  
 OY 61 GGTGGAAGATTCAGCTGACAGACGACTGCTCCGCCGAGTTCATTGTGATTCAC 120  
 |||||||  
 DB 346 GTGTGAAGATTCAGCTGACAGACGACTGCTCCGCCGAGTTCATTGTGATTCAC 405  
 |||||||  
 OY 121 GGTGAAGCTTCAGACATGTGTGAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 180  
 |||||||  
 DB 406 GGTGAAGCTTCAGACATGTGTGAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 465  
 |||||||  
 OY 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACCACTCTT 240  
 |||||||  
 DB 466 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACCACTCTT 525  
 |||||||  
 OY 241 CTGCTCTCCAGGGAAGTAACTCACTGATTCAGTCTGCAACACCCCTTTGTAA 300  
 |||||||  
 DB 526 CTGCTCTCCAGGGAAGTAACTCACTGATTCAGTCTGCAACACCCCTTTGTAA 585  
 |||||||  
 OY 301 CGGGCCCAAGGCGCAAGAAAGGGAAGTCTGCTCGGCGCTCAGCCAT -GGCTCCGCA 359  
 |||||||  
 DB 586 CGGGCCCAAGGCGCAAGAAAGGGAAGTCTGCTCGGCGCTCAGCCATGGGCTCCGCA 645  
 |||||||

OY 360 CCACCATCTCT 369  
 |||||||  
 DB 646 CCACCATCTCT 655

RESULT 6  
 AL538562  
 LOCUS AL538562 920 bp mRNA linear EST 16-FEB-2001  
 DEFINITION AL538562 LTI\_FL013\_FBrn1 Homo sapiens cDNA clone CSODF024Y004 5  
 prime, mRNA sequence.  
 ACCESSION AL538562  
 VERSION AL538562.1 GI:12866967  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 920)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
 source  
 1..920  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="CSODF024Y004"  
 /clone\_lib="LTI\_FL013\_FBrn1"  
 /dev\_stage="pooled tissue from post conception fetuses (20  
 week, 24 week and 26 week)"  
 /lab\_host="DH10B"  
 /note="Organ: Fetal brain; Vector: PCMVSPORT 6; 1st strand  
 cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-stranded cDNA was digested with Not I  
 and cloned into the Not I and Eco RV sites of the  
 PCMVSPORT 6 vector. Library was constructed by Life  
 Technologies. Contact : Feng Liang Life Technologies, a  
 division of invitrogen 9800 Medical Center Drive Rockville  
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
 fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"

BASE COUNT 172 a 285 c 257 g 199 t  
 ORIGIN

Query Match 95.8%; Score 353.4; DB 9; Length 920;  
 Best Local Similarity 98.9%; Pred. No. 5.4e-99;  
 Matches 365; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 60  
 |||||||  
 DB 279 GGCAACTTTTGGGATTTCTTGTTCAGAGCTTTGGCTGCAATCCAGTCTACCA 338  
 |||||||  
 OY 61 GGTGGAAGATTCAGCTGACAGACGACTGCTCCGCCGAGTTCATTGTGATTCAC 120  
 |||||||  
 DB 339 GTGTGAAGATTCAGCTGACAGACGACTGCTCCGCCGAGTTCATTGTGATTCAC 398  
 |||||||  
 OY 121 GGTGAAGCTTCAGACATGTGTGAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 180  
 |||||||  
 DB 399 GGTGAAGCTTCAGACATGTGTGAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 458  
 |||||||  
 OY 181 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACCACTCTT 240  
 |||||||  
 DB 459 CCGCAAGTCTGTGATCATCATCAGCGGCTGTCTCATCGCTCTGCCGGGTACCACTCTT 518  
 |||||||  
 OY 241 CTGCTCTCCAGGGAAGTAACTCACTGATTCAGTCTGCAACACCCCTTTGTAA 300  
 |||||||  
 DB 519 CTGCTCTCCAGGGAAGTAACTCACTGATTCAGTCTGCAACACCCCTTTGTAA 578  
 |||||||  
 OY 301 CGGGCCCAAGGCGCAAGAAAGGGAAGTCTGCTCGGCGCTCAGCCATGGCTCCGCA 360  
 |||||||

Db 579 CGGGCCAGAGCCCAAGAAAGGGAGATTCTGCTCGGCCCTCAGG-CAGGGCTCCGAGC 637  
QY 361 CACCATCCT 369  
|||||  
Db 638 CACCATCCT 646

RESULT 7  
BI554034 698 bp mRNA linear EST 05-SEP-2001  
LOCUS 603235426F1 NCI\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:5309527  
DEFINITION 5', mRNA sequence.  
ACCESSION BI554034  
VERSION BI554034.1 GI:15441348  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11784 row: d column: 08  
High quality sequence stop: 687.  
Location/Qualifiers

FEATURES  
source  
1..698  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5309527"  
/clone\_lib="NCI CGAP\_Brn67"  
/tissue\_type="anaplastic oligodendroglioma with 1p/19q  
loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NCI;  
Site:2: Salt; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 131 a 231 c 204 g 132 t  
ORIGIN

Query Match 95.6%; Score 352.8; DB 13; Length 698;  
Best Local Similarity 98.6%; Pred. No. 6.9e-99;  
Matches 365; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GGCACATTTTGGCGATGTTCTTGTTCAGGCTTGGCGTCAAAATCCAGTGTACCA 60  
|||||  
Db 278 GGCACATTTTGGCGATGTTCTTGTTCAGGCTTGGCGTCAAAATCCAGTGTACCA 337

QY 61 GGTGAAGAAATTCAGCTGACAGACAGACAGCTCCCGCGAGTCAATGTTGAATTCAC 120  
|||||  
Db 338 GGTGAAGAAATTCAGCTGACAGACAGCTCCCGCGAGTCAATGTTGAATTCAC 397

QY 121 GGTGAAGCTTCAAGACATGTGTACAGAA-GAAGTGAAGAGCAAGTCCGGGATCATGT 179  
|||||  
Db 398 GGTGAAGCTTCAAGACATGTGTACAGAAAGAGTGAAGCAAGTCCGGGATCATGT 457

QY 180 ACCGCAAGTCTGTGATCATATCAGCGGCTGTCTCATCGCTTCCGGGGTACAGTCTT 239  
|||||  
Db 458 ACCGCAAGTCTGTGATCATATCAGCGGCTGTCTCATCGCTTCCGGGGTACAGTCTT 517

QY 240 TTGCTCCCGAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 299  
|||||  
Db 518 TTGCTCCCGAGGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 577

QY 300 ACGGGCCAGAGCCCAAGAAAGGGAGATTCTGCTCGGCCCTCAGGCGATGCTCCGCA 359  
|||||  
Db 578 ACGGGCCAGAGCCCAAGAAAGGGAGATTCTGCTCGGCCCTCAGGCGATGCTCCGCA 637

QY 360 CCACATCCT 369  
|||||  
Db 638 CCACATCCT 647

RESULT 8  
BI669845 690 bp mRNA linear EST 12-SEP-2001  
LOCUS 603293440F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5312889 5',  
DEFINITION mRNA sequence.  
ACCESSION BI669845  
VERSION BI669845.1 GI:15584078  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki  
Toshnyuki and Piero Carninci (RIKEN)  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11792 row: p column: 10  
High quality sequence stop: 690.  
Location/Qualifiers

FEATURES  
source  
1..690  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5312889"  
/clone\_lib="NIH\_MGC\_96"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescript (modified  
pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgaag  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTNN-3',  
size-selected for average insert size 2.3 kb and  
normalized to ROT 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library."  
BASE COUNT 127 a 231 c 202 g 130 t  
ORIGIN

Query Match 93.1%; Score 343.4; DB 13; Length 690;  
Best Local Similarity 98.9%; Pred. No. 5.9e-96;  
Matches 366; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 GGCACATTTTGGCGATGTTCTTGTTCAGGCTTGGCGTCAAAATCCAGTGTACCA 60  
|||||  
Db 303 GGCACATTTTGGCGATGTTCTTGTTCAGGCTTGGCGTCAAAATCCAGTGTACCA 361

QY 61 -GTGAAGAAATTCAGCTGACAGACAGCTCCCGCGAGTCAATGTTGAATTCGA 119  
|||||  
Db 362 GTGAAGAAATTCAGCTGACAGACAGCTCCCGCGAGTCAATGTTGAATTCGA 421

QY 120 CGGTGAAGCTTCAAGACATGTGTACAGAAAGAGTGAAGCAAGTCCGGGATCATGT 179  
|||||  
Db 422 CGGTGAAGCTTCAAGACATGTGTACAGAAAGAGTGAAGCAAGTCCGGGATCATGT 481

QY 180 ACCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 239  
DB 482 ACCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 541  
QY 240 TCTGCTCCCGAGGAAGTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 299  
DB 542 TCTGCTCCCGAGGAAGTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 601  
QY 300 ACGGGCCAAAGGCGCCAAAGGAAGTCTGCTGCGGCGCTGCGGCGCTGCGGCG 359  
DB 602 ACGGGCCAAAGGCGCCAAAGGAAGTCTGCTGCGGCGCTGCGGCGCTGCGGCG 661  
QY 360 CCACCATCTCT 369  
DB 662 CCACCATCTCT 671

RESULT 9  
BF345141 1010 bp mRNA linear EST 22-NOV-2000

LOCUS 60201831BF1 NCI\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4153684  
DEFINITION 5', mRNA sequence.

ACCESSION BF345141 GI:11292606  
VERSION BF345141.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1010)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LTM9422 row: d column: 05  
High quality sequence stop: 649.

FEATURES  
source  
1..1010  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4153684"  
/clone\_lib="NCI\_CGAP\_Brn67"  
/tissue\_type="anaplastic oligodendroglioma with 1p/19q  
loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NotI;  
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 266 a 344 c 254 g 146 t  
ORIGIN

Query Match 92.6%; Score 341.8; DB 12; Length 1010;  
Best Local Similarity 98.4%; Pred. No. 2.4e-95;  
Matches 365; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 GGCAACTTTTGGGATTTGTTCTTNC-AGGCTTGGCGTGCAGAAATCAGTGTACC 59  
DB 227 GGCAACTTTTGGGATTTGTTCTTNCAGGCTTTCGCTGCAAAATCAGTGTACC 286  
QY 60 AGTGTAGAGATTTCCAGTGAACAGAGTCTCTCTCCCGAGTTCATTTGAATTGCA 119  
DB 287 AGTGTAGAGATTTCCAGTGAACAGAGTCTCTCTCCCGAGTTCATTTGAATTGCA 346

QY 120 CGGTGAACGTTCCAGACATGTCTCAGAAAAGATGTAGAGCAAGTCCGGGATCATGT 179  
DB 347 CGGTGAACGTTCCAGACATGTCTCAGAAAAGATGTAGAGCAAGTCCGGGATCATGT 406  
QY 180 ACCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 239  
DB 407 ACCGCAAGTCTGTGCATCATGAGCGGCTGTCTCATGCGCTCTGCGGGTACCACTCT 466  
QY 240 TCTGCTCCCGAGGAAGTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 299  
DB 467 TCTGCTCCCGAGGAAGTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 526  
QY 300 A-CGGGCCAAAGGCGCCAAAGGAAGTCTGCTGCGGCGCTGCGGCGCTGCGGCG 358  
DB 527 ACGGGCCAAAGGCGCCAAAGGAAGTCTGCTGCGGCGCTGCGGCGCTGCGGCG 586  
QY 359 ACCACCATCTCT 369  
DB 587 ACCACCATCTCT 597

RESULT 10  
BE386060 593 bp mRNA linear EST 21-JUL-2000

LOCUS 601276753F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3617749 5',  
DEFINITION mRNA sequence.

ACCESSION BE386060  
VERSION BE386060.1 GI:9331425  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 593)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
Plate: LTM285 row: 1 column: 14  
High quality sequence stop: 593.

FEATURES  
source  
1..593  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3617749"  
/clone\_lib="NIH\_MGC\_20"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pORF7; Site: 1; XhoI; Site: 2;  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 139 a 166 c 183 g 105 t  
ORIGIN

Query Match 91.2%; Score 336.4; DB 10; Length 593;  
Best Local Similarity 99.4%; Pred. No. 8.2e-94;  
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 AGGCTTGGCGTGCAGAAATCAGTGTGAGAAATTCAGTGAACAGACTG 90  
DB 246 AGGCTTGGCGTGCAGAAATCAGTGTGAGAAATTCAGTGAACAGACTG 305

QY 91 CTCCTCCCGAGTTCATTTGTAATTCGACGGTGAACATCATGTGTGACAAAAGA 150  
 |||||  
 Db 306 CTCCTCCCGAGTTCATTTGTAATTCGACGGTGAACATCATGTGTGACAAAAGA 365  
 |||||  
 QY 151 AGTATGAGCAAGATCCCGGATCATGTACCGAAGTCCGTGCATCATAGCGGCTTG 210  
 |||||  
 Db 366 AGTATGAGCAAGATCCCGGATCATGTACCGAAGTCCGTGCATCATAGCGGCTTG 425  
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 QY 211 TCTCATGCGCTTCCCGGGTACCAAGTCTTCTGCTCCCGAAGAACTGAATCATGTTTG 270  
 |||||  
 Db 426 TCTCATGCGCTTCCCGGGTACCAAGTCTTCTGCTCCCGAAGAACTGAATCATGTTTG 485  
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 QY 271 CATCAGTGTGTGAACACCCCTCTTTTATACGGCCCAAGGCCCAAGAAAGGGAGTTTC 330  
 |||||  
 Db 486 CATCAGTGTGTGAACACCCCTCTTTTATACGGCCCAAGGCCCAAGAAAGGGAGTTTC 545  
 |||||  
 QY 331 TGCCTGCGCCCTGACGCGATGCTCCGACACCATCTCT 369  
 |||||  
 Db 546 TGCCTGCGCCCTGACGCGATGCTCCGACACCATCTCT 584  
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RESULT 11  
 LOCUS B1823714 704 bp mRNA linear EST 04-OCT-2001  
 DEFINITION 603040833F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5181585 5',  
 mRNA sequence.  
 B1823714  
 VERSION B1823714.1 GI:15935264  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 704)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabp-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14M1453 row: a column: 10  
 High quality sequence stop: 692.

## FEATURES

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 /note="Organ: pooled brain, lung, testis; Vector:  
 pcwv-sport6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH-MGC Library."

## BASE COUNT

135 a 227 c 205 g 137 t

Query Match 89.7%; Score 331; DB 13; Length 704;  
 Best Local Similarity 97.5%; Pred. No. 4, 4e-92;  
 Matches 356; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 1 GGCACATTTTGGCGATTTGTTCTGCTTNCAGGCTTGGCGTGAACATTCAGTGTACCA 60  
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 Db 280 GGCACATTTTGGCGATTTGTTCTGCTTNCAGGCTTGGCGTGAACATTCAGTGTACCA 339  
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 QY 61 GTGTGAAGATTTCCAGCTGAACACGATCTCTCCCGAGTTTCATTTGTAATTCAC 120  
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 Db 340 GTGTGAAGATTTCCAGCTGAACACGATCTCTCCCGAGTTTCATTTGTAATTCAC 399  
 |||||  
 QY 121 GGTGAAGTTTCAAGATGTCAGAAAGATGATGAGCAAAAGTCCCGGATCATGTA 180  
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 Db 400 GGTGAAGTTTCAAGATGTCAGAAAGATGATGAGCAAAAGTCCCGGATCATGTA 459  
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 QY 181 CCGCAAGTCTGTGATCATACAGGCGCTGTCTCATGCGCTTGCAGGATACAGTCTT 240  
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 Db 460 CCGCAAGTCTGTGATCATACAGGCGCTGTCTCATGCGCTTGCAGGATACAGTCTT 519  
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 QY 241 CTGCTCCCGAGGAACTGATCACTGATTTGATCATGCTGTGCAACACCCCTC-TTTGTA 299  
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 Db 520 CTGCTCCCGAGGAACTGATCACTGATTTGATCATGCTGTGCAACACCCCTCATTGTA 579  
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 QY 300 ACGGCGCAA-GGCGCAAGAAAGGGAAGTTGCGCTCGGCGCTCAGCCATGCTGCTCCG 358  
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 Db 580 ACGGCGCAATGGCCCAAGAAAGGGAAGTTTGTGCTCAGGCGCTCAGCCATGCTGCTCAG 639  
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 QY 359 ACCAC 363  
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 Db 640 ACCAC 644

RESULT 12  
 LOCUS B6753353 705 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602731780F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:4875499 5',  
 mRNA sequence.  
 B6753353  
 VERSION B6753353.1 GI:14064006  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 705)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabp-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14CMT1756 row: o column: 20  
 High quality sequence stop: 481.

## FEATURES

location/Qualifiers  
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 /clone\_image="IMAGE:4875499"  
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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; Vector: pORF7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH-MGC Library. |"

## BASE COUNT

156 a 214 c 172 g 163 t

ORIGIN

Query Match	89.1%;	Score 328.6;	DB 12;	Length 705;
Best Local Similarity	96.5%;	Pred. No. 2.5e-91;		
Matches 356;	Conservative 0;	Mismatches 11;	Indels 2;	Gaps 2

QY	1	GGCAACATTTTGGCGATTGTCTTGGCTTNCAGGCTTTGGCTGCAAAATCCAGTCCACCA	80
Db	32	GGCAACTTTTGGGGATTGTCTTGGCTCCAGGCTTTGGCGTGCACATACAGTGCCTACCA	91
QY	61	GTTGAGAGAAATTCACAGCTGGAACAACGACCTGCTCTCCCGGAGTTCAATTGATTTGCAC	120
Db	92	GTTGAGAGAA-TCCAGCTGGAACAACGACCTGCTCTCCCGGAGTTCAATTGAAATTCAC	150
QY	121	GGTGACGTTTCAAGACATGTGTCAAGAAAGAGTAGATGAGCAAAAGTGGCGGGATCATGTA	180
Db	151	GGTGAACTTTCAAGACATGTGTCAAGAAAGAGTAGATGAGCATGTGTGCGGGATCATGTA	210
QY	181	CGGCAAGTCTGTGTCATATCAGCGGCTGTATCTCATCCCTCTGCGGGATACAGTCTCT	240
Db	211	CGGCAAGTCTGTGTCATATCAGCGG-CTGTCTCATGCGCTCTGCGGGATACAGTCTCT	269
QY	241	CTGCTCTCCCAAGGGAATCGAATCTCAGTTTGATCATCGTGTGCAACACCCCTCTTTGTAA	300
Db	270	CTGCTCTCCCAAGGGAATCGAATCTCAGTTTGATCATCGTGTGCAACACCCCTCTTTGTAA	329
QY	301	CGGCGCAAGGCCCAAGAAAAGGGGAAGTTTCCTCTCGGCGCTCAGGCGATGGCTCCGAC	360
Db	330	CGGCGCAAGGCCCAAGAAAAGGGGAAGTTTCCTCTCGGCGCTCAGGCGCAAGGGCTCCGAC	389
QY	361	CACCATCTCT 369	
Db	390	CACCATCTCT 398	

RESULT	13
LOCUS	BE736301
DEFINITION	601307087F1 NIH_MGC_39 Homo sapiens CDNA clone IMAGE:3641660 5',
	850 bp mRNA linear EST 15-SEP-2000
	BE736301

BASE COUNT  
ORIGIN

following 5' adaptor: GGCAAGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
a 276 G 265 g 147 t

Query Match	87.28;	Score 321.6;	DB 12;	Length 850;
Best Local Similarity	95.1%;	Pred. No. 4.3e-89;		
Matches 352;	Conservative	0;	Mismatches 16;	Indels 2;
			Gaps	2

QY	1	GGCAACTTTTGGCGATTGTTCTTCTGTTNAGGCTTTGGCTTCCAATCCAGTGTACCA	80
Db	253	GGCAACTTTTGGCGATGTTCTTCTGTTCCAGGCTTTGGCTTCCAATCCAGTGTACCA	312
QY	61	GTGTGAAGAAATTCACGCTGAACAACGACTCTCTCCCCGGAGTTCATTGTGAATT-GCA	119
Db	313	GTGTGAAGAAATTCACGCTGAACAACGACTGATCTCCCCGGAGTTCATTGTGAATTGGCA	372
QY	120	CGGTGAACGTTCAAGACATGTGTGTGAGAAAGAAAGATGAGGAAAGCGCGGATCATGT	179
Db	373	CGGTGAACGTTCAAGACATGTGTGTGAGAAAGAAAGATGAGGAAAGTCCGGGATATGT	432
QY	180	ACCGGAAGTCCGTGAGCATCATCAGCGGCTCTCTCATCGGCTGTGCGGGTACAGTCT	239
Db	433	ACCGGAAGTCCGTGAGCATCATCAGCGGCTCTCTCATCGGCTGTGCGGGTACAGTCT	492
QY	240	TCTGCTCCCAAGGGCAACTGCACTCAAGTTTGATCAGCTGTGTGACACACCCCTCTTTGTA	299
Db	493	TACTGTCCCAAGGGCAACTGCACTCAAGTTTGATCAGCTGTGTGCA- AACCTCTTTGTA	551
QY	300	ACGGGCGCAAGGCCCAAGAAAAAGGGAAGTTGTGCTGGGCGCTCAGNCAGTAAGGCTCCGA	359
Db	552	ACGGGCGCAAGGCCCAAGAAAAAGGGAAGTTGTGCTGCGGCTCAGGCCAAGGCTCCGCA	611
QY	360	CCACCATCT 369	
Db	612	CCACCATCT 621	

ACCESSION	BE736501.1	GI:10150293
VERSION	BE736501.1	
KEYWORDS	human.	
SOURCE	Est.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 850)	
AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens					
Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:					
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.					
1 (pages 1 to 340)					
Hillier, L., Clark, N., Duboucq, T., Elliston, K., Hawkins, M., Holman					
M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons,					
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Watersto					
, R., Williamson, A. Nohlmann, P. and Wilson, R.					
The Washu-Merck Est Project					
Unpublished. (1995)					
Contact: Wilson RK					

**FEATURES**  
**source**

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3641660"
/clone_lib="NH.MGC.39"
/clone_type="adenocarcinoma"
/vector="DH10 (phage resistant)"
/laost_host="DH10s"
/laost_note="Organ: pancreas; Vector: pOM7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo dT priming. Directionally cloned into EcoRI/XhoI sites using the

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 15:03:08 ; Search time 133.06 Seconds  
(without alignments)  
11437.514 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agttctccttgcaagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: OLIGO-NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 10

Total number of hits satisfying chosen parameters: 802347

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

N.Geneseq\_101002:\*

- 1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
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- 8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
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- 22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	625	ABT03280	Human ovarian carc
2	625	100.0	625	ABL40348	Ovarian carcinoma
3	625	100.0	625	ABL87898	Human ovarian carc
4	606	97.0	1897	ABT03284	Human ovarian carc
5	606	97.0	1897	ABL40352	Ovarian carcinoma
6	555	88.8	1608	ABO54231	Human ovarian anti
7	555	88.8	1953	AAE22400	Human secreted pro
8	555	88.8	1953	AAE64188	Human secreted pro
9	549	87.8	1890	AAE93845	Human CDNA encodin

10	486	77.8	1619	24	ABT03277	Human ovarian carc
11	486	77.8	1619	24	ABT03281	Human ovarian carc
12	486	77.8	1619	24	ABL40345	Ovarian carcinoma
13	486	77.8	1619	24	ABL40349	Ovarian carcinoma
14	393	62.9	1524	24	ABK33543	CDNA encoding huma
15	365	58.4	587	22	AAE94186	Primer specific fo
16	359	57.4	1362	24	ABT03279	Human ovarian carc
17	359	57.4	1362	24	ABL40347	Ovarian carcinoma
18	359	57.4	2528	22	AAH18690	Human G protein co
19	352	56.3	444	22	AAH50766	Human tumor assoc
20	352	56.3	373	24	ABL78538	Human ovarian carc
21	307	49.1	349	24	ABL79431	Human ovarian carc
22	263	42.1	409	24	ABL81262	Human ovarian carc
23	166	26.6	201	24	ABL85916	Human ovarian carc
24	154	24.6	390	24	ABL78554	Human ovarian carc
25	120	19.2	558	24	ABL79397	Human ovarian carc
26	92	14.7	381	24	ABL84848	Human ovarian carc
27	26	4.2	50	22	AAE33985	Human SNP oligonuc
28	26	4.2	50	22	AAE33986	Human SNP oligonuc
29	25	4.0	51	22	AAE27277	Human SNP oligonuc
30	23	3.7	263	22	ABL18284	Human nervous syst
31	23	3.7	377	22	ABL10167	Human breast cance
32	23	3.7	1539	23	ABV23163	Human prostate exp
33	23	3.7	1539	23	ABV29003	Human prostate exp
34	22	3.5	256	24	ABK53839	Human head and nec
35	22	3.5	377	23	ABV08332	Human prostate exp
36	22	3.5	442	22	AAE87949	Human polynucleoti
37	22	3.5	1329	24	ABL90482	Human polynucleoti
38	22	3.5	1388	24	ABK65378	Human polynucleoti
39	22	3.5	1823	22	AAH34281	Arabidopsis CDNA e
40	22	3.5	2049	24	ABL90818	Human colon cancer
41	21	3.4	259	22	AAH69474	Human polynucleoti
42	21	3.4	288	22	AAE09957	Human cervical can
43	21	3.4	288	23	ABV05091	Human breast cance
44	21	3.4	294	23	ABV05770	Human prostate exp
45	21	3.4	359	22	AAH68574	Human prostate exp

#### ALIGNMENTS

RESULT 1  
ABT03280  
ID ABT03280 standard; CDNA; 625 BP.  
XX  
AC ABT03280;  
DT 05-SEP-2002 (first entry)  
XX  
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.  
XX  
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; Immunotherapy;  
KW Cytostatic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200239885-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 13-NOV-2001; 2001WO-US45395.  
XX  
PR 14-NOV-2000; 2000US-0713550.  
XX  
PR 03-APR-2001; 2001US-0825294.  
XX  
PR 02-OCT-2001; 2001US-0970966.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesch DA;  
XX WPI; 2002-500186/53.  
XX  
PT Novel ovarian cancer polypeptide and polynucleotide, useful for



QY 301 CATGATCCCTCCGAATCTGGTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360  
DB 301 CATGATCCCTCCGAATCTGGTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360  
QY 361 TGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
DB 361 TGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
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QY 541 AACACTGTTTCAACCCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600  
DB 541 AACACTGTTTCAACCCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600  
QY 601 ACAGTGNAAAAAAGAAAAA 625  
DB 601 ACAGTGNAAAAAAGAAAAA 625

## RESULT 3

ABL87898 standard; DNA; 625 BP.

ABL87898;

17-MAY-2002 (first entry)

Human ovarian cancer related DNA clone SEQ ID NO:10876.

Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.

Homo sapiens.

WO200192581-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US17756.

26-MAY-2000; 2000US-207484P.

(CORI-) CORIXA CORP.

Algate PA, Harlocker SL, Jones R;

WPI: 2002-122075/16.

Composition for therapy and diagnosis of ovarian cancer comprising

polypeptide of an ovarian tumor polypeptide, polynucleotide encoding

polypeptide, antibody specific to polypeptide or T cell expressing

polypeptide -

Claim 1: SEQ ID 10876; 489pp: English.

The present invention describes a composition (I) comprising: carriers

and immunostimulants; and a polypeptide (II) of an ovarian tumour

polypeptide encoded by a polynucleotide (III) having a CDNA sequence

(SI) from the 10912 nucleotide sequences as given in ABL77023 to

ABLB7934, (III) encoding (II) having a sequence (S2), a T cell

population of (II), or antigen presenting cells that express (II).

(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to

(SI) can be used for detecting ovarian cancer in a patient's biological

sample preferably serum or ovarian tissue. The method comprises

contacting a biological sample from a patient with (IV), detecting the

amount of polynucleotide hybridising to (IV) and comparing the amount to

a predetermined cutoff value and thereby detecting ovarian cancer in the

CC patient, where the amount of polynucleotide hybridising to (IV) is

CC detected preferably by polymerase chain reaction (PCR). (I) comprising

CC (III) and/or (II) is useful for stimulating and/or expanding T cells

CC specific for an ovarian tumour protein comprising contacting T cells

CC with (III) or (II). (III) is useful in design and preparation of

CC ribozyme molecules for inhibiting expression of the tumour polypeptides

CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour CDNA library using well known

CC techniques.

XX

Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match 100.0%; Score 625; DB 24; Length 625;

Best Local Similarity 100.0%; Pred. No. 5.2e-239;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCTCTTGCAGAGGACTGGCCGCGGAGCCGGAAGACAAACGGGCGCTGCACAAAGG 60

DB 1 AGTTCCTCTTGCAGAGGACTGGCCGCGGAGCCGGAAGACAAACGGGCGCTGCACAAAGG 60

QY 61 GCGCGTGTGCGGTGAGTGGAGTGGCATGTACGCGCAGGCGCTTCTGTTGGTGGCGTGTG 120

DB 61 GCGCGTGTGCGGTGAGTGGAGTGGCATGTACGCGCAGGCGCTTCTGTTGGTGGCGTGTG 120

QY 121 CAGCGACAGCGCGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180

DB 121 CAGCGACAGCGCGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180

QY 181 CGTGTACAGAGAGCGGGTGTGATGACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240

DB 181 CGTGTACAGAGAGCGGGTGTGATGACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240

QY 241 GAGGATCATGTATGAGCGCCGGAAGTAGGACCTGTCAGTGTGTTGGTGGTGGCGCAGC 300

DB 241 GAGGATCATGTATGAGCGCCGGAAGTAGGACCTGTCAGTGTGTTGGTGGTGGCGCAGC 300

QY 301 CATGATCCCTCCGAATCTGGTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360

DB 301 CATGATCCCTCCGAATCTGGTGGGATCCAGCATACGCCAATGTCAACAATCAGCCC 360

QY 361 TGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420

DB 361 TGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420

QY 421 TAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480

DB 421 TAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480

QY 481 GGTACCAATTTTTCAGTGTGGACCTTGACAGCTCTTTTCCACAAGCAGAGAAATTT 540

DB 481 GGTACCAATTTTTCAGTGTGGACCTTGACAGCTCTTTTCCACAAGCAGAGAAATTT 540

QY 541 AACACTGTTTCAACCCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600

DB 541 AACACTGTTTCAACCCCGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG 600

QY 601 ACAGTGNAAAAAAGAAAAA 625

DB 601 ACAGTGNAAAAAAGAAAAA 625

RESULT 4

ABT03284

ID ABT03284 standard; CDNA; 1897 BP.

XX

ABT03284;

AC

XX

DT

05-SEP-2002 (first entry)

XX

DE

Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.

XX

Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

cytostatic; gene; ss.

KW

XX Homo sapiens.  
 OS  
 XX  
 XX WO200239885-A2.  
 PN  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 13-NOV-2001; 2001WO-US45395.  
 XX  
 PR 14-NOV-2000; 2000US-0713550.  
 PR 03-APR-2001; 2001US-0825294.  
 PR 02-OCT-2001; 2001US-0970966.  
 XX  
 PA (CORI-) CORINA CORP.  
 XX  
 XX  
 PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;  
 XX  
 DR WPI: 2002-500186/53.  
 XX  
 XX Novel ovarian cancer polypeptide and polynucleotide, useful for  
 PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
 PT  
 PS  
 XX  
 XX Claim 2; Page 196; 197pp; English.  
 CC  
 CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.  
 CC  
 XX  
 SQ Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;  
 Query Match 97.0%; Score 606; DB 24; Length 1897;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-231;  
 Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTTCTCCTTGCAGAGAGCTGGCCCGGAGCGCAAGAGCAAGCGGCGCTGCACAAACCG 60  
 DB 1271 AGTTCTCCTTGCAGAGAGCTGGCCCGGAGCGCAAGAGCAAGCGGCGCTGCACAAACCG 1330  
 QY 61 GCGGCTGCGGTGGTGGAGTCCGATGACCGCGAGGCGGCTTCTGCTGGGCTGCTG 120  
 DB 1331 GCGGCTGCGGTGGTGGAGTCCGATGACCGCGAGGCGGCTTCTGCTGGGCTGCTG 1390  
 QY 121 CAGGACAGCGCGGAGCAGACACCTGCGACAGAACCCCGCGAAGCTCTCGAGGACAC 180  
 DB 1391 CAGGACAGCGCGGAGCAGACACCTGCGACAGAACCCCGCGAAGCTCTCGAGGACAC 1450  
 QY 181 CGTGTACAGAGCGGCTTGTATGACCGAGCTGAGGTAGAAAAAGCTTCTCGAGAGGAG 240  
 DB 1451 CGTGTACAGAGCGGCTTGTATGACCGAGCTGAGGTAGAAAAAGCTTCTCGAGAGGAG 1510  
 QY 241 GAGGATCATGTAGCGCCGGAGAGTGGACCTGCTGACGCTGCTGGTGGTGGCGGACG 300  
 DB 1511 GAGGATCATGTAGCGCCGGAGAGTGGACCTGCTGACGCTGCTGGTGGTGGCGGACG 1570  
 QY 301 CATGATCCTCGAATCTGTTGGCATCCAGCATACGCCAATGTCAACAATCAGGCC 360  
 DB 1571 CATGATCCTCGAATCTGTTGGCATCCAGCATACGCCAATGTCAACAATCAGGCC 1630  
 QY 361 TGGGACAGACGAGCAGAGGAGGAGACAGAGAAAAAGAAAAACACAGCATAGAGAACAG 420  
 DB 1631 TGGGACAGACGAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATAGAGAACAG 1690  
 QY 421 TAAATGAATAAACCATTAATATTAGCCCCCTGTTCTGTCTGTACTGGCCAGGAAT 480  
 DB 1691 TAAATGAATAAACCATTAATATTAGCCCCCTGTTCTGTCTGTACTGGCCAGGAAT 1750  
 QY 481 GGTACCAATTTTTCAGTGTGGACTGACAGCTTCTTTGGCAACAAGAGAGAAATTT 540  
 DB 1751 GGTACCAATTTTTCAGTGTGGACTGACAGCTTCTTTGGCAACAAGAGAGAAATTT 1810

OY 541 AACACTGTTTCAACCCGGGAGGAGTGGCTGTAAAGAAAGACCATTAATGCTTAG 600  
 DB 1811 AACACTGTTTCAACCCGGGAGGAGTGGCTGTAAAGAAAGACCATTAATGCTTAG 1870  
 OY 601 ACAGTG 606  
 DB 1871 ACAGTG 1876  
 RESULT 5  
 ABL40352  
 ID ABL40352 standard; cDNA; 1897 BP.  
 XX  
 XX ABL40352;  
 XX  
 XX 28-JUN-2002 (first entry)  
 XX  
 DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.  
 XX  
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 260..685  
 FT /\*tag= a  
 FT /product= "Ovarian carcinoma protein O1034C/O591S"  
 XX  
 PN US2002004491-A1.  
 PD 10-JAN-2002.  
 XX  
 XX 03-APR-2001; 2001US-0825294.  
 XX  
 PR 10-SEP-1999; 99US-0394374.  
 PR 01-MAY-2000; 2000US-0561778.  
 PR 15-AUG-2000; 2000US-0640173.  
 PR 07-SEP-2000; 2000US-0656668.  
 PR 14-NOV-2000; 2000US-0713550.  
 XX  
 PA (XUJ/) XU J.  
 PA (STOL/) STOLK J A.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PI Xu J, Stolk JA, Algate PA, Fling SP;  
 XX  
 XX WPI: 2002-171027/22.  
 DR P-PSDB; ABB09417.  
 XX  
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
 PT prevention and/or treatment of cancer, especially ovarian cancer  
 XX  
 PS Claim 1a; Page 127-128; 131pp; English.  
 XX  
 CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma O1034C/O591S consensus  
 CC nucleotide sequence.



QY 181 CGTGCACAGAGGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCGAAGAGGGAG 240  
|||||  
Db 1105 CGTGCACAGAGGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCGAAGAGGGAG 1164  
QY 241 GAGGATCATGTACGCCGGAAGTAGACCTGCTCCAGTCTGCTTTGGCTTTGGCCGACG 300  
|||||  
Db 1165 GAGGATCATGTACGCCGGAAGTAGACCTGCTCCAGTCTGCTTTGGCTTTGGCCGACG 1224  
QY 301 CATGATCTCTCCGAATCTGTTGGGCTATCCAGCATACGGCCAAATGTCAACAATAGGCC 360  
|||||  
Db 1225 CATGATCTCTCCGAATCTGTTGGGCTATCCAGCATACGGCCAAATGTCAACAATAGGCC 1284  
QY 361 TGGCGACAGACAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACAG 420  
|||||  
Db 1285 TGGCGACAGACAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACAG 1344  
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480  
|||||  
Db 1345 TAAATRAATTAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 1404  
QY 481 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 540  
|||||  
Db 1405 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 1464  
QY 541 AACACTGTTTCAAAACCCGCGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600  
|||||  
Db 1465 AACACTGTTTCAAAACCCGCGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 1524  
QY 601 ACAGTG 606  
|||||  
Db 1525 ACAGTG 1530

RESULT 7  
AAF22400/C  
ID AAF22400 standard; cDNA; 1953 BP.  
XX  
AC AAF22400;  
XX  
DT 26-MAR-2001 (first entry)  
XX  
DE Human secreted protein gene 28 SEQ ID NO:38.  
XX  
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antiinfective; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;  
KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;  
KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;  
KW angiodysplasia; nervous system disorder; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing; skin aging;  
KW food additive; preservative; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200061629-A1.  
XX  
PD 19-OCT-2000.  
XX  
PE 06-APR-2000; 2000WO-US09071.  
XX  
PR 09-APR-1999; 99US-0128694.  
XX  
PR 20-JAN-2000; 2000US-0176931.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (ROSE/) ROSEN C A.  
XX  
PI Ruben SM, Komatsoulis G;  
XX  
DR WPI: 2000-647420/62.  
XX  
DR P-PSDB; AAB6161.

PT Isolated nucleic acid molecule encoding a human secreted protein is  
XX used in preventing, treating or ameliorating a medical condition -  
PS Claim 1; Page 440; 533pp; English.

XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134  
CC to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins  
CC and polypeptides homologous to them. Human secreted proteins have  
CC activities based on the tissues and cells the genes are expressed in.  
CC Examples of activities include: immunosuppressive; antiarthritic;  
CC antiinfective; antiproliferative; cytostatic; cardiant; vasotropic;  
CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
CC fungicide; and ophthalmological. The polynucleotides and proteins can be  
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are  
CC also used in diagnosing a pathological condition or susceptibility to a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular  
CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral  
CC ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's  
CC disease, infections caused by bacteria, viruses and fungi and ocular  
CC disorders e.g. corneal infection. The polypeptides can also be used to  
CC aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. AAF22364 to  
CC AAF22372 and AAB63133 represent sequences used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 1953 BP; 428 A; 540 C; 524 G; 458 T; 3 other;

Query Match 88.8%; Score 555; DB 21; Length 1953;  
Best Local Similarity 99.8%; Pred. No. 2.9e-211;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTCAGAGAGAGTGGCCGCGGAGCGAAGAGCAACGGCCCTGCACAAACG 60  
|||||  
Db 684 AGTTCTCCTTCAGAGAGAGTGGCCGCGGAGCGAAGAGCAACGGCCCTGCACAAACG 625  
QY 61 GCGCGTTCGCTGCTGAGTGGCGCATGTACGCGGCGCTTCTGCTGGCTGCTG 120  
|||||  
Db 624 GCGCGTTCGCTGCTGAGTGGCGCATGTACGCGGCGCTTCTGCTGGCTGCTG 565  
QY 121 CAGCGACAGGGGCGACAGACCTGACAGCAACCGCGCAACTCTGTGAGAGAC 180  
|||||  
Db 564 CAGCGACAGGGGCGACAGACCTGACAGCAACCGCGCAACTCTGTGAGAGAC 505  
QY 181 CGTGCACAGAGGCGGTTGATGACCGAGCTGAGTAAAGAAAAACGTCCTCGAAGAGGGAG 240  
|||||  
Db 504 CGTGCACAGAGGCGGTTGATGACCGAGCTGAGTAAAGAAAAACGTCCTCGAAGAGGGAG 445  
QY 241 GAGGATCATGTACGCCGGAAGTAGACCTGCTCCAGTCTGCTTTGGCCGACG 300  
|||||  
Db 444 GAGGATCATGTACGCCGGAAGTAGACCTGCTCCAGTCTGCTTTGGCCGACG 385  
QY 301 CATGATCTCTCCGAATCTGTTGGGCTATCCAGCATACGGCCAAATGTCAACAATAGGCC 360  
|||||  
Db 384 CATGATCTCTCCGAATCTGTTGGGCTATCCAGCATACGGCCAAATGTCAACAATAGGCC 325  
QY 361 TGGCGACAGACAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACAG 420  
|||||  
Db 324 TGGCGACAGACAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACAG 265  
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480  
|||||  
Db 264 TAAATRAATTAACCATTAATATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 205  
QY 481 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 540  
|||||  
Db 204 GGTACCAATTTTTCAGTGTGAGCTGACCTCTTTTGCACAGAAAGAGAAATTT 145

QY 541 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAACCATTAATGCTTTAG 600  
 DB 144 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAACCATTAATGCTTTAG 85  
 QY 601 ACAGTG 606  
 DB 84 ACAGTG 79

RESULT 8  
 AAF64188/c  
 ID AAF64188 standard: cDNA: 1956 BP.  
 XX AAF64188;  
 AC AAF64188;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human secreted protein gene 13 SEQ ID NO:23.  
 XX

Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 anti-proliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
 neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
 optalmalological; vulnerary; autoimmune disease; cardiovascular disorder;  
 hyperproliferative disorders; cerebrovascular disorder; wound healing;  
 nervous system disorder; ocular disorder; skin ageing; chemotaxis;  
 food additive; ss.

OS Homo sapiens.  
 XX WO200077026-A1.  
 PN 21-DEC-2000.  
 XX 01-JUN-2000; 2000WO-US14973.  
 PF 11-JUN-1999; 99US-0138630.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM, Komatsoulis GA;  
 DR WPI: 2001-071258/08.  
 XX P-PSDB: AAB75518.  
 DR  
 PT Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers -  
 XX  
 PS Claim 1; Page 443-444; 542pp: English.

Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide  
 sequences AAF64176 - AAF64224. The specification includes amino acid  
 sequences AAB75555 - AAB75606 which represent fragments of the human  
 secreted proteins, and protein sequences with which they share homology.  
 The proteins and polynucleotides, their agonists and antagonists have  
 activities dependent on the tissues and cells in which they are  
 expressed, examples of these activities include, immunosuppressive;  
 antiarthritic; antirheumatic; anti-proliferative; cytostatic; cardiant;  
 vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
 virucide; fungicide; optalmalological; and vulnerary. The proteins,  
 polynucleotides, agonists and antagonists can be used to treat or detect  
 or diagnose various diseases and disorders including, autoimmune  
 diseases e.g. Rheumatoid arthritis, hyperproliferative disorders  
 e.g. neoplasms of the breast or liver, cardiovascular disorders  
 e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,  
 angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
 infections caused by bacteria, viruses and fungi and ocular disorders  
 e.g. corneal infection. The polypeptides can also be used to aid wound  
 healing and epithelial cell proliferation, to prevent skin ageing due to  
 sunburn, to maintain organs before transplantation, for supporting cell  
 culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 polypeptides can also be used as a food additive or preservative to

CC Increase or decrease storage capabilities. Included in the invention are  
 CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which  
 CC are used in the isolation, identification and characterisation of the  
 CC proteins of the invention.  
 XX

SQ Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;

Query Match 88.8%; Score 555; DB 22; Length 1956;  
 Best Local Similarity 99.8%; Pred. No. 2,9e-211;  
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTTCCTTTCAGAGAGACTGGCCGGGACGGGAAAGACAGCGGCGTGCACAAACG 60  
 DB 684 AGTTTCCTTTCAGAGAGACTGGCCGGGACGGGAAAGACAGCGGCGTGCACAAACG 625  
 QY 61 GGCGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120  
 DB 624 GGCGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 565  
 QY 121 CAGCGACAGCGGCGGACAGACAGCCTGACAGAACACCCGCGAAATGCTGCGAGACAC 180  
 DB 564 CAGCGACAGCGGCGGACAGACAGCCTGACAGAACACCCGCGAAATGCTGCGAGACAC 505  
 QY 181 CGTTGTACAGAGAGCGGCTGTGATGACCGAGCTGAGGTAGAAAACGCTCCGAGAAAGGAG 240  
 DB 504 CGTTGTACAGAGAGCGGCTGTGATGACCGAGCTGAGGTAGAAAACGCTCCGAGAAAGGAG 445  
 QY 241 GAGGATCATGTACGCGCGGAGTAGAGACCTGTCGAGTGTGCTGTGCTGTGCTGTGCTG 300  
 DB 444 GAGGATCATGTACGCGCGGAGTAGAGACCTGTCGAGTGTGCTGTGCTGTGCTGTGCTG 385  
 QY 301 CATGATCTCTCGAATCTGTGTTGGCATCCAGCATAGCGGCAATGTCAACAATCAGCCC 360  
 DB 384 CATGATCTCTCGAATCTGTGTTGGCATCCAGCATAGCGGCAATGTCAACAATCAGCCC 325  
 QY 361 TGGGACAGACAGACAGAGGAGGAGAGACAGAAAAGAAAACACACATGAGAACACAG 420  
 DB 324 TGGGACAGACAGACAGAGGAGGAGAGACAGAAAAGAAAACACACATGAGAACACAG 265  
 QY 421 TAAATGAATAAACCATTAATATTTAGCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 480  
 DB 264 TAAATGAATAAACCATTAATATTTAGCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 205  
 QY 481 GGTACCAATTTTCACTGTGACCTTGACAGCTTCTTTTCCACAGCAGAGAGAAATT 540  
 DB 204 GGTACCAATTTTCACTGTGACCTTGACAGCTTCTTTTCCACAGCAGAGAGAAATT 145  
 QY 541 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAACCATTAATGCTTTAG 600  
 DB 144 AACACTGTTTCAAAACCCGGGGAGTTGCTGTGTTAAAGAAACCATTAATGCTTTAG 85  
 QY 601 ACAGTG 606  
 DB 84 ACAGTG 79

RESULT 9  
 AAF93845  
 ID AAF93845 standard: cDNA: 1890 BP.  
 XX AAF93845;  
 AC AAF93845;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0181.  
 XX  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067182-A2.  
 XX





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|||||
Db 1052 GGGGCTGTCGGTGGTGGATGCGCATGTACGCGAGGCGCTTCTGCTGGTGGCGTGGTG 1111
OY 121 CACGACAGCGCGGACGACGACACC-TGCAGCAACACCCGCGAAGACGTCGCGAGACA 179
Db 1112 CACGACAGCGCGGACGACGACACCCTTGACAGAACCCGCGAAGACGTCGCGAGACA 1171
OY 180 CCGTGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTCCGAGAGGGA 239
Db 1172 CCGTGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAAGCTCCGAGAGGGA 1231
OY 240 GAGAGATCATGTACGCGCGGAGTAGAAGCTGTCAGTGTGCTGGGTTGGCCGAG 299
Db 1232 GAGAGATCATGTACGCGCGGAGTAGAAGCTGTCAGTGTGCTGGGTTGGCCGAG 1291
OY 300 CCATGATCTCCGAAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCTCCGAAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 1351
OY 360 CTGGGACAGACAGACGAGAGGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA 419
Db 1352 CTGGGACAGACAGACGAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA 1411
OY 420 GTAAATGAATAAACCATTAATTTTAAAGCCCTCTGCTGTGCTTACTGCGCAGAAA 479
Db 1412 GTAAATGAATAAACCATTAATTTTAAAGCCCTCTGCTGTGCTTACTGCGCAGAAA 1471
OY 480 TGGTACCAATTTTTCAGTGTGACCTGACAGCTTTTCCCAACAGCAGAGAGAAAT 539
Db 1472 TGGTACCAATTTTTCAGTGTGACCTGACAGCTTTTCCCAACAGCAGAGAGAAAT 1531
OY 540 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTA 599
Db 1532 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTA 1591
OY 600 GACAGTG 606
Db 1592 GACAGTG 1598

RESULT 11
ABT03281
ID ABT03281 standard; cDNA; 1619 BP.
XX
AC ABT03281;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.
XX
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX
KW cytoskeletal; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200239885-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US45395.
XX
PR 14-NOV-2000; 2000US-0713550.
XX
PR 03-APR-2001; 2001US-0825294.
XX
PR 02-OCT-2001; 2001US-0970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
DR WPI; 2002-500186/53.
XX
PT Novel ovarian cancer polypeptide and polynucleotide, useful for
PT detecting the presence of ovarian cancer in a patient, and in

```

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PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT
XX
PS Claim 2; page 195; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 77.8%; Score 486; DB 24; Length 1619;
Best local similarity 99.8%; Pred. No. 7.8e-184;
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 AGTTCTCTTTCAGAGAGCTGCGCGCGGAGCGGAGAGCAACGCGCTGCACAAACG 60
Db 992 AGTTCTCTTTCAGAGAGCTGCGCGCGGAGCGGAGAGCAACGCGCTGCACAAACG 1051
OY 61 GCGGCTGTGCTGTGAGAGTGCATGTACGCGAGCGCTTCTGCTGCTGCTGCTG 120
Db 1052 GCGGCTGTGCTGTGAGAGTGCATGTACGCGAGCGCTTCTGCTGCTGCTGCTG 1111
OY 121 CACGACAGCGCGGACGACAGCAC-TCACAGAACACCGCGCAACTGCTGCGAGGACA 179
Db 1112 CACGACAGCGCGGACGACAGCACCTTTCACAGAACACCGCGCAACTGCTGCGAGGACA 1171
OY 180 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTGAAAAAGCTCTCCGAGAGGGA 239
Db 1172 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTGAAAAAGCTCTCCGAGAGGGA 1231
OY 240 GAGAGATCATGTACGCGCGGAGTAGAAGCTGTCAGTGTGCTGGGTTGGCCGAG 299
Db 1232 GAGAGATCATGTACGCGCGGAGTAGAAGCTGTCAGTGTGCTGGGTTGGCCGAG 1291
OY 300 CCATGATCTCCGAAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCTCCGAAATCTGGTGGCATCCAGCATACGCGCAATGTCAACAATCAGCC 1351
OY 360 CTGGGACAGACAGACGAGAGGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA 419
Db 1352 CTGGGACAGACAGACGAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA 1411
OY 420 GTAAATGAATAAACCATTAATTTTAAAGCCCTCTGCTGTGCTTACTGCGCAGAAA 479
Db 1412 GTAAATGAATAAACCATTAATTTTAAAGCCCTCTGCTGTGCTTACTGCGCAGAAA 1471
OY 480 TGGTACCAATTTTTCAGTGTGACCTGACAGCTTTTCCCAACAGCAGAGAAAT 539
Db 1472 TGGTACCAATTTTTCAGTGTGACCTGACAGCTTTTCCCAACAGCAGAGAAAT 1531
OY 540 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTA 599
Db 1532 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTA 1591
OY 600 GACAGTG 606
Db 1592 GACAGTG 1598

RESULT 12
ABL40345
ID ABL40345 standard; cDNA; 1619 BP.
XX
AC ABL40345;
XX
DT 28-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 57887 extended cDNA.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
KW ss.

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XX OS Homo sapiens.
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-0825294.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGN/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI XU J, Stolk JA, Algate PA, Fling SP;
XX DR WPI; 2002-171027/22.
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX PS Claim 1a; Page 119-120; 131pp; English.
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX CC that may be utilised in cancer therapy, for example in a vaccine or
XX CC gene therapy. Polypeptides and polynucleotides of the invention are
XX CC useful for detecting a cancer in a patient, for stimulating and/or
XX CC expanding T-cells specific for a tumour protein, and for inhibiting the
XX CC development of a cancer in a patient. They are also useful for
XX CC stimulating an immune response in a patient, and for treating a cancer in
XX CC a patient and for determining the presence of a cancer in a patient.
XX CC The isolated polynucleotides of the invention are useful for their
XX CC ability to selectively form duplex molecules with complementary stretches
XX CC of the entire desired gene or gene fragments, and for designing and
XX CC preparing ribozyme molecules for inhibiting expression of tumour
XX CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX CC invention are also useful in recombinant DNA molecules to direct
XX CC expression of a polypeptide in appropriate host cells. The current
XX CC sequence represents the extended cDNA sequence of ovarian carcinoma
XX CC isolate 57887 given in record ABL48956.
XX SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;
XX
XX Query Match 77.8%; Score 486; DB 24; Length 1619;
XX Best Local Similarity 99.8%; Pred. No. 7.8e-184;
XX Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 AGTTCTCTTGCAGAGACTGGCCGGGAGCGCAAGACAGACGGCGCTGCACAAACG 60
XX DB 992 AGTTCTCTTGCAGAGACTGGCCGGGAGCGCAAGACAGACGGCGCTGCACAAACG 1051
XX
XX QY 61 GGCCTGTCCGTTGGTGGATGTCATGCGGAGCGGCTTCTGTGGTTGGCTGCTG 120
XX DB 1052 GGCCTGTCCGTTGGTGGATGTCATGCGGAGCGGCTTCTGTGGTTGGCTGCTG 1111
XX
XX QY 121 CAGCAGACGGCGGAGCAGACACC-TTCACAGAACACCCGCCGAAACTGCTCGAGAGACA 179
XX DB 1112 CAGCAGACGGCGGAGCAGACACCCTTGCAGAACACCCGCCGAAACTGCTCGAGAGACA 1171
XX
XX QY 180 CCGTGTACAGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAAAGGGA 239
XX DB 1172 CCGTGTACAGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAAAGGGA 1231
XX
XX QY 240 GGAGGATCATGTAGCCCGGAGGTAGGACCTGTCCAGTCGCTGGTTGGCCGCGAG 299
XX DB 1232 GGAGGATCATGTAGCCCGGAGGTAGGACCTGTCCAGTCGCTGGTTGGCCGCGAG 1291

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QY 300 CCATGATCTCTCCGAATCTGTTGGCATCCAGCATACGGCCATGTCACAATCAGCC 359
DB 1292 CCATGATCTCTCCGAATCTGTTGGCATCCAGCATACGGCCATGTCACAATCAGCC 1351
QY 360 CTGGGCGAGACAGCAGCAGAGGAGAGACAGAAAAAAGAAACACAGCATGAGAACACA 419
DB 1352 CTGGGCGAGACAGCAGCAGAGGAGAGACAGAAAAAAGAAACACAGCATGAGAACACA 1411
QY 420 GTAATGAAATAAACCATAAATATTTTAGCCCTCTGTCTGTCTTACTGCGCAGAGAAA 479
DB 1412 GTAATGAAATAAACCATAAATATTTTAGCCCTCTGTCTGTCTTACTGCGCAGAGAAA 1471
QY 480 TGGTACCAATTTTTCAGTGTGACCTGACAGCCTTTTGGCCACAAGACAGAAATT 539
DB 1472 TGGTACCAATTTTTCAGTGTGACCTGACAGCCTTTTGGCCACAAGACAGAAATT 1531
QY 540 TAACACTGTTTCAAAACCCGGGAGTTGGCTGTCTTAAAGAAAGCATTAAATGCTTTA 599
DB 1532 TAACACTGTTTCAAAACCCGGGAGTTGGCTGTCTTAAAGAAAGCATTAAATGCTTTA 1591
QY 600 GACAGTG 606
DB 1592 GACAGTG 1598

```

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RESULT 13
ABL40349
ID ABL40349 standard; cDNA; 1619 BP.
XX AC ABL40349;
XX DT 28-JUN-2002 (first entry)
XX DE Ovarian carcinoma O5915 nucleotide sequence.
XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX SS.
XX OS Homo sapiens.
XX PN US2002004491-A1.
XX PD 10-JAN-2002.
XX PF 03-APR-2001; 2001US-0825294.
XX PR 10-SEP-1999; 99US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX PA (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGN/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PI XU J, Stolk JA, Algate PA, Fling SP;
XX DR WPI; 2002-171027/22.
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX PS Claim 1a; Page 125-126; 131pp; English.
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX CC that may be utilised in cancer therapy, for example in a vaccine or
XX CC gene therapy. Polypeptides and polynucleotides of the invention are
XX CC useful for detecting a cancer in a patient, for stimulating and/or
XX CC expanding T-cells specific for a tumour protein, and for inhibiting the
XX CC development of a cancer in a patient. They are also useful for
XX CC stimulating an immune response in a patient, and for treating a cancer in

```



Db 1132 AGTTCCTTGCAGAGAGACTGGCCGGGACGCGAAGACAAAGGGCGCTGCACAAAGCG 1191  
 QY 61 GAGCGTGTGGTGTGAGTGGCGCATGTACGCGAGCGGCTTCTGCTGGTGGCGTGTG 120  
 Db 1192 GCGCGTGTGGTGTGAGTGGCGCATGTACGCGAGCGGCTTCTGCTGGTGGCGTGTG 1251  
 QY 121 CAGCGACAGCGCGGCGAGCAGACACCTGACAGAACACCCGCGAAACTCTGCGAGAGAC 180  
 Db 1252 CAGCGACAGCGCGGCGAGCAGACACCTGACAGAACACCCGCGAAACTCTGCGAGAGAC 1311  
 QY 181 CGTGTACAGAGAGCGGGTGTGATGACCGAGCTAGAGTAAAGAAACGTCCTCGAAGAGGGAG 240  
 Db 1312 CGTGTACAGAGAGCGGGTGTGATGACCGAGCTAGAGTAAAGAAACGTCCTCGAAGAGGGAG 1371  
 QY 241 GAGGATCATGTACGCGCGGAGTGTAGACCTGTCAGTGTGCTGGGTTGGCCGAGC 300  
 Db 1372 GAGGATCATGTACGCGCGGAGTGTAGACCTGTCAGTGTGCTGGGTTGGCCGAGC 1431  
 QY 301 CATGATCCTCCGAATCTGTGGGCGATCCAGCATACGGCCAAATGTACAGCATAGCC 360  
 Db 1432 CATGATCCTCCGAATCTGTGGGCGATCCAGCATACGGCCAAATGTACAGCATAGCC 1491  
 QY 361 TGGGAGACAGAGAGAGGAGGAGAGACAGA 393  
 Db 1492 TGGGAGACAGAGAGGAGGAGAGAGACAGA 1524

## RESULT 15

AAFP4186/c

ID AAFP4186 standard; DNA; 587 BP.

AC AAFP4186;

DT 23-MAY-2001 (first entry)

XX Primer specific for DNA encoding secretory/membrane protein SEQ ID 620.

DE Human; secretory protein; membrane protein; vaccine; gene therapy;

KW rheumatoid arthritis; diabetes; PCR primer; ss.

OS Synthetic.

PN EPI067182-A2.

PD 10-JAN-2001.

PF 07-JUL-2000; 2000EP-0114090.

PR 08-JUL-1999; 99JP-0194179.

PR 11-JAN-2000; 2000JP-0118775.

PR 02-MAY-2000; 2000JP-0183766.

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

DR WPI; 2001-093989/11.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in

PT gene therapy or as candidate target molecules in drug development -

XX Claim 5; SEQ ID 620; 609pp + CD ROM; English.

PS This invention relates to nucleic acid sequences AAFP3744 - AAFP3916

CC which encode human secretory or membrane proteins represented by

CC AAB8317 - AAB88419. Included in the invention are primers

CC AAFP3917 - AAFP4295 and AAFP5232 - AAFP6235 which are used to isolate the

CC cDNA sequences of the invention. The invention also includes methods for

CC the production of antibodies directed against the proteins, and cDNA

CC sequences, which can be used in vaccines. The polynucleotide sequences

CC can be used in gene therapy. The polynucleotide sequences and the

CC proteins they encode may be used in the prevention, treatment and

CC diagnosis of diseases associated with inappropriate secretory

CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies and antagonists may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
 CC (ELISA). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.

S0 Sequence 587 BP; 117 A; 162 C; 140 G; 162 T; 6 other;

Query Match 58.4%; Score 365; DB 22; Length 587;

Best Local Similarity 99.8%; Pred. No. 1e-135;

Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 191 AGCGGTTGATGACCGAGCTGAGTAAAGAAACGTCCTCGAAGAGGAGGAGATCATG 250  
 Db 417 AGCGGTTGATGACCGAGCTGAGTAAAGAAACGTCCTCGAAGAGGAGGAGATCATG 358  
 QY 251 TACGCCCGGAAGTAGAGACTGCTCCAGTCGTGCTGGGTTGGCCGAGACCATGATCTC 310  
 Db 357 TACGCCCGGAAGTAGAGACTGCTCCAGTCGTGCTGGGTTGGCCGAGACCATGATCTC 298  
 QY 311 CGAATCTGTGGGCGATCCAGCATACGGCCAAATGTACAGCATAGCCCTGGCAGACA 370  
 Db 297 CGAATCTGTGGGCGATCCAGCATACGGCCAAATGTACAGCATAGCCCTGGCAGACA 238  
 QY 371 CGAGCAGAGGAGAGAGACAGAGAAAGAAACACAGCATGAGACAGTAATGATTA 430  
 Db 237 CGAGCAGAGGAGAGAGACAGAGAAAGAAACACAGCATGAGACAGTAATGATTA 178  
 QY 431 AAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTTGGCCAGAAATGTTACCAAT 490  
 Db 177 AAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTTGGCCAGAAATGTTACCAAT 118  
 QY 491 TTTCACTGTGGACTTGAACAGCTTCTTTGCCACAGAGAGAAATTTAACTATGTT 550  
 Db 117 TTTCACTGTGGACTTGAACAGCTTCTTTGCCACAGAGAGAAATTTAACTATGTT 58  
 QY 551 CAAACCGGGGAGTGGCTGTAAAGAAAGACCATTAATGCTTTAGACAGTG 606  
 Db 57 CAAACCGGGGAGTGGCTGTAAAGAAAGACCATTAATGCTTTAGACAGTG 2

## RESULT 16

ABT03279/c

ID ABT03279 standard; cDNA; 1362 BP.

XX ABT03279;

AC ABT03279;

DT 05-SEP-2002 (first entry)

DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 208.

KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;

KW cytosolic; gene; ss.

OS Homo sapiens.

PN WO200239885-A2.

PD 23-MAY-2002.

PF 13-NOV-2001; 2001WO-US45395.

PR 14-NOV-2000; 2000US-0713550.

PR 03-APR-2001; 2001US-0825294.

```

PR 02-OCT-2001; 2001US-0970966.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX
XX WPI: 2002-500186/53.
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for
XX detecting the presence of ovarian cancer in a patient, and in
XX pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
XX
XX Claim 2; Page 193; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
XX and coding sequences. The sequences can be used in the diagnosis and
XX treatment of ovarian cancers. The present sequence is a coding sequence
XX of the invention.
XX
XX Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other;
XX
XX Query Match 57.4%; Score 359; DB 24; Length 1362;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-133;
XX Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGTTCCTCTTGACAGAGACTGGCCGCGGACGCGAAGAGCAGCGGCGCTGCACAAAGCG 60
XX DB 1215 AGTTCCTCTTGACAGAGACTGGCCGCGGACGCGAAGAGCAGCGGCGCTGCACAAAGCG 1156
XX
XX QY 61 GCGCGCTGCTGGTGGTGGATGCCATGTACGCGCAGGCGCTTCTCGTGGTGGCGTCTG 120
XX DB 1155 GCGCGCTGCTGGTGGTGGATGCCATGTACGCGCAGGCGCTTCTCGTGGTGGCGTCTG 1096
XX
XX QY 121 CAGCGACAGCGCGGACAGACAGCTGCAGACAGACACCGCGGAACGTGCGGAGGACAC 180
XX DB 1095 CAGCGACAGCGCGGACAGACAGCTGCAGACAGACACCGCGGAACGTGCGGAGGACAC 1036
XX
XX QY 181 CGTGTACAGAGCGGGGTGATGACCGAGCTGAGAGTGAAGAAAGCTCTCCGAGAGGGAG 240
XX DB 1035 CGTGTACAGAGCGGGGTGATGACCGAGCTGAGAGTGAAGAAAGCTCTCCGAGAGGGAG 976
XX
XX QY 241 GAGGATCATGTACGCGCGGAGTGCCTGCTGCTGGTGGTGGCGGACG 300
XX DB 975 GAGGATCATGTACGCGCGGAGTGCCTGCTGCTGGTGGTGGCGGACG 916
XX
XX QY 301 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 359
XX DB 915 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 857
XX
XX RESULT 17
XX ABL40347/c
XX ID ABL40347 standard; cDNA; 1362 BP.
XX
XX AC ABL40347;
XX
XX XX 28-JUN-2002 (first entry)
XX
XX DE Ovarian carcinoma GPR39 cDNA.
XX
XX KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
XX 98.
XX
XX OS Homo sapiens.
XX
XX XX Key Location/Qualifiers
XX FT CDS 1..1362
XX FT /tag= a
XX FT /product= "Ovarian carcinoma protein GPR39"
XX
XX US2002004491-A1.

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PD 10-JAN-2002.
XX
XX PF 03-APR-2001; 2001US-0825294.
XX
XX PR 10-SEP-1999; 990US-0394374.
XX PR 01-MAY-2000; 2000US-0561778.
XX PR 15-AUG-2000; 2000US-0640173.
XX PR 07-SEP-2000; 2000US-0656668.
XX PR 14-NOV-2000; 2000US-0713550.
XX
XX PA (XUJ/) XU J.
XX PA (STOL/) STOLK J A.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX
XX PI Xu J, Stolk JA, Algate PA, Fling SP;
XX
XX DR WPI: 2002-171027/22.
XX
XX DR P-PSDB; ABB09416.
XX
XX PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
XX prevention and/or treatment of cancer, especially ovarian cancer.
XX
XX PS Claim 1a; Page 123-124; 131pp; English.
XX
XX CC The invention relates to ovarian tumour polynucleotides and polypeptides
XX that may be utilised in cancer therapy, for example in a vaccine or
XX gene therapy. Polypeptides and polynucleotides of the invention are
XX useful for detecting a cancer in a patient, for stimulating and/or
XX expanding T-cells specific for a tumour protein, and for inhibiting the
XX development of a cancer in a patient. They are also useful for
XX stimulating an immune response in a patient, and for treating a cancer in
XX a patient and for determining the presence of a cancer in a patient.
XX
XX CC The isolated polynucleotides of the invention are useful for their
XX ability to selectively form duplex molecules with complementary stretches
XX of the entire desired gene or gene fragments, and for designing and
XX preparing ribozyme molecules for inhibiting expression of tumour
XX polypeptides in tumour cells. Polypeptides and polynucleotides of the
XX invention are also useful in recombinant DNA molecules to direct
XX expression of a polypeptide in appropriate host cells. The current
XX sequence represents the ovarian carcinoma GPR39 cDNA.
XX
XX SQ Sequence 1362 BP; 263 A; 435 C; 362 G; 302 T; 0 other;
XX
XX Query Match 57.4%; Score 359; DB 24; Length 1362;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-133;
XX Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGTTCCTCTTGACAGAGACTGGCCGCGGACGCGAAGAGCAGCGGCGCTGCACAAAGCG 60
XX DB 1215 AGTTCCTCTTGACAGAGACTGGCCGCGGACGCGAAGAGCAGCGGCGCTGCACAAAGCG 1156
XX
XX QY 61 GCGCGCTGCTGGTGGTGGATGCCATGTACGCGCAGGCGCTTCTCGTGGTGGCGTCTG 120
XX DB 1155 GCGCGCTGCTGGTGGTGGATGCCATGTACGCGCAGGCGCTTCTCGTGGTGGCGTCTG 1096
XX
XX QY 121 CAGCGACAGCGCGGACAGACAGCTGCAGACAGACACCGCGGAACGTGCGGAGGACAC 180
XX DB 1095 CAGCGACAGCGCGGACAGACAGCTGCAGACAGACACCGCGGAACGTGCGGAGGACAC 1036
XX
XX QY 181 CGTGTACAGAGCGGGGTGATGACCGAGCTGAGTGAAGAAAGCTCTCCGAGAGGGAG 240
XX DB 1035 CGTGTACAGAGCGGGGTGATGACCGAGCTGAGTGAAGAAAGCTCTCCGAGAGGGAG 976
XX
XX QY 241 GAGGATCATGTACGCGCGGAGTGCCTGCTGCTGGTGGTGGCGGACG 300
XX DB 975 GAGGATCATGTACGCGCGGAGTGCCTGCTGCTGGTGGTGGCGGACG 916
XX
XX QY 301 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 359
XX DB 915 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 857

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RESULT 18
AA18690/c
ID AAD18690 standard; cDNA: 2528 BP.
XX
XX AAD18690;
XX
XX 18-DEC-2001 (first entry)
XX
DE Human G protein coupled receptor (GPCR) 4941 cDNA.
XX
XX Human; cardiovascular: tumorigenic disorder; aberrant angiogenesis;
XX gene therapy; aberrant vascularisation; arteriosclerosis; ovarian cancer;
XX ischemia/reperfusion injury; hypertension; arterial inflammation;
XX psoriasis; endothelial cell disorder; diabetic retinopathy; restenosis;
XX myocardial infarction; Grave's disease; G protein coupled receptor;
XX GPCR 4941; vasotropic; hypotensive; antiinflammatory; cytosolic;
XX antidiabetic; antipsoriatic; leukaemia; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 42..1403
XX FT /*tag= a
XX FT /product= "Human GPCR 4941"
XX FT /note= "The CDS is specifically claimed in claim 1 of
XX the specification"
XX
XX WO200181634-A2.
XX
XX PD 01-NOV-2001.
XX
XX 25-APR-2001; 2001WO-US13788.
XX
XX 26-APR-2000; 2000US-199908P.
XX PR 09-AUG-2000; 2000US-0635521.
XX
XX (MIL-) MILLENNIUM PHARM INC.
XX
XX PI Galvin KA, Rudolph-owen LA;
XX
XX WPI: 2001-611743/70.
XX DR P-PSDB; AAE11751.
XX
XX Identifying nucleic acids for the diagnosis and treatment of
XX PT cardiovascular and tumorigenic disorders, comprises identifying G
XX protein coupled receptor (GPCR)-4941 -
XX
XX Example 1: Fig 1: 118pp; English.
XX
XX The present invention relates to a method for identifying a nucleic acid
XX molecule (G protein coupled receptor gene, GPCR 4941) associated with a
XX cardiovascular or tumorigenic disorder. The method comprising contacting
XX a sample containing a nucleic acid molecule with a hybridisation probe or
XX amplification primers and detecting the presence. The invention is used
XX in gene therapy. The method of the invention is used for identifying
XX CC nucleic acids or polypeptides associated with a cardiovascular or
XX CC tumorigenic disorder such as aberrant angiogenesis, aberrant
XX CC vascularisation, arteriosclerosis, or ovarian cancer, ischaemia/
XX CC reperfusion injury, hypertension, restenosis, arterial inflammation,
XX CC endothelial cell disorders, diabetic retinopathy, psoriasis, myocardial
XX CC infarction, Grave's disease and leukaemia. The methods can also detect
XX CC mRNA or genomic DNA in a sample. The present sequence is G protein
XX CC coupled receptor (GPCR) 4941 cDNA.
XX
XX Sequence 2528 BP: 516 A; 766 C; 677 G; 567 T; 2 other:
XX
Query Match 57.4%; Score 359; DB 22; Length 2528;
Best Local Similarity 100.0%; Pred. No. 2..1e-133;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGTTCCTCTTCAGAGACTGGCGGAGCGGAGCAAGCAAGCGGCGCTGCACAAACGG 60
DB 1256 AGTTCCTCTTCAGAGACTGGCGGAGCGGAGCAAGCAAGCGGCGCTGCACAAACGG 1197

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OY 61 GCGCTGTGCGTGAGTGGAGTCCGATGTACGCGAGCGGCTTCTGTTGGCTGCTG 120
DB 1196 GCGCTGTGCGTGAGTGGAGTCCGATGTACGCGAGCGGCTTCTGTTGGCTGCTG 1137
OY 121 CAGCGACAGCGCGGACAGACACACCTTCACAGAACACCCCGGAAACCTGTCAGAGAC 180
DB 1136 CAGCGACAGCGCGGACAGACACACCTTCACAGAACACCCCGGAAACCTGTCAGAGAC 1077
OY 181 CGTGTACAGAGCGGCTTGTATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAGGAG 240
DB 1076 CGTGTACAGAGCGGCTTGTATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAGGAG 1017
OY 241 GAGGATCATGTACGCCCGGAGATGAGACCTGCTCACTGCTGTTGGCTTGGCCGACG 300
DB 1016 GAGGATCATGTACGCCCGGAGATGAGACCTGCTCACTGCTGTTGGCTTGGCCGACG 957
OY 301 CATGATCTCTCCGATCTGCTTGGGATCCAGCAATACGCCCAATGTCACAAATCAGCC 359
DB 956 CATGATCTCTCCGATCTGCTTGGGATCCAGCAATACGCCCAATGTCACAAATCAGCC 898

RESULT 19
AAH50766/c
ID AAH50766 standard; cDNA: 444 BP.
XX
XX AAH50766;
XX
XX 23-AUG-2001 (first entry)
XX
XX Human tumour associated cDNA #95.
XX
XX Human; cancer specific gene expression; gene therapy;
XX KM age related differential expression; ss.
XX
XX Homo sapiens.
XX
XX WO200136685-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US1809.
XX
XX 17-NOV-1999; 99US-0166056.
XX PR 17-NOV-1999; 99US-0166106.
XX
XX (NYXI-) NYXIS NEURO THERAPIES INC.
XX
XX PI Kroes RA, Moskal JR, Yamamoto H;
XX
XX WPI: 2001-355647/37.
XX
XX Novel nucleic acid molecules differentially expressed in brain cancers,
XX PT useful for ascertaining propensity of cell for malignant phenotype or
XX PT ascertaining suitability of anti-neoplastic drug candidate -
XX
XX Claim 28; Page 50; 82pp; English.
XX
XX The present invention provides the sequences of 184 cDNA fragments which
XX CC are differentially expressed in cancer cell depending on the age of the
XX CC patient. They can be used to diagnose and identify treatments for
XX CC cancers, particularly brain cancers such as haemangioblastoma, teratoma,
XX CC haemangioma, glioblastoma, schwannoma, osteoma and pinealoma. The
XX CC present sequence is a cancer-associated cDNA of the invention.
XX
XX Sequence 444 BP: 95 A; 113 C; 94 G; 142 T; 0 other:
XX
Query Match 56.3%; Score 352; DB 22; Length 444;
Best Local Similarity 99.8%; Pred. No. 1..6e-130;
Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 204 CCGAGCTAGGTAGAAAAAGTCTCCGAGAGGAGAGATCATGTACGCCGGAAGT 263

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PT polypeptide -  
 XX  
 PS Claim 1: SEQ ID 2409; 489pp; English.  
 CC The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of an ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.  
 CC  
 XX Sequence 349 BP; 79 A; 84 C; 78 G; 108 T; 0 other;

Query Match 49.1%; Score 307; DB 24; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-112;  
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCAATGATCTCCGAATCTGGTTGGGATCCAGATACGGCCCAATGTCAACAATCAGCC 359  
 |||||  
 Db 310 CCAATGATCTCCGAATCTGGTTGGGATCCAGATACGGCCCAATGTCAACAATCAGCC 251  
 |||||  
 QY 360 CTGGGCGACACGACGACGAGGAGAGACAGAGAAAAAACAACAGATGAGACACA 419  
 |||||  
 Db 250 CTGGGCGACACGACGAGGAGGAGAGACAGAGAAAAAACAACAGATGAGACACA 191  
 |||||  
 QY 420 GTAAATGATTAATAACCAATTAATTTAGCCCTCTGCTGCTTACTGGCCAGGAAA 479  
 |||||  
 Db 190 GTAAATGATTAATAACCAATTAATTTAGCCCTCTGCTGCTTACTGGCCAGGAAA 131  
 |||||  
 QY 480 TGGTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTTGCCACAAGCAGAGAGAAAT 539  
 |||||  
 Db 130 TGGTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTTGCCACAAGCAGAGAAAT 71  
 |||||  
 QY 540 TAACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAATGCTTTA 599  
 |||||  
 Db 70 TAACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAATGCTTTA 11  
 |||||  
 QY 600 GACAGTG 606  
 |||||  
 Db 10 GACAGTG 4

RESULT 22  
 ABL81262/c  
 ID ABL81262 standard; cDNA; 409 BP.  
 XX  
 AC ABL81262;  
 XX  
 DT 17-MAY-2002 (first entry)  
 XX  
 DE Human ovarian cancer related cDNA clone SEQ ID NO:4240.  
 KW Human: ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192581-A2.  
 XX

PD 06-DEC-2001.  
 XX  
 XX 29-MAY-2001; 2001WO-US17756.  
 PE  
 XX  
 PR 26-MAY-2000; 2000US-207484P.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 PI Algate PA, Harlocker SL, Jones R;  
 XX  
 DR WPI; 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide -  
 PS Claim 1; SEQ ID 4240; 489pp; English.

CC The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of an ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (S1) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a  
 CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.  
 CC  
 XX Sequence 409 BP; 89 A; 106 C; 87 G; 127 T; 0 other;

Query Match 42.1%; Score 263; DB 24; Length 409;  
 Best Local Similarity 99.7%; Pred. No. 3.0e-95;  
 Matches 313; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 293 GCCGAGCAGATGATCTCCGAATCTGGTTGGGATCCAGATACGGCCCAATGTCAACA 352  
 |||||  
 Db 315 GCCGAGCAGATGATCTCCGAATCTGGTTGGGATCCAGATACGGCCCAATGTCAACA 256  
 |||||  
 QY 353 ATCAGCCCTGGGCGACACGACGAGGAGAGAGACAGAGAAAAAACAACAGATGA 412  
 |||||  
 Db 255 ATCAGCCCTGGGCGACACGACGAGGAGAGAGACAGAGAAAAAACAACAGATGA 196  
 |||||  
 QY 413 GAACACAGTAAATGATTAATAACCAATTAATTTAGCCCTCTGCTGCTTACTGGC 472  
 |||||  
 Db 195 GAACACAGTAAATGATTAATAACCAATTAATTTAGCCCTCTGCTGCTTACTGGC 136  
 |||||  
 QY 473 CAGGAATGTTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTTGCCACAAGCAAGA 532  
 |||||  
 Db 135 CAGGAATGTTACCAATTTTTCAGTGTGACTTGACAGCTTCTTTTGCCACAAGCAAGA 76  
 |||||  
 QY 533 GAGAAATTTAACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAA 592  
 |||||  
 Db 75 GAGAAATTTAACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAACATTAAA 16  
 |||||  
 QY 593 TGCTTTAGACAGTG 606  
 |||||  
 Db 15 TGCTTTAGACAGTG 2

RESULT 23







DB 209 GCGCGTGTGCGTGAGTGGCAGTATACGC 240

## RESULT 27

AL33985/C  
ID AAL33985 standard; DNA; 50 BP.

AC AAL33985;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #7193.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -

XX Claim 1: Page 3451; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX histones, kinases, colony stimulating factors, complement related  
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
XX G-protein coupled receptors and thioesterases. The present sequence is  
XX one such oligonucleotide. The oligonucleotides and the peptides encoded  
XX by them may be used in the prevention, diagnosis and treatment of  
XX diseases associated with inappropriate expression of the proteins listed  
XX above. Disorders that may be prevented, diagnosed and/or treated include  
XX multifactorial diseases with a genetic component, such as autoimmune  
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer  
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,  
XX leukaemia), diseases of the nervous system and an infection of pathogenic  
XX organisms.

XX Sequence 50 BP; 14 A; 13 C; 17 G; 6 T; 0 other;

XX Query Match 4.2%; Score 26; DB 22; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 0.68;  
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GCGGAGCATGATCTCGAATCTG 318

DB 26 GCGGAGCATGATCTCGAATCTG 1

## RESULT 28

AL33986/C  
ID AAL33986 standard; DNA; 50 BP.

AC AAL33986;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #7194.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -

XX Claim 1: Page 3451; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX histones, kinases, colony stimulating factors, complement related  
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
XX G-protein coupled receptors and thioesterases. The present sequence is  
XX one such oligonucleotide. The oligonucleotides and the peptides encoded  
XX by them may be used in the prevention, diagnosis and treatment of  
XX diseases associated with inappropriate expression of the proteins listed  
XX above. Disorders that may be prevented, diagnosed and/or treated include  
XX multifactorial diseases with a genetic component, such as autoimmune  
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer  
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,  
XX leukaemia), diseases of the nervous system and an infection of pathogenic  
XX organisms.

XX Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 other;

XX Query Match 4.2%; Score 26; DB 22; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 0.68;  
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 ACCTGTCAGTGTCTGTTGGTTTG 292

DB 50 ACCTGTCAGTGTCTGTTGGTTTG 25

## RESULT 29

AAL27277/C  
ID AAL27277 standard; DNA; 51 BP.

XX AL27277;  
AC 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #485.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200147944-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 28-DEC-2000; 2000WO-US35498.  
XX  
XX 28-DEC-1999; 99US-0173419.  
XX  
XX 27-DEC-2000; 2000US-0173419.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shinkets RA, Leach M;  
PI  
DR WPI; 2001-465210/50.  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections.  
XX  
XX Claim 1; Page 1529; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid protein, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 51 BP; 9 A; 5 C; 10 G; 27 T; 0 other;  
XX  
XX Query Match 4.0%; Score 25; DB 22; Length 51;  
XX Best Local Similarity 100.0%; Pred No. 1.7;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 23-JAN-2002 (first entry)  
XX  
XX Human nervous system related polynucleotide SEQ ID NO 10615.  
DE  
XX  
KW Human; nocotropic; neuroprotective; cytostatic; dermatological; vlrucide;  
KW Immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulvareary;  
KW antiparkinsonian; antisticking; antinaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200159063-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01334.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX  
XX 04-FEB-2000; 2000US-0180628.  
XX  
XX 24-FEB-2000; 2000US-0184664.  
XX  
XX 02-MAR-2000; 2000US-0186350.  
XX  
XX 16-MAR-2000; 2000US-0186874.  
XX  
XX 17-MAR-2000; 2000US-0190076.  
XX  
XX 18-APR-2000; 2000US-0198123.  
XX  
XX 19-MAY-2000; 2000US-0205515.  
XX  
XX 07-JUN-2000; 2000US-0209467.  
XX  
XX 28-JUN-2000; 2000US-0214886.  
XX  
XX 30-JUN-2000; 2000US-0215135.  
XX  
XX 07-JUL-2000; 2000US-0216647.  
XX  
XX 07-JUL-2000; 2000US-0216880.  
XX  
XX 11-JUL-2000; 2000US-0217487.  
XX  
XX 11-JUL-2000; 2000US-0217496.  
XX  
XX 14-JUL-2000; 2000US-0218290.  
XX  
XX 26-JUL-2000; 2000US-0220963.  
XX  
XX 26-JUL-2000; 2000US-0220964.  
XX  
XX 14-AUG-2000; 2000US-0224518.  
XX  
XX 14-AUG-2000; 2000US-0224519.  
XX  
XX 14-AUG-2000; 2000US-0225213.  
XX  
XX 14-AUG-2000; 2000US-0225214.  
XX  
XX 14-AUG-2000; 2000US-0225266.  
XX  
XX 14-AUG-2000; 2000US-0225267.  
XX  
XX 14-AUG-2000; 2000US-0225268.  
XX  
XX 14-AUG-2000; 2000US-0225270.  
XX  
XX 14-AUG-2000; 2000US-0225447.  
XX  
XX 14-AUG-2000; 2000US-0225757.  
XX  
XX 14-AUG-2000; 2000US-0225758.  
XX  
XX 14-AUG-2000; 2000US-0225759.  
XX  
XX 18-AUG-2000; 2000US-0226279.  
XX  
XX 22-AUG-2000; 2000US-0226681.  
XX  
XX 22-AUG-2000; 2000US-0226688.  
XX  
XX 22-AUG-2000; 2000US-0227182.  
XX  
XX 23-AUG-2000; 2000US-0227009.  
XX  
XX 30-AUG-2000; 2000US-0228924.  
XX  
XX 01-SEP-2000; 2000US-0229287.  
XX  
XX 01-SEP-2000; 2000US-0229343.  
XX  
XX 01-SEP-2000; 2000US-0229344.  
XX  
XX 01-SEP-2000; 2000US-0229345.  
XX  
XX 05-SEP-2000; 2000US-0229509.  
XX  
XX 05-SEP-2000; 2000US-0229513.  
XX  
XX 06-SEP-2000; 2000US-0230437.  
XX  
XX 06-SEP-2000; 2000US-0230438.  
XX  
XX 08-SEP-2000; 2000US-0231242.  
XX  
XX 08-SEP-2000; 2000US-0231243.  
XX  
XX 08-SEP-2000; 2000US-0231244.  
XX  
XX 08-SEP-2000; 2000US-0231245.  
XX  
XX 08-SEP-2000; 2000US-0231413.  
XX  
XX 08-SEP-2000; 2000US-0231414.  
XX  
XX 08-SEP-2000; 2000US-0232080.  
XX  
XX 08-SEP-2000; 2000US-0232081.  
XX  
XX 12-SEP-2000; 2000US-0231968.  
XX  
XX 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 20-OCT-2000; 2000US-0242221.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246539.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250391.  
PR 01-DEC-2000; 2000US-0251160.  
PR 05-DEC-2000; 2000US-0251030.

PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-541565/60.  
XX  
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating nervous system  
PT cancers and metastases -  
XX  
XX  
PS Disclosure: SEQ ID NO 10615; 1701pp + Sequence listing; English.  
XX  
XX  
CC The invention relates to novel genes (ABAI1004-ABAI21534) and proteins  
CC (ABAI4678-ABAI8001) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
SQ Sequence 263 BP; 88 A; 36 C; 67 G; 71 T; 1 other;  
XX  
XX  
Query Match 3.7%; Score 23; DB 22; Length 263;  
Best Local Similarity 100.0%; Pred No. 8.7;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 603 AGTGNAAAAAAAAAAAAAAAAA 625  
Db 241 AGTGNAAAAAAAAAAAAAAAAA 263  
|||||  
RESULT 31  
AAI10167/c  
ID AAI10167 standard; cDNA; 377 BP.  
XX  
XX AAI10167;  
XX  
XX 07-DEC-2001 (first entry)  
XX  
XX Human breast cancer expressed polynucleotide 2624.  
XX  
XX Human breast cancer; cell marker; cytostatic; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200151628-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 10-JAN-2001; 2001WO-US00798.  
XX  
XX



CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) determining the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
SQ Sequence 1539 BP; 577 A; 372 C; 435 G; 146 T; 9 other;  
Query Match 3.7%; Score 23; DB 23; Length 1539;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 385 AGACAGAGAGAGAGAGAGAGAG 407  
DB 878 AGACAGAGAGAGAGAGAGAGAG 900  
RESULT 34  
ABK53839  
ID ABK53839 standard; cDNA; 256 BP.  
AC ABK53839;  
XX  
XX  
XX 05-JUN-2002 (first entry)  
DE Human head and neck tumour CDNA, SEQ ID No 34.  
XX  
XX Human; head and neck cancer; tumour; cytostatic; immunogenic; vaccine;  
XX gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200212329-A2.  
XX  
XX 14-FEB-2002.  
XX  
XX 01-AUG-2001; 2001WO-US24226.  
XX  
XX 03-AUG-2000; 2000US-223281P.  
XX  
XX 16-NOV-2000; 2000US-249933P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Fan L;  
XX  
XX WPI: 2002-257467/30.  
XX  
XX Novel polynucleotide encoding head and neck tumour polypeptides, useful  
XX in pharmaceutical compositions, e.g. vaccines, for treating head and  
XX neck cancers -  
XX  
XX Claim 1; Page 123; 200pp; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising  
XX sequences selected from 273 sequences fully defined in the specification.  
XX (I), including its encoded polypeptide (II), an antibody binding to (II),  
XX a fusion protein comprising (II) and a T-cell population stimulated by  
XX (I) or (II) are useful for stimulating an immune response in a patient  
XX and treating head and neck cancer in a patient. An oligonucleotide (III)  
XX that hybridizes to (I) is useful for determining the presence of cancer  
XX in a patient, by obtaining a biological sample from the patient,  
XX contacting the sample with (III), detecting in the sample an amount of a  
XX polynucleotide that hybridizes to the oligonucleotide, and comparing the

CC amount of polynucleotide that hybridizes to the oligonucleotides to a  
CC predetermined cut-off value. (I) and (II) are useful in pharmaceutical  
CC compositions, e.g. vaccines, and other compositions for the diagnosis and  
CC treatment of head and neck cancer. ABK53806-ABK54078 represent human head  
CC and neck cancer cDNA sequences of the invention.  
XX  
SQ Sequence 256 BP; 83 A; 31 C; 52 G; 83 T; 7 other;  
Query Match 3.5%; Score 22; DB 24; Length 256;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 604 GTGNNAAAAAAAAAAAAAAAAAAAA 625  
DB 213 GTGNNAAAAAAAAAAAAAAAAAAAA 234  
RESULT 35  
ABV08332/C  
ID ABV08332 standard; cDNA; 377 BP.  
XX  
XX ABV08332;  
XX  
XX 13-SEP-2002 (first entry)  
DE Human prostate expression marker CDNA 8323.  
XX  
XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX Pharmacogenomic marker; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200160860-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 20-FEB-2001; 2001WO-US05171.  
XX  
XX 17-FEB-2000; 2000US-183319P.  
XX  
XX 16-MAR-2000; 2000US-189862P.  
XX  
XX 25-MAY-2000; 2000US-207454P.  
XX  
XX 09-JUN-2000; 2000US-211314P.  
XX  
XX 18-JUL-2000; 2000US-219007P.  
XX  
XX 13-DEC-2000; 2000US-255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI: 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
XX prostate cells and correlating with presence of prostate cancer, useful  
XX for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
XX Claim 1; Page 1324; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
XX specification or its complement. (I) is useful for:  
XX (a) assessing whether a patient is afflicted with prostate cancer;  
XX (b) monitoring the progression of prostate cancer in a patient;  
XX (c) assessing the efficacy of a test compound to inhibit prostate  
XX cancer in a patient;  
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
XX in a patient;  
XX (e) selecting a composition for inhibiting prostate cancer in a patient;  
XX (f) determining the prostate cell carcinogenic potential of a compound;  
XX (g) determining whether prostate cancer has metastasized in a patient;  
XX (h) assessing the aggressiveness or indolence of prostate cancer in a  
XX patient;  
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

SO Sequence 377 BP; 89 A; 75 C; 63 G; 123 T; 27 other;

Query Match 3.5%; Score 22; DB 23; Length 377;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNNAAAAAAAAAAAAA 625  
DB 78 GTGNNAAAAAAAAAAAAA 57

## RESULT 36

AA187949  
ID AA187949 standard; cDNA; 442 BP.

AC AA187949;

DT 06-NOV-2001 (first entry)

DE Human polynucleotide SEQ ID NO 8009.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KM tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation; ss.

XX Homo sapiens.

OS WO200164835-A2.

PN 07-SEP-2001.

PD 26-FEB-2001; 2001WO-US04927.

PF 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-514838/56.

DR P-PSDB; AAC08018.

XX Isolated nucleic acids and polypeptides, useful for preventing

PT diagnosing and treating e.g. leukaemia, inflammation and immune

PT disorders -

PS Claim 1; SEQ ID NO 8009; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and

CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 442 BP; 167 A; 65 C; 102 G; 85 T; 23 other;

SO Query Match 3.5%; Score 22; DB 22; Length 442;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNNAAAAAAAAAAAAA 625  
DB 1294 GTGNNAAAAAAAAAAAAA 1315

DB 226 GTGNNAAAAAAAAAAAAA 247

## RESULT 37

ABL90482  
ID ABL90482 standard; cDNA; 1329 BP.

AC ABL90482;

DT 24-MAY-2002 (first entry)

DE Human polynucleotide SEQ ID NO 1044.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;

KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;

KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;

KW neurological disease; infection; human; secreted protein; gene; ss.

XX Homo sapiens.

OS WO200190304-A2.

PN 29-NOV-2001.

PD 18-MAY-2001; 2001WO-US16450.

PF 19-MAY-2000; 2000US-205515P.

PR (HDMA-) HUMAN GENOME SCI INC.

PA Birse CE, Rosen CA;

PI WPI; 2002-122018/16.

DR P-PSDB; ABB90073.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

PT prevention of neural, immune system, muscular, reproductive,

PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

PT disorders -

PS Claim 4; SEQ ID NO 1044; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins

CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are

CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (ant)agonists are useful

CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone

CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative

CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;

CC (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal

CC epilepsy; and (f) infectious diseases.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1329 BP; 263 A; 407 C; 369 G; 288 T; 2 other;

SO Query Match 3.5%; Score 22; DB 24; Length 1329;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNNAAAAAAAAAAAAA 625

DB 1294 GTGNNAAAAAAAAAAAAA 1315



RESULT 38  
 ABK65378  
 ID ABK65378 standard; cDNA: 1388 BP.  
 XX  
 XX ABK65378;  
 AC  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 XX Arabidopsis cDNA encoding a transcription factor #230.  
 DE  
 XX  
 XX Plant; ss: gene; transcription factor; transgenic;  
 KM agriculture; metabolic chemical; environmental stress; drought;  
 KM microbial disease resistance; herbicide resistance; seed yield;  
 KM fruit yield; growth rate; leaf senescence; flower senescence.  
 XX  
 OS Arabidopsis thaliana.  
 OS  
 XX MO200215675-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 XX 22-AUG-2001; 2001MO-US26189.  
 PF  
 XX 22-AUG-2000; 2000US-227439P.  
 PR 16-NOV-2000; 2000US-0713994.  
 PR 16-APR-2001; 2001US-0837944.  
 XX  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 PA (PIIG/) PILGRIM M.  
 PA (GREG/) CREELMAN R.  
 PA (DUBE/) DUBELL A J.  
 PA (HEAR/) HEARD J.  
 PA (JIAN/) JIANG C.  
 PA (KEDD/) KEDDIE J.  
 PA (ADAM/) ADAM L.  
 PA (RATC/) RATCLIFF O.  
 PA (REUB/) REUBER J L.  
 PA (RIEC/) RIECHMANN J L.  
 PA (YUGG/) YU G.  
 PA (PINE/) PINEDA O.  
 XX  
 PI Pilgrim M, Creelman R, Dubell AJ, Heard J, Jiang C, Keddie J;  
 PI Adam L, Ratcliff O, Reuber JL, Riechmann JL, Yu G, Pineda O;  
 DR WPI: 2002-292022/33.  
 DR P-PSDB: AA093192.  
 XX  
 PT An isolated or recombinant polynucleotide used to produce a transgenic  
 PT plant -  
 XX  
 PS Claim 4: Page 927-929; 941pp; English.

CC pest tolerance, environmental stress response (e.g. drought), microbial  
 CC disease resistance, herbicide resistance, seed and fruit yield, growth  
 CC rate, leaf and flower senescence and many other traits listed in the  
 CC specification). The present sequence is one of the 232 polynucleotides  
 CC encoding an A. thaliana transcription factor.  
 CC  
 XX  
 SQ Sequence 1388 BP; 398 A; 282 C; 319 G; 389 T; 0 other;  
 Query Match 3.5%; Score 22; DB 24; Length 1388;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 374 GCAGAGGAGAGACAGAGAAA 395  
 DB 991 GCAGAGGAGAGACAGAGAAA 1012  
 ||||||||||||||||||||  
 RESULT 39  
 AAH34281  
 ID AAH34281 standard; cDNA: 1823 BP.  
 XX  
 AC AAH34281;  
 XX  
 DT 03-SEP-2001 (first entry)  
 DT  
 XX  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1363.  
 XX  
 KM Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KM colorectal carcinoma; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN MO200122920-A2.  
 PD  
 XX 05-APR-2001.  
 XX  
 PF 28-SEP-2000; 2000MO-US26524.  
 XX  
 PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 PT WPI: 2001-235357/24.  
 PT P-PSDB: AAG74876.  
 DR  
 XX  
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 XX useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX  
 PS Claim 1: Page 3077-3078; 9803pp; English.

AAH2993 to AAH37195 and AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patient's own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated P,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAG77789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

Sequence 1823 BP; 355 A; 609 C; 516 G; 335 T; 8 other;

Query Match 3.5%; Score 22; DB 22; Length 1823;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAA 625

DB 1726 GTGNAAAAAAAAAAAAAA 1747

#### RESULT 40

ABL90818/c

ID ABL90818 standard; cDNA; 2049 BP.

AC ABL90818;

DT 24-MAY-2002 (first entry)

DE Human polynucleotide SEQ ID NO 1380.

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor; antiviral; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiactant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.

OS Homo sapiens.

PN WO200190304-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US16450.

PR 19-MAY-2000; 2000US-205515P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barse CE, Rosen CA;

DR WPI: 2002-122018/16.

DR P-PSDB; ABB90409.

Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -

Claim 4; SEQ ID NO 1380; 2081pp + Sequence Listing; English.

The invention relates to novel genes (ABL89449-AB190853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune disease, hemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 2049 BP; 383 A; 571 C; 686 G; 400 T; 9 other;

Query Match 3.5%; Score 22; DB 24; Length 2049;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 GTGNAAAAAAAAAAAAAA 625

DB 325 GTGNAAAAAAAAAAAAAA 304

#### RESULT 41

AAH69474/c

ID AAH69474 standard; cDNA; 259 BP.

AC AAH69474;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 748.

Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

PN WO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US33312.

PR 08-DEC-1999; 99US-0169681.

PR 21-DEC-1999; 99US-0171350.

PR 14-MAR-2000; 2000US-0189315.

PR 12-MAY-2000; 2000US-0203791.

PR 09-JUN-2000; 2000US-0210600.

PR 21-JUL-2000; 2000US-0220114.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;

DR WPI: 2001-375006/39.

PF New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer -

Claim 1; Page 232; 1051pp; English.

The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.

Sequence 259 BP; 73 A; 33 C; 37 G; 87 T; 29 other;

Query Match 3.4%; Score 21; DB 22; Length 259;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAA 625

DB 63 TGNAAAAAAAAAAAAA 43

#### RESULT 42

AAI09957/c

ID AAI09957 standard; cDNA; 288 BP.

AC AAI09957;

DT 07-DEC-2001 (first entry)

XX DE Human breast cancer expressed polynucleotide 2414.  
XX KM Human; breast cancer; cell marker; cytostatic; ss.  
XX OS Homo sapiens.  
XX PN WO200151628-A2.  
XX PD 19-JUL-2001.  
XX PF 10-JAN-2001; 2001WO-US00798.  
XX PR 14-JAN-2000; 2000US-0176077.  
PR 14-MAR-2000; 2000US-0189167.  
PR 24-MAR-2000; 2000US-0192099.  
PR 29-MAR-2000; 2000US-0193480.  
PR 15-MAY-2000; 2000US-0205230.  
PR 09-JUN-2000; 2000US-0211315.  
PR 25-JUL-2000; 2000US-0220534.  
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Lille J, Xu Y, Wang Y, Steinmann K;  
XX WPI; 2001-451856/48.  
XX PT New peptide useful as a marker for the diagnosis of breast cancer -  
XX PS Claim 1; Page 462; 3695pp; English.  
XX CC The invention relates to human breast cancer expressed polynucleotides  
CC (AA107544-AA126789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.  
XX SQ Sequence 288 BP; 76 A; 53 C; 75 G; 79 T; 5 other;  
Query Match 3.4%; Score 21; DB 22; Length 288;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 605 TGNAAAAAAAAAAAAAAAAAAAA 625  
DB 70 TGNAAAAAAAAAAAAAAAAAAAA 50  
RESULT 43  
ABV05091/C  
ID ABV05091 standard; cDNA; 288 BP.  
XX AC ABV05091;  
XX DT 13-SEP-2002 (first entry)  
XX DE Human prostate expression marker cDNA 5082.  
XX KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200160860-A2.  
XX PD 23-AUG-2001.  
XX PF 20-FEB-2001; 2001WO-US05171.  
XX PR 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAR-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX DR Novel isolated nucleic acid molecule associated with cancerous state of  
XX PT prostate cells and correlating with presence of prostate cancer, useful  
XX PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX PS Claim 1; Page 864; 11750pp; English.  
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX SQ Sequence 288 BP; 76 A; 37 C; 29 G; 112 T; 34 other;  
Query Match 3.4%; Score 21; DB 23; Length 288;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 605 TGNAAAAAAAAAAAAAAAAAAAA 625  
DB 55 TGNAAAAAAAAAAAAAAAAAAAA 35  
RESULT 44  
ABV05770/C  
ID ABV05770 standard; cDNA; 294 BP.  
XX AC ABV05770;  
XX DT 13-SEP-2002 (first entry)  
XX DE Human prostate expression marker cDNA 5761.  
XX KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200160860-A2.  
XX PD 23-AUG-2001.  
XX PF 20-FEB-2001; 2001WO-US05171.  
XX PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAR-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.

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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI: 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1: Page 962; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
(a) assessing whether a patient is afflicted with prostate cancer;  
(b) monitoring the progression of prostate cancer in a patient;  
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
(e) selecting a composition for inhibiting prostate cancer in a patient;  
(f) assessing the prostate cell carcinogenic potential of a compound;  
(g) determining whether prostate cancer has metastasized in a patient;  
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
(i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 294 BP; 79 A; 52 C; 34 G; 119 T; 10 other;

Query Match 3.4%; Score 21; DB 23; Length 294;

Best Local Similarity 100.0%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAAAAAAAAA 625  
| | | | | | | | | | | | | | | | | |  
DB 31 TGNAAAAAAAAAAAAAAAAAAAA 11

RESULT 45

AAH68974/C  
ID AAH68974 standard; CDNA; 359 BP.

XX  
AC AAH68974;

DT 19-SEP-2001 (first entry)

DE Human cervical cancer marker nucleic acid 248.

KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

OS Homo sapiens.

WO200142467-A2.

PD 14-JUN-2001.

PF 08-DEC-2000; 2000WO-US33312.

PR 08-DEC-1999; 99US-0169681.

PR 21-DEC-1999; 99US-0171350.

PR 14-MAR-2000; 2000US-0189315.

PR 12-MAY-2000; 2000US-0203791.

PR 09-JUN-2000; 2000US-0210600.

PR 21-JUL-2000; 2000US-0220114.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Deeds J, Berger A, Zhao X;

WPI: 2001-375006/39.

PT New isolated nucleic acid for diagnosing and treating cervical cancer  
PT and for assessing and detecting compounds for treating the cancer -  
XX  
XX  
PS Claim 1: Page 147; 1051pp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with  
CC cervical cancer with cytostatic activity. The nucleic acids and encoded  
CC polypeptides are useful: to assess if a patient is afflicted with  
CC cervical cancer or has a pre-malignant condition; to monitor the  
CC progression of cervical cancer or a premalignant condition in a patient;  
CC and to select and/or assess the efficacy of a compound or therapy for  
CC inhibiting cervical cancer in a patient. The nucleic acids may also be  
CC useful for gene therapy.

SO Sequence 359 BP; 96 A; 62 C; 48 G; 131 T; 22 other;

Query Match 3.4%; Score 21; DB 22; Length 359;

Best Local Similarity 100.0%; Pred. No. 52; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAAAAAAAAA 625  
| | | | | | | | | | | | | | | | | |  
DB 82 TGNAAAAAAAAAAAAAAAAAAAA 62

Search completed: November 7, 2002, 18:15:34  
Job time : 142.06 secs

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:00:33 ; Search time 23.4202 Seconds  
(without alignments)  
8184.096 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agtctctctgcagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: OLIGO\_NDC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 10

Total number of hits satisfying chosen parameters: 97832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: Issued\_Patents\_NA.\*
- 2: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	3.4	377	3	US-08-946-026-41
2	21	3.4	407	4	US-09-385-982-519
3	21	3.4	631	4	US-09-149-476-67
4	21	3.4	804	4	US-09-149-476-125
5	21	3.4	2176	4	US-08-974-549A-3
6	21	3.4	2369	4	US-09-149-476-309
7	21	3.2	265	1	US-08-686-878A-46
8	20	3.2	265	4	US-09-175-928-45
9	20	3.2	296	2	US-09-032-684-13
10	20	3.2	500	2	US-08-967-101-82
11	20	3.2	500	2	US-08-592-541-82
12	20	3.2	500	3	US-09-124-698-82
13	20	3.2	500	4	US-09-127-480-82
14	20	3.2	500	4	US-08-496-841C-82
15	20	3.2	789	4	US-09-124-523-82
16	20	3.2	789	4	US-09-020-956-32
17	20	3.2	789	4	US-09-030-607-32
18	20	3.2	789	4	US-09-605-785-32
19	20	3.2	789	4	US-09-439-313-32
20	20	3.2	789	4	US-09-352-616A-32
21	20	3.2	789	4	US-08-232-149A-32
22	20	3.2	1062	4	US-09-149-476-108
23	20	3.2	1210	4	US-09-443-041A-29
24	19	3.0	30	4	US-09-648-040-4
25	19	3.0	40	2	US-08-859-106A-4
26	19	3.0	40	4	US-09-011-540-11
27	19	3.0	51	4	US-09-051-079-5

c 28	19	3.0	52	3	US-08-618-100B-9	Sequence 9, Appl
c 29	19	3.0	69	1	US-08-702-344-7	Sequence 7, Appl
c 30	19	3.0	69	1	US-08-702-344-72	Sequence 22, Appl
c 31	19	3.0	69	4	US-09-209-911A-7	Sequence 7, Appl
c 32	19	3.0	84	1	US-08-664-596B-3	Sequence 3, Appl
c 33	19	3.0	84	1	US-08-738-367-3	Sequence 266, App
c 34	19	3.0	193	4	US-08-991-789A-266	Sequence 37, Appl
c 35	19	3.0	193	4	US-09-062-451-266	Sequence 98, Appl
c 36	19	3.0	208	1	US-08-686-878A-37	Sequence 98, Appl
c 37	19	3.0	208	2	US-08-967-101-98	Sequence 98, Appl
c 38	19	3.0	208	3	US-09-124-698-98	Sequence 98, Appl
c 39	19	3.0	208	4	US-09-127-480-98	Sequence 37, Appl
c 40	19	3.0	208	4	US-08-496-841C-98	Sequence 98, Appl
c 41	19	3.0	208	4	US-09-175-928-98	Sequence 98, Appl
c 42	19	3.0	208	4	US-08-124-523-98	Sequence 98, Appl
c 43	19	3.0	244	1	US-08-686-878A-43	Sequence 43, Appl
c 44	19	3.0	310	4	US-09-328-111-715	Sequence 715, App
c 45	19	3.0				

## ALIGNMENTS

RESULT 1  
US-08-946-026-41  
; Sequence 41, Application US/08946026  
; Patent No. 6034218

GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Dillon, Davin C.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Mitcham, Jennifer L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/946,026  
FILING DATE: 07-OCT-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Markl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.424C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ. ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-946-026-41

Query Match 3.4%; Score 21; DB 3; Length 377;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

605 TGNAAAAAAAAAAAAAAAAA 625  
349 TGNAAAAAAAAAAAAAAAAA 369

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RESULT 2
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; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
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; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
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; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(407)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-519

Query Match          3.4%: Score 21; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAA 625
Db 33 TGNAAAAAAAAAAAAA 13

RESULT 3
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; Sequence 67, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 166 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
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; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/057, 650  
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EARLIER APPLICATION NUMBER: 60/057, 669  
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EARLIER APPLICATION NUMBER: 60/049, 610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061, 060  
EARLIER FILING DATE: 1997-10-02

Query Match 3.4% Score 21; DB 4; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAA 625  
Db 573 TGNAAAAAAAAAAAAA 593

RESULT 4  
US-09-149-476-125  
Sequence 125, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040, 162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038, 621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 626  
EARLIER FILING DATE: 1997-03-07  
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EARLIER APPLICATION NUMBER: 60/040, 336  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 615  
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EARLIER APPLICATION NUMBER: 60/047, 597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 502  
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EARLIER APPLICATION NUMBER: 60/047, 633  
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EARLIER APPLICATION NUMBER: 60/047, 583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 617  
EARLIER FILING DATE: 1997-05-23

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42	EARLIER	APPLICATION NUMBER:	60/047,593	
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44	EARLIER	APPLICATION NUMBER:	60/047,614	
45	EARLIER	FILING DATE:	1997-05-23	578
46	EARLIER	APPLICATION NUMBER:	60/043,578	
47	EARLIER	FILING DATE:	1997-04-11	576
48	EARLIER	APPLICATION NUMBER:	60/043,576	
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67	EARLIER	FILING DATE:	1997-08-22	



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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      3.4%; Score 21; DB 4; Length 804;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAA 625
Db 767 TGNAAAAAAAAAAAAAA 787

RESULT 5
US-08-974-549A-3
; Sequence 3, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
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; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2176
; OTHER INFORMATION: /note="clone 712562"
; NAME/KEY: CDS
; LOCATION: 23..802
; US-08-974-549A-3

Query Match      3.4%; Score 21; DB 4; Length 2176;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAA 625
Db 2148 TGNAAAAAAAAAAAAAA 2168

RESULT 6
US-09-149-476-309/C
; Sequence 309, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 3.4%; Score 21; DB 4; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 605 TGNAAAAAAAAAAAAA 625  
DB 28 TGNAAAAAAAAAAAAA 8

RESULT 7  
US-08-686-878A-46  
Sequence 46, Application US/08686878A  
Patent No. 5708157  
GENERAL INFORMATION:  
APPLICANT: McCoy, John  
APPLICANT: Lavalley, Edward  
APPLICANT: Racie, Lisa  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Evans, Cheryl  
APPLICANT: Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/686,878A  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-686-878A-46

Query Match 3.2%; Score 20; DB 1; Length 265;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
DB 245 GNAAAAAAAAAAAAAA 264

RESULT 8  
US-09-175-928-45  
Sequence 45, Application US/09175928A  
Patent No. 6312921  
GENERAL INFORMATION:  
APPLICANT: McCoy, John M.  
APPLICANT: Lavalley, Edward R.  
APPLICANT: Collins-Racie, Lisa A.  
APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: M, Sha  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
FILE REFERENCE: 6006B,A1172A  
CURRENT APPLICATION NUMBER: US/09/175,928A  
CURRENT FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 45  
LENGTH: 265  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (2)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (67)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (75)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (79)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (101)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (104)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (111)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (121)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (133)  
FEATURE:

NAME/KEY: unsure  
LOCATION: (136)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (157)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (162)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (164)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (172)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (175)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (183)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (187)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (192)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (199)..(200)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (208)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (211)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (223)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (225)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (227)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (243)..(244)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (246)  
US-09-175-928-45

Query Match 3.2%; Score 20; DB 4; Length 265;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
DB 245 GNAAAAAAAAAAAAAA 264

RESULT 9  
US-09-032-684-13/c  
Sequence 13, Application US/09032684  
Patent No. 5882874  
GENERAL INFORMATION:  
APPLICANT: FISHER, PAUL B.  
TITLE OF INVENTION: RECIPROCAL SUBTRACTION DIFFERENTIAL  
TITLE OF INVENTION: DISPLAY  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,684  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 55551/JPW/AMG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-032-684-13

Query Match 3.2%; Score 20; DB 2; Length 296;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
DB 60 GNAAAAAAAAAAAAAA 41

RESULT 10  
US-08-967-101-82/c  
Sequence 82, Application US/08967101  
Patent No. 5840540  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,101  
FILING DATE: 10-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100

;; INFORMATION FOR SEQ ID NO: 82:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 500 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-967-101-82

Query Match 3.2%; Score 20; DB 2; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
|||  
DB 34 GNAAAAAAAAAAAAAA 15

## RESULT 11

US-08-592-541-82/c  
; Sequence 82, Application US/08592541  
; Patent No. 5986054

;; GENERAL INFORMATION:  
;; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
;; APPLICANT: ROMMENS, JOHANNA M  
;; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
;; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
;; NUMBER OF SEQUENCES: 183  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
;; STREET: High Street Tower - 125 High Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/592,541  
;; FILING DATE:  
;; CLASSIFICATION: 800

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Pitcher, Edmund R.  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 248-7000  
;; TELEFAX: (617) 248-7100  
;; INFORMATION FOR SEQ ID NO: 82:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 500 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-592-541-82

Query Match 3.2%; Score 20; DB 2; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
|||  
DB 34 GNAAAAAAAAAAAAAA 15

RESULT 12  
US-09-124-698-82/c  
; Sequence 82, Application US/09124698  
; Patent No. 6117978  
; GENERAL INFORMATION:

;; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
;; APPLICANT: ROMMENS, JOHANNA M  
;; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
;; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
;; NUMBER OF SEQUENCES: 183  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
;; STREET: High Street Tower - 125 High Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/124,698  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/592,541  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Pitcher, Edmund R.  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 248-7000  
;; TELEFAX: (617) 248-7100  
;; INFORMATION FOR SEQ ID NO: 82:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 500 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-09-124-698-82

Query Match 3.2%; Score 20; DB 3; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
|||  
DB 34 GNAAAAAAAAAAAAAA 15

RESULT 13  
US-09-127-480-82/c  
; Sequence 82, Application US/09127480  
; Patent No. 6194153

;; GENERAL INFORMATION:  
;; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
;; APPLICANT: ROMMENS, JOHANNA M  
;; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
;; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
;; NUMBER OF SEQUENCES: 183  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
;; STREET: High Street Tower - 125 High Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/127,480

FILED DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-127-480-82

Query Match 3.2%; Score 20; DB 4; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
Db 34 GNAAAAAAAAAAAAAA 15

## RESULT 14

US-08-496-841C-82/C  
Sequence 82, Application US/08496841C  
Patent No. 6210919

## GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H  
ROMMENS, JOHANNA M  
FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 175

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/496,841C  
FILING DATE: 28-Jun-1995

## CLASSIFICATION: &lt;Unknown&gt;

## ATTORNEY/AGENT INFORMATION:

NAME: Paul F. Fehner, Ph.D.  
REGISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 527-7700  
TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:

US-08-496-841C-82

Query Match 3.2%; Score 20; DB 4; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
Db 34 GNAAAAAAAAAAAAAA 15

## RESULT 15

US-09-124-523-82/C  
Sequence 82, Application US/09124523  
Patent No. 6395960

## GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H  
ROMMENS, JOHANNA M  
FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/124,523  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/592,541  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-09-124-523-82

Query Match 3.2%; Score 20; DB 4; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
Db 34 GNAAAAAAAAAAAAAA 15

## RESULT 16

US-09-020-956-32/C  
Sequence 32, Application US/09020956  
Patent No. 6261562

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
Dillon, David C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS  
NUMBER OF SEQUENCES: 178

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle

STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020, 956  
FILING DATE: 09-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-020-956-32

Query Match 3.2%; Score 20; DB 4; Length 789;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
|||||  
Db 66 GNAAAAAAAAAAAAAA 47

RESULT 17  
US-09-030-607-32/C  
Sequence 32, Application US/09030607  
Patent No. 6262245  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
NUMBER OF SEQUENCES: 224  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030, 607  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.427C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-030-607-32

Query Match 3.2%; Score 20; DB 4; Length 789;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
|||||  
Db 66 GNAAAAAAAAAAAAAA 47

RESULT 18  
US-09-605-785-32/C  
Sequence 32, Application US/09605785  
Patent No. 6321716  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aljun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C16  
CURRENT APPLICATION NUMBER: US/09/605, 785  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-605-785-32

Query Match 3.2%; Score 20; DB 4; Length 789;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAA 625  
|||||  
Db 66 GNAAAAAAAAAAAAAA 47

RESULT 19  
US-09-439-313-32/C  
Sequence 32, Application US/09439313  
Patent No. 6329505  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan Louise  
APPLICANT: Jiang Yugu  
APPLICANT: Reed, Steven G.

```
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: fastseq for windows version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-32
```

```
Query Match          3.2%: Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 606 GNAAAAAAAAAAAAAAAAAA 625
Db 66 GNAAAAAAAAAAAAAAAAAA 47
```

```
RESULT 20
US-09-352-616A-32/C
; Sequence 32, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jlangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: fastseq for windows version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-32
```

```
Query Match          3.2%: Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 606 GNAAAAAAAAAAAAAAAAAA 625
Db 66 GNAAAAAAAAAAAAAAAAAA 47
```

```
RESULT 21
US-09-232-149A-32/C
; Sequence 32, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
```

```
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: fastseq for windows version 3.0
SEQ ID NO 32
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-32
```

```
Query Match          3.2%: Score 20; DB 4; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 606 GNAAAAAAAAAAAAAAAAAA 625
Db 66 GNAAAAAAAAAAAAAAAAAA 47
```

```
RESULT 22
US-09-149-476-108
; Sequence 108, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
```



[illegible]

```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 1062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
Db 1030 GNAAAAAAAAAAAAAA 1049

RESULT 23
US-09-443-041A-29
; Sequence 29, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Triflicum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1129
; OTHER INFORMATION: any nucleotide
US-09-443-041A-29

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 1210;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625
Db 1129 GNAAAAAAAAAAAAAA 1148

RESULT 24
US-09-648-040-4
; Sequence 4, Application US/09648040
; Patent No. 6436665
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; FILE REFERENCE: 50036/032002
; CURRENT APPLICATION NUMBER: US/09/648,040
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,261
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
```

```
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Encoding molecule
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-09-648-040-4

Query Match
Best Local Similarity 100.0%; Score 19; DB 4; Length 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 10 NAAAAAAAAAAAAAAAAA 28

RESULT 25
US-08-859-106A-4/C
; Sequence 4, Application US/08859106A
; Patent No. 5965422
; GENERAL INFORMATION:
; APPLICANT: LOFFLER, Fridolin
; APPLICANT: NGUYEN, Quoc Khanh
; APPLICANT: SCHUSTER, Erwin
; APPLICANT: SPROHLER, Bruno
; APPLICANT: THOMAS, Lutz
; APPLICANT: WOLF, Sabine
; TITLE OF INVENTION: LYSOPHOSPHOLIPASE PRODUCED FROM
; TITLE OF INVENTION: ASPERGILLUS BY RECOMBINANT METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,106A
; FILING DATE: 20-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19620649.9
; FILING DATE: 22-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 015200-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 40
; OTHER INFORMATION: /product= "N is A, C or G"
US-08-859-106A-4
```

Query Match 3.0%; Score 19; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 607 NAAAAAAAAAAAAAAAAA 625  
DB 40 NAAAAAAAAAAAAAAAAA 22

RESULT 26  
US-09-011-540-11/c  
Sequence 11, Application US/09011540  
Patent No. 6228632  
GENERAL INFORMATION:  
APPLICANT: SCHUSTER, Erwin  
APPLICANT: SPROESSLER, Bruno  
APPLICANT: TITZE, Kornelia  
APPLICANT: GOTTSCHALK, Michael  
APPLICANT: KHANH, Nguyen Quoc  
APPLICANT: WOLF, Sabine  
APPLICANT: PLAINER, Hermann  
TITLE OF INVENTION: LEUCINE AMINOPEPTIDASES PRODUCED RECOMBINANTLY FROM  
FILE REFERENCE: 015200-051  
CURRENT FILING DATE: 1998-04-20  
EARLIER FILING DATE: 1998-04-20  
EARLIER APPLICATION NUMBER: DE 19526485.1  
EARLIER FILING DATE: 1995-07-20  
EARLIER APPLICATION NUMBER: PCT/EP96/04330  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 11  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Aspergillus sojae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (39)..(40)  
OTHER INFORMATION: N is A, C or G.  
US-09-011-540-11

Query Match 3.0%; Score 19; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 607 NAAAAAAAAAAAAAAAAA 625  
DB 40 NAAAAAAAAAAAAAAAAA 22

RESULT 27  
US-09-051-079-5/c  
Sequence 5, Application US/09051079A  
Patent No. 6214549  
GENERAL INFORMATION:  
APPLICANT: WEINDEL, Kurt  
APPLICANT: SEIDEL, Christoph  
APPLICANT: LASSONCZYK, Gerhard  
TITLE OF INVENTION: METHOD OF DETECTING A SUBSTANCE TO BE ANALYZED  
FILE REFERENCE: 101614-07096  
CURRENT FILING DATE: US/09/051,079A  
EARLIER FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: PCT/EP96/04358  
EARLIER FILING DATE: 1996-10-08  
EARLIER APPLICATION NUMBER: DE/195 37 952.7  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 5  
LENGTH: 51  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)  
OTHER INFORMATION: n means DNP bound via DNP-TEG.  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (21)  
OTHER INFORMATION: n means DNP bound via DNP-TEG.  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-09-051-079-5

Query Match 3.0%; Score 19; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 607 NAAAAAAAAAAAAAAAAA 625  
DB 21 NAAAAAAAAAAAAAAAAA 3

RESULT 28  
US-08-618-100B-9/c  
Sequence 9, Application US/08618100B  
Patent No. 6088976  
GENERAL INFORMATION:  
APPLICANT: Brilgers, Michael R.  
APPLICANT: Auwerx, Johan  
APPLICANT: de Vos, Piet  
APPLICANT: Steels, Bart  
APPLICANT: Croston, Glenn E.  
TITLE OF INVENTION: MODULATORS OF OB GENE AND  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,100B  
FILING DATE: March 19, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/558,588  
FILING DATE: October 30, 1995  
APPLICATION NUMBER: 08/510,584  
FILING DATE: August 2, 1995  
APPLICATION NUMBER: 08/418,096  
FILING DATE: April 5, 1995  
APPLICATION NUMBER: 08/408,584  
FILING DATE: March 20, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: "N" represents any base.

US-08-618-100B-9

Query Match 3.0%; Score 19; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625  
|||||  
DB 51 NAAAAAAAAAAAAAAAAA 33

RESULT 29

US-08-702-344-7  
Sequence 7, Application US/08702344  
Patent No. 5723315

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Lavallee, Edward

APPLICANT: Racie, Lisa

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

TITLE OF INVENTION: ENCODING THEM

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/702,344

APPLICATION NUMBER: US/08/702,344

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 69 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-702-344-7

Query Match 3.0%; Score 19; DB 1; Length 69;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625  
|||||  
DB 5 NAAAAAAAAAAAAAAAAA 23

RESULT 30

US-08-702-344-22

Sequence 22, Application US/08702344

Patent No. 5723315

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Lavallee, Edward

APPLICANT: Racie, Lisa

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

TITLE OF INVENTION: ENCODING THEM

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/702,344

APPLICATION NUMBER: US/08/702,344

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 69 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-702-344-22

Query Match 3.0%; Score 19; DB 1; Length 69;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625  
|||||  
DB 22 NAAAAAAAAAAAAAAAAA 40

RESULT 31

US-09-269-911A-7/c

Sequence 7, Application US/09269911A

Patent No. 6228589

GENERAL INFORMATION:

APPLICANT: Brenner, Sydney

TITLE OF INVENTION: MEASUREMENT OF GENE EXPRESSION PROFILES

TITLE OF INVENTION: IN TOXICITY-DETERMINATION

FILE REFERENCE: 5525-0025.10

CURRENT APPLICATION NUMBER: US/09/269,911A

CURRENT FILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 69

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: conjugate  
NAME/KEY: misc\_feature  
LOCATION: (65)...(65)  
OTHER INFORMATION: n = cDNA from library  
NAME/KEY: misc\_feature  
LOCATION: (66)...(69)  
OTHER INFORMATION: n = A,T,C or G  
US-09-269-911A-7

Query Match 3.0%; Score 19; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625  
|||||  
DB 65 NAAAAAAAAAAAAAAAAA 47

## RESULT 32

US-08-664-596B-3  
Sequence 3, Application US/08664596B  
Patent No. 5807703

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Lavelle, Edward

APPLICANT: Racie, Lisa

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Evans, Cheryl

APPLICANT: Spaulding, Vikki

APPLICANT: Bowman, Michael

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF INVENTION: ENCODING THEM

CORRESPONDENCE ADDRESSES: 37

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/664,596B

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-664-596B-3

QY 607 NAAAAAAAAAAAAAAAAA 625  
|||||  
DB 8 NAAAAAAAAAAAAAAAAA 26

Query Match 3.0%; Score 19; DB 1; Length 84;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 33

US-08-738-367-3  
Sequence 3, Application US/08738367  
Patent No. 5827688

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Lavelle, Edward

APPLICANT: Racie, Lisa

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF INVENTION: ENCODING THEM

CORRESPONDENCE ADDRESSES: 8

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,367

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-738-367-3

QY 607 NAAAAAAAAAAAAAAAAA 625  
|||||  
DB 8 NAAAAAAAAAAAAAAAAA 26

Query Match 3.0%; Score 19; DB 1; Length 84;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-991-789A-266/C

Sequence 266, Application US/08991789A

Patent No. 6225054

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.

SMITH, John M.

REED, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 292

CORRESPONDENCE ADDRESS:

ADDRESS: Seed IP Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington



Patent No. 5840540  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
ATTORNEY/AGENT INFORMATION:  
NAME: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,101  
FILING DATE: 10-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-967-101-98  
Query Match 3.0%; Score 19; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 607 NAAAAAAAAAAAAAAAAA 625  
DB 159 NAAAAAAAAAAAAAAAAA 141  
RESULT 38  
US-08-592-541-98/C  
Sequence 98, Application US/08592541  
Patent No. 5986034  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
ATTORNEY/AGENT INFORMATION:  
NAME: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-592-541-98  
Query Match 3.0%; Score 19; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 607 NAAAAAAAAAAAAAAAAA 625  
DB 159 NAAAAAAAAAAAAAAAAA 141  
RESULT 39  
US-09-124-698-98/C  
Sequence 98, Application US/09124698  
Patent No. 6117978  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
ATTORNEY/AGENT INFORMATION:  
NAME: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,698  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-124-698-98  
Query Match 3.0%; Score 19; DB 3; Length 208;  
Best Local Similarity 100.0%; Pred. No. 14;

	Matches	19; Conservative	0; Mismatches	0; Indels	0; Gaps
Oy	607	NNNNNNNNNNNNNNNNNNNN	625		
Db	159	NNNNNNNNNNNNNNNNNNNN	141		

```

RESULT 40
US-09-127-480-98/c
; Sequence 98, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLÖP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-98

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Query Match          3.0%; Score 19: DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625
      |||||||
Db 159 NAAAAAAAAAAAAAAAAAAAA 141

RESULT 41
US-08-496-841C-98/C
; Sequence 98, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
;

```

```

1 STREET: 805 Third Avenue
2 CITY: New York
3 STATE: New York
4 COUNTRY: U.S.A.
5 ZIP: 10022
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/496,841C
15 FILING DATE: 28-Jun-1995
16 CLASSIFICATION: <Unknown>
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Paul F. Fehner, Ph.D.
20 REGISTRATION NUMBER: 35,135
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (212) 527-7700
23 TELEFAX: (212) 753-6237
24
25 INFORMATION FOR SEQ. ID NO: 98:
26
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 208 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32
33 MOLECULE TYPE: DNA (genomic)
34 SEQUENCE DESCRIPTION: SEQ ID NO: 98:
35
36 US-08-496-841C-98

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		Query Match	3.0%;	Score 19;	DB 4;	Length 208;	
		Best Local Similarity	100.0%;	Pred. No. 14;			
		Matches 19;	Conservative	0;	Mismatches	0;	Gaps 0;
QY	607	AAAAAAAAAAAAAAAAAAAAA	625				
Db	159	AAAAAAAAAAAAAAAAAAAAA	141				

```

RESULT 42
US-09-175-928-37
: Sequence 37, Application US/09175928A
: Patent No. 6312921
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John M.
: APPLICANT: Lavallee, Edward R.
: APPLICANT: Collins-Racie, Lisa A.
: APPLICANT: Evans, Cheryl
: APPLICANT: Werberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Mi, Sha
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
: FILE REFERENCE: 60065.A1172A
: CURRENT APPLICATION NUMBER: US/09/175,928A
: NUMBER OF SEQ ID NOS: 62
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 37
: LENGTH: 208
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (8)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (29)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (31)
: FEATURE:

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NAME/KEY: unsure  
LOCATION: (42)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (55)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (65)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (75)  
FEATURE:  
NAME/KEY: unsure  
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NAME/KEY: unsure  
LOCATION: (91)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (98)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (100)...(101)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (113)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (119)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (121)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (128)  
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NAME/KEY: unsure  
LOCATION: (130)...(131)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (133)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (137)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (161)  
US-09-175-928-37

Query Match  
Best Local Similarity 100.0%; Score 19; DB 4; Length 208;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625  
DB 161 NAAAAAAAAAAAAAAAAAAAA 179

RESULT 43  
US-09-124-523-98/C  
Sequence 98; Application US/09124523  
Patent No. 6395960  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBRAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston

STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ. ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-124-523-98

Query Match  
Best Local Similarity 100.0%; Score 19; DB 4; Length 208;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625  
DB 159 NAAAAAAAAAAAAAAAAAAAA 141

RESULT 44  
US-08-686-878A-43  
Sequence 43; Application US/08686878A  
Patent No. 5708157  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John  
APPLICANT: Lavallee, Edward  
APPLICANT: Racine, Lisa  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Evans, Cheryl  
APPLICANT: Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/686,878A  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 244 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-686-878A-43

Query Match 3.0%; Score 19; DB 1; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAAAAAA 624  
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 DB 226 GNAAAAAAAAAAAAAAAAAA 244

## RESULT 45

US-09-328-111-715  
 : Sequence 715, Application US/09328111  
 : Patent No. 6262333  
 : GENERAL INFORMATION:  
 : APPLICANT: Endege, Wilson O.  
 : APPLICANT: Steinmann, Kathleen E.  
 : APPLICANT: Astle, Jon H.  
 : APPLICANT: Burgess, Christopher C.  
 : APPLICANT: Bushnell, Steven E.  
 : APPLICANT: Carroll III, Eddie  
 : APPLICANT: Carino, Theodore J.  
 : APPLICANT: Derli, Adnan  
 : APPLICANT: Ford, Donna M.  
 : APPLICANT: Lewis, Marcia E.  
 : APPLICANT: Monahan, John E.  
 : APPLICANT: Schlegel, Robert  
 : TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
 : TITLE OF INVENTION: PRODUCTS  
 : FILE REFERENCE: CCD-257 (US)  
 : CURRENT APPLICATION NUMBER: US/09/328,111  
 : CURRENT FILING DATE: 1999-06-08  
 : EARLIER APPLICATION NUMBER: US 60/088,801  
 : EARLIER FILING DATE: 1998-06-10  
 : NUMBER OF SEQ ID NOS: 850  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 715  
 : LENGTH: 310  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: misc-feature  
 : LOCATION: (1)..(310)  
 : OTHER INFORMATION: n = A,T,C or G  
 US-09-328-111-715

Query Match 3.0%; Score 19; DB 4; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAA 625  
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 DB 280 NAAAAAAAAAAAAAAAAA 298

Search completed: November 7, 2002, 23:12:21  
 Job time : 31.4202 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 23:08:43 : Search time 27.1619 Seconds  
(without alignments)  
8163.686 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agttctctctgcagagact.....gnaaaaaaaaaaaaaaaaa 625

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapept 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 10

Total number of hits satisfying chosen parameters: 149939

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published\_Applications\_NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCR\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	625	US-09-825-294-210	Sequence 210, App
2	625	100.0	625	US-09-867-701-10876	Sequence 10876, A
3	606	97.0	1897	US-09-825-294-214	Sequence 214, App
4	486	77.8	1619	US-09-825-294-205	Sequence 205, App
5	486	77.8	1619	US-09-825-294-211	Sequence 211, App
6	359	57.4	1362	US-09-825-294-208	Sequence 208, App
7	314	50.2	373	US-09-867-701-1516	Sequence 1516, App
8	307	49.1	349	US-09-867-701-2409	Sequence 2409, App
9	263	42.1	409	US-09-867-701-4240	Sequence 4240, App
10	166	26.6	201	US-09-867-701-8894	Sequence 8894, App
11	154	24.6	390	US-09-867-701-1532	Sequence 1532, App
12	120	19.2	58	US-09-867-701-2375	Sequence 2375, App
13	92	14.7	381	US-09-867-701-7826	Sequence 7826, App
14	22	3.5	9	US-09-938-842A-1283	Sequence 1283, App
15	21	3.4	322	US-09-783-590-6936	Sequence 6936, App
16	21	3.4	508	US-09-925-299-698	Sequence 698, App
17	21	3.4	547	US-09-834-975-379	Sequence 379, App
18	21	3.4	600	US-09-783-590-7037	Sequence 7037, App
19	21	3.4	1350	US-09-925-301-539	Sequence 539, App

20	21	3.4	1402	10	US-09-925-297-171	Sequence 171, App
21	20	3.2	58	10	US-09-783-590-2406	Sequence 2406, App
22	20	3.2	60	10	US-09-919-580-419	Sequence 419, App
23	20	3.2	66	10	US-09-925-301-759	Sequence 759, App
24	20	3.2	97	10	US-09-815-343-241	Sequence 241, App
25	20	3.2	217	10	US-09-895-828-248	Sequence 248, App
26	20	3.2	226	9	US-10-046-935-291	Sequence 291, App
27	20	3.2	265	12	US-10-040-916-46	Sequence 46, App
28	20	3.2	291	10	US-09-834-975-374	Sequence 374, App
29	20	3.2	451	10	US-09-777-564-625	Sequence 625, App
30	20	3.2	456	10	US-09-783-590-10830	Sequence 10830, App
31	20	3.2	648	10	US-09-925-301-819	Sequence 819, App
32	20	3.2	789	10	US-09-759-143-32	Sequence 32, App
33	20	3.2	789	10	US-09-780-669-32	Sequence 32, App
34	20	3.2	789	10	US-09-030-606-32	Sequence 32, App
35	20	3.2	789	10	US-09-822-827-32	Sequence 32, App
36	20	3.2	789	10	US-09-115-453-32	Sequence 32, App
37	20	3.2	368004	10	US-09-949-654-3	Sequence 3, App
38	19	3.0	51	10	US-09-783-590-8086	Sequence 8086, App
39	19	3.0	52	10	US-09-783-590-5881	Sequence 5881, App
40	19	3.0	53	10	US-09-919-580-705	Sequence 705, App
41	19	3.0	53	10	US-09-783-590-3220	Sequence 3220, App
42	19	3.0	56	10	US-09-919-580-171	Sequence 171, App
43	19	3.0	56	10	US-09-919-580-677	Sequence 677, App
44	19	3.0	56	10	US-09-919-580-713	Sequence 713, App
45	19	3.0	60	10	US-09-925-301-758	Sequence 758, App

#### ALIGNMENTS

RESULT 1  
US-09-825-294-210  
Sequence 210, Application US/09825294  
Patent No. US200200491A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C5  
CURRENT APPLICATION NUMBER: US/09/825,294  
NUMBER OF SEQ ID NOS: 215  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 210  
LENGTH: 625  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(625)  
OTHER INFORMATION: n = A,T,C or G  
US-09-825-294-210

Query Match 100.0%; Score 625; DB 10; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1.4e-242;  
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTGAGAGAGAGTGGCGGAGCGGAGCAAGCAAGGGGCTGCACAAACG 60  
DB 1 AGTTCTCCTTGAGAGAGAGTGGCGGAGCGGAGCAAGCAAGGGGCTGCACAAACG 60  
QY 61 GGGCGTGTGCGTGTGAGTGGCGATGTACGCGAGCGGCTTCTCGTGTGGTGGTCTG 120  
DB 61 GGGCGTGTGCGTGTGAGTGGCGATGTACGCGAGCGGCTTCTCGTGTGGTGGTCTG 120  
QY 121 CACGACAGGCGGAGAGAGAGTGGCGATGTACGCGAGCGGCTTCTCGTGTGGTGGTCTG 180  
DB 121 CACGACAGGCGGAGAGAGAGTGGCGATGTACGCGAGCGGCTTCTCGTGTGGTGGTCTG 180

QY	181	CGGTACACAGGACGGGTTTGATGACCCAGCTGAGGTTAGAAAAACGTTCCGACGAAGGGAG	240
Db	181	CGTGTACAGAGCGGGGTTTGATGACCCAGCTGAGGTTAGAAAAACGTTCCGACGAAGGGAG	240
QY	241	GAGGATCATGTACGCCCGCGGAAGTAGACCTCGTCCAGTCGTGTTGGGTTGGCCGACG	300
Db	241	GAGGATCATGTACGCCCGCGGAAGTAGACCTCGTCCAGTCGTGTTGGGTTGGCCGACG	300
QY	301	CATATTCCTCCGATCTGTGGTGGGCATTCACGCAATGTCACAAACATTCAGCCC	360
Db	301	CATATTCCTCCGATCTGTGGTGGGCATTCACGCAATGTCACAAACATTCAGCCC	360
QY	361	TGGCGACAGACAGACAGAGGAGGAGACAGAAAAAAGAAAAACACAGCATAGAAACACAG	420
Db	361	TGGCGACAGACAGACAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATAGAAACACAG	420
QY	421	TAAATGAATAAACCATTAATATTATGAGCCCTCTCTGTCTGTACTGTCGCTTACTGGCCAGGAAT	480
Db	421	TAAATGAATAAACCATTAATATTATGAGCCCTCTCTGTCTGTACTGTCGCTTACTGGCCAGGAAT	480
QY	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCCAAGCAAGACAGAAATT	540
Db	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCCAAGCAAGACAGAAATT	540
QY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG	600
QY	601	ACACTGNAAAAAAAAAAAAAA 625	
Db	601	ACACTGNAAAAAAAAAAAAAA 625	

## RESULT 2

```

US-09-867-701-10876
: Sequence 10876, Application US/09867701
: Patent No. US20020132237A1
: GENERAL INFORMATION:
: APPLICANT: Agilate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlocker, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF INFLAMMATORY DISEASES AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ. ID NOS: 10912
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 10876
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
: US-09-867-701-10876

```

Query Match	100.0%;	Score 625;	DB 10;	Length 625;
Best Local Similarity	100.0%;	Pred. No. 1.4e-242;		

	Matches	625; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	1	AGTTTCCTCTGCAGAGGACTGGCGCGGGAGCGCAAGAGCAACGGGCGCTGCACAAAGCG	60		
Db	1	AGTTTCCTCTTGCAGAGGACTGGCGCGGGAGCGCAAGAGCAACGGGCGCTGCACAAAGCG	60		
QY	61	GGCGCTGTGCGTGGAGAGTGGCAGTGTACGGGAGCGCCTTCTGTTGGCGTGTG	120		
Db	61	GGCGCTGTGCGTGGAGAGTGGCAGTGTACGGGAGCGCCTTCTGTTGGCGTGTG	120		
QY	121	CAGGACACAGGGGGGACAGACACCTGCACGAAACCCGGCCGAACCTGTTGGAGAGACAC	180		
Db	121	CAGGACACAGGGGGGACAGACACCTGCACGAAACCCGGCCGAACCTGTTGGAGAGACAC	180		

QY	181	CGGTACACAGGAGGGGGTTGATGACACGAGCTGAGGTAGAAAAACGTCGCGAAGGGGAG	240
Db	181	CGTGTACAGGGAGGGGTTGATGAGCCGAGCTGAGGTAGAAAAACGTCGCGAAGGGGAG	240
QY	241	GAGGATCATGTACGCCCGGGAAAGTAGAGACCTGCTCAGCTCGTGTGGGTTTGGCCGAGC	300
Db	241	GAGGATCATGTACGCCCGGGAAAGTAGAGACCTGCTCAGCTCGTGTGGGTTTGGCCGAGC	300
QY	301	CATGATCCTCCGATCTGTGTTGGGCATCCAGCATACGGCCAAATGTCAACAATTCAGCCC	360
Db	301	CATGATCCTCCGATCTGTGTTGGGCATCCAGCATACGGCCAAATGTCAACAATTCAGCCC	360
QY	361	TGGCGACAGACGACGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACAG	420
Db	361	TGGCGACAGACGACGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACAG	420
QY	421	TAAATGAATAAAACCATAAATATTTAGCCCTCTGTTCTGTGTGCTTACGCGAGGAAT	480
Db	421	TAAATGAATAAAACCATAAATATTTAGCCCTCTGTTCTGTGTGCTTACTGCCAGGAAT	480
QY	481	GGTACCAATTTTAAAGTGTGAGCTTACAGCTTCCTTTGCCAACAAGACAGAGAAATT	540
Db	481	GGTACCAATTTTAAAGTGTGAGCTTACAGCTTCCTTTGCCAACAAGACAGAGAAATT	540
QY	541	AACACTGTTTCAAAACCCGGGGAGATTGGCTGTGTTAAAGAAAGACATTTAAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGAGATTGGCTGTGTTAAAGAAAGACATTTAAATGCTTTAG	600
QY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	

### RESULT 3

```

US-09-825-294-214
: Sequence 214, Application US/09825294
: Patent No. US20020004491A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stoltz, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS
: OF TREATING CANCER
:
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS
: OF CANCER
:
: FILE REFERENCE: 210121.48405
:
: CURRENT APPLICATION NUMBER: US/09/825,294
:
: CURRENT FILING DATE: 2001-04-03
:
: NUMBER OF SEQ ID NOS: 215
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO: 214
:
: LENGTH: 1897
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)...(1897)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-09-825-294-214

```

Query Match	97.0%;	Score 606;	DB 10;	Length 1897;
Best Local Similarity	100.0%;	Pred. No. 5.7e-235;		
Matches 606;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	AGTCTCCTTGGACAGAGGACTGGGCCGGGACGGAGGACCAACGGGCGTGTGCACAAACG	60
Db	1271	AGTCTCCTTGGACAGAGGACTGGGCCGGGACGGAGGACCAACGGGCGTGTGCACAAACG	1330
QY	61	GGCGCTTCGGTGGGTGAGAGTGCACATGTACAGCCACAGGCGCTTCTCGTGGTGGCCTGCTG	120
Db	1331	GGCGCTTCGGTGGGTGAGAGTGCACATGTACAGCCACAGGCGCTTCTCGTGGTGGCCTGCTG	1390
QY	121	CAGCGACAGGCGGAGGCACAGCACCTGTGCAGCAACACCGCCGAAACTGCTGTGGAGGACAC	180

```
Db 1391 CAGCGAAGGCGGACGACACACCTGACAGACACCCGCGAAACGTCGTGGAGAGAC 1450
|
|
|
Qy 181 CGGTACAGAGCGGCTTGATGACGAGCTAGAGAAAAAGTCCTCGAGAAAGGAG 240
|
|
|
Db 1451 CGGTACAGAGCGGCTTGATGACGAGCTAGAGAAAAAGTCCTCGAGAAAGGAG 1510
|
|
|
Qy 241 GAGGATCATGTAGACCCCGGAAGTAGACCTGCTCCAGTCGTGGTTGGCCGACG 300
|
|
|
Db 1511 GAGGATCATGTAGACCCCGGAAGTAGACCTGCTCCAGTCGTGGTTGGCCGACG 1570
|
|
|
Qy 301 CAGATCCTCCGAATCTGTTGGGCGATTCAGATTCAGGCAATGTCACAAATCAGCCC 360
|
|
|
Db 1571 CAGATCCTCCGAATCTGTTGGGCGATTCAGATTCAGGCAATGTCACAAATCAGCCC 1630
|
|
|
Qy 361 TGGGACAGACGACGAGAGGAGAGACAGAAAAAGAAAAACAGAGATGAGAACAG 420
|
|
|
Db 1631 TGGGACAGACGACGAGAGGAGAGACAGAAAAAGAAAAACAGAGATGAGAACAG 1690
|
|
|
Qy 421 TAAATGAATAAACCATTAATATTTAGCCCCCTCTGTTCTGTGCTTACTGGCCAGGAAT 480
|
|
|
Db 1691 TAAATGAATAAACCATTAATATTTAGCCCCCTCTGTTCTGTGCTTACTGGCCAGGAAT 1750
|
|
|
Qy 481 GGTACCAATTTTTCAGTGTGACTTGACACTTCTTTTGCACAAAGAGAGAAATTT 540
|
|
|
Db 1751 GGTACCAATTTTTCAGTGTGACTTGACACTTCTTTTGCACAAAGAGAGAAATTT 1810
|
|
|
Qy 541 AACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
|
|
|
Db 1811 AACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1870
|
|
|
Qy 601 ACAAGTG 606
|
|
|
Db 1871 ACAAGTG 1876
|
|
|
```

## RESULT 4

```
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolj, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205
```

Query Match 77.8%; Score 486; DB 10; Length 1619;  
Best Local Similarity 99.8%; Pred. No. 9,7e-187;  
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy 1 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 60
|
|
|
Db 992 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 1051
|
|
|
Qy 61 GGGCGTGTGCTGTGAGAGTGCAGATGTAGCGCGAGCGGCTTCGTCGTGGTGGCTGCTG 120
|
|
|
Db 1052 GGGCGTGTGCTGTGAGAGTGCAGATGTAGCGCGAGCGGCTTCGTCGTGGTGGCTGCTG 1111
|
|
|
Qy 121 CAGCGACAGGCGGACAGACAGACAC--TGACAGAAACACCCCGGAACCTGTCGAGAGACA 179
|
|
|
Db 1112 CAGCGACAGGCGGACAGACAGACACCTTTCAGAGAAACACCCCGGAACCTGTCGAGAGACA 1171
|
|
|
```

```
Qy 180 CCGTGTACAGAGCGGCTTGATGACAGAGCTAGAGTAAAGAAACGTCCTCCGAAAGGGA 239
|
|
|
Db 1172 CCGTGTACAGAGCGGCTTGATGACAGAGCTAGAGTAAAGAAACGTCCTCCGAAAGGGA 1231
|
|
|
Qy 240 GGAAGATCATGTAGACCCCGGAAGTAGACCTGCTCCAGTCGTGGTTGGCCGAG 299
|
|
|
Db 1232 GGAAGATCATGTAGACCCCGGAAGTAGACCTGCTCCAGTCGTGGTTGGCCGAG 1291
|
|
|
Qy 300 CCAATGATCCTCCGAATCTGTTGGGCGATTCAGATTCAGGCAATGTCACAAATCAGCCC 359
|
|
|
Db 1292 CCAATGATCCTCCGAATCTGTTGGGCGATTCAGATTCAGGCAATGTCACAAATCAGCCC 1351
|
|
|
Qy 360 CTGGGACAGACGACGAGAGGAGAGACAGAAAAAGAAAAACAGACATGAGAACACA 419
|
|
|
Db 1352 CTGGGACAGACGACGAGAGGAGAGACAGAAAAAGAAAAACAGACATGAGAACACA 1411
|
|
|
Qy 420 GTAAATGAATAAACCATTAATATTTAGCCCCCTCTGTTCTGTGCTTACTGGCCAGGAAA 479
|
|
|
Db 1412 GTAAATGAATAAACCATTAATATTTAGCCCCCTCTGTTCTGTGCTTACTGGCCAGGAAA 1471
|
|
|
Qy 480 TGGTACCAATTTTTCAGTGTGACTTGACACTTCTTTTGCACAAAGAGAGAAATTT 539
|
|
|
Db 1472 TGGTACCAATTTTTCAGTGTGACTTGACACTTCTTTTGCACAAAGAGAGAAATTT 1531
|
|
|
Qy 540 TAAACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTA 599
|
|
|
Db 1532 TAAACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTA 1591
|
|
|
Qy 600 GACAGTG 606
|
|
|
Db 1592 GACAGTG 1598
|
|
|
```

## RESULT 5

```
US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolj, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211
```

Query Match 77.8%; Score 486; DB 10; Length 1619;  
Best Local Similarity 99.8%; Pred. No. 9,7e-187;  
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy 1 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 60
|
|
|
Db 992 AGTTCTCTTTCAGAGAGACTGGCGCGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 1051
|
|
|
Qy 61 GGGCGTGTGCTGTGAGAGTGCAGATGTAGCGCGAGCGGCTTCGTCGTGGTGGCTGCTG 120
|
|
|
Db 1052 GGGCGTGTGCTGTGAGAGTGCAGATGTAGCGCGAGCGGCTTCGTCGTGGTGGCTGCTG 1111
|
|
|
Qy 121 CAGCGACAGGCGGACAGACAGACAC--TGACAGAAACACCCCGGAACCTGTCGAGAGACA 179
|
|
|
Db 1112 CAGCGACAGGCGGACAGACAGACACCTTTCAGAGAAACACCCCGGAACCTGTCGAGAGACA 1171
|
|
|
Qy 180 CCGTGTACAGAGCGGCTTGATGACAGAGCTAGAGTAAAGAAACGTCCTCCGAAAGGGA 239
|
|
|
```

```
|||||
Db 1172 CGGTATACAGAGCGGGTTGATGACCGAGCTAGTAGAAAAAAGCTCTCCGAGAAAGGGA 1231
QY 240 GGAGGATCATGTATACCCCGGAAGTAGAGACCTGTCAGTGTGTGGTTGGCCGAG 299
Db 1232 GGAGGATCATGTATACCCCGGAAGTAGAGACCTGTCAGTGTGTGGTTGGCCGAG 1291
QY 300 CCATATCTCCGAAATCTGGTTGGGATCCAGCATACGGCCAAATGTCACAAATCAGCC 359
Db 1292 CCATATCTCCGAAATCTGGTTGGGATCCAGCATACGGCCAAATGTCACAAATCAGCC 1351
QY 360 CTGGGACAGACAGCAGGAGGAGAGACAGAAAAAGAAAAACAGCATGAGAACACA 419
Db 1352 CTGGGACAGACAGCAGGAGGAGAGACAGAAAAAGAAAAACAGCATGAGAACACA 1411
QY 420 GTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 479
Db 1412 GTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1471
QY 480 TGGTACCAATTTTTCAGTGTGAGCTGTGACCTCTTTTGCACAGACAGAGAAAT 539
Db 1472 TGGTACCAATTTTTCAGTGTGAGCTGTGACCTCTTTTGCACAGACAGAGAAAT 1531
QY 540 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599
Db 1532 TAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591
QY 600 GACAGTG 606
Db 1592 GACAGTG 1598
|||||
```

## RESULT 6

```
; US-09-825-294-208/c
; Sequence 208, Application US/09825294
; Patent No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-208
```

## Query Match

```
Best Local Similarity 57.4%; Score 359; DB 10; Length 1362;
Best Local Similarity 100.0%; Pred. No. 1.1e-135;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AGTTCCTCTTGACAGAGACTGGCCCGGAGCGGAAGACAGACGGCGCTGCACAAAGG 60
Db 1215 AGTTCCTCTTGACAGAGACTGGCCCGGAGCGGAAGACAGACGGCGCTGCACAAAGG 1156
QY 61 GGGCGTGTGGTGTGAGTGTGCGCATGTACGGCGACAGCGCTTCTGTGGTGGCGTGTG 120
Db 1155 GGGCGTGTGGTGTGAGTGTGCGCATGTACGGCGACAGCGCTTCTGTGGTGGCGTGTG 1096
QY 121 CAGCGACAGCGCGACAGACAGCACTGACGAAACACCCCGAACTGCTGCGAGAGAC 180
Db 1095 CAGCGACAGCGCGACAGACAGCACTGACGAAACACCCCGAACTGCTGCGAGAGAC 1036
QY 181 CGGTATACAGAGCGGGTGTATGACGAGCTGAGAGTGAAGAAAGCTCTCCGAGAAAGGAG 240
Db 1035 CGGTATACAGAGCGGGTGTATGACGAGCTGAGGTAGAAAAAGCTCTCCGAGAAAGGAG 976
|||||
```

```
QY 241 GAGATCATGTATACGCCCGGAAGTAGAGACCTGTCAGTGTGTGGTTGGCCGAGC 300
Db 975 GAGATCATGTATACGCCCGGAAGTAGAGACCTGTCAGTGTGTGGTTGGCCGAGC 916
QY 301 CATGATCTCTCCGAATCTGGTTGGGATCCAGCATACGGCCAAATGTCACAAATCAGCC 359
Db 915 CATGATCTCTCCGAATCTGGTTGGGATCCAGCATACGGCCAAATGTCACAAATCAGCC 857
|||||
```

## RESULT 7

```
; US-09-867-701-1516/c
; Sequence 1516, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1516
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-1516
```

## Query Match

```
Best Local Similarity 50.2%; Score 314; DB 10; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 293 GCCGACGACATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCAAATGTCACACA 352
Db 315 GCCGACGACATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCAAATGTCACACA 256
QY 353 ATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
Db 255 ATCAGCCCTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 413 GAGACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 472
Db 195 GAGACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 136
QY 473 CAGGAATGTGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGCAAG 532
Db 135 CAGGAATGTGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGCAAG 76
QY 533 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAA 592
Db 75 GAGAAATTAACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAA 16
QY 593 TGCTTTAGACAGTG 606
Db 15 TGCTTTAGACAGTG 2
|||||
```

## RESULT 8

```
; US-09-867-701-2409/c
; Sequence 2409, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
```

```
;; NUMBER OF SEQ ID NOS: 10912
;; SOFTWARE: fastseq for windows version 4.0
;; SEQ ID NO 2409
;; LENGTH: 349
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-867-701-2409
```

```
Query Match          49.1%; Score 307; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.4e-115;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 300 CCATATCTCTCCGAATCTGTGGGATCCAGCATCGCCCAATGTCCAAATCAGCC 359
    |||||||
DB 310 CCATATCTCTCCGAATCTGTGGGATCCAGCATCGCCCAATGTCCAAATCAGCC 251
    |||||||
QY 360 CTGGCAGACAGCAGCAGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGACACA 419
    |||||||
DB 250 CTGGCAGACAGCAGCAGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGACACA 191
    |||||||
QY 420 GTAAATGATAAACCATTAAATATTATTACCCCTCTGTCTGTCTTACTGCGCAGGAA 479
    |||||||
DB 190 GTAAATGATAAACCATTAAATATTATTACCCCTCTGTCTGTCTTACTGCGCAGGAA 131
    |||||||
QY 480 TGTGACCAATTTTTCAGTGTGACTTGACAGCTTTCTTTGCCACAAGCAGAGAAAT 539
    |||||||
DB 130 TGTGACCAATTTTTCAGTGTGACTTGACAGCTTTCTTTGCCACAAGCAGAGAAAT 71
    |||||||
QY 540 TAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAAGACATTAAATGCTTTA 599
    |||||||
DB 70 TAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAAGACATTAAATGCTTTA 11
    |||||||
QY 600 GACAGTG 606
    |||||||
DB 10 GACAGTG 4
```

```
RESULT 9
US-09-867-701-4240/c
; Sequence 4240, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240
```

```
Query Match          42.1%; Score 263; DB 10; Length 409;
Best Local Similarity 99.7%; Pred. No. 4.5e-97;
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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QY 293 GCGGCAGCCATGATCTCCGAATCTGTGGGATCCAGCATCGGCCCAATGTCCACACA 352
    |||||||
DB 315 GCGGCAGCCATGATCTCCGAATCTGTGGGATCCAGCATCGGCCCAATGTCCACACA 256
    |||||||
QY 353 ATGAGCCCTGGGAGACAGCAGAGGAGAGACAGAGAAAAGAAAACACAGCATGA 412
    |||||||
DB 255 ATGAGCCCTGGGAGACAGCAGAGGAGAGACAGAGAAAAGAAAACACAGCATGA 196
    |||||||
QY 413 GAACACAGTAAATATAAATTAATTAATTTAGCCCTCTGTCTGTGCTTACTGCG 472
    |||||||
DB 195 GAACACAGTAAATATAAATTAATTAATTTAGCCCTCTGTCTGTGCTTACTGCG 136
    |||||||
```

```
QY 473 CAGNAATGTATCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGACAGA 532
    |||||||
DB 135 CAGNAATGTATCAATTTTTCAGTGTGACTTGACAGCTTCTTTGCCACAAGACAGA 76
    |||||||
QY 533 GAGAAATTAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAAGCAATTAA 592
    |||||||
DB 75 GAGAAATTAACACTGTTTCAACCCGGGAGTGTGCTGTAAAGAAAAGCAATTAA 16
    |||||||
QY 593 TGCCTTACAGAGTG 606
    |||||||
DB 15 TGCCTTACAGAGTG 2
```

```
RESULT 10
US-09-867-701-8894/c
; Sequence 8894, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8894
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8894
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Query Match          26.6%; Score 166; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.5e-58;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 231 AGAAGGGAGAGAGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGGGGTT 290
    |||||||
DB 181 AGAAGGGAGAGAGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGGGGTT 122
    |||||||
QY 291 TGGCCGAGCATATCTCCGAATCTGTGGGATCCAGCATCGGCCCAATGTCCACA 350
    |||||||
DB 121 TGGCCGAGCATATCTCCGAATCTGTGGGATCCAGCATCGGCCCAATGTCCACA 62
    |||||||
QY 351 CAATCAGCCCTGGGAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
    |||||||
DB 61 CAATCAGCCCTGGGAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 16
    |||||||
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```
RESULT 11
US-09-867-701-1532
; Sequence 1532, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1532
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
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```

? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 698
? LENGTH: 508
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (358)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (449)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (480)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (496)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (499)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc_feature
? LOCATION: (505)
? OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-698

Query Match
Best Local Similarity 100.0%; Score 21; DB 10; Length 508;
Pred. No. 8.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 603 AGTGNAAAAAAAAAAAAAAAAA 623
|||||
DB 445 AGTGNAAAAAAAAAAAAAAAAA 465

RESULT 17
US-09-834-975-379
? Sequence 379, Application US/09834975
? Patent No. US20020110815A1
? GENERAL INFORMATION:
? APPLICANT: Lillie, James
? APPLICANT: Brown, Jeffrey
? APPLICANT: Bolt, Andrew
? APPLICANT: Van Hufel, Christophe
? TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
? TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPPY
? FILE REFERENCE: MRI-016B
? CURRENT APPLICATION NUMBER: US/09/834,975
? CURRENT FILING DATE: 2001-04-13
? PRIOR APPLICATION NUMBER: 60/197,538
? PRIOR FILING DATE: 2000-04-14
? NUMBER OF SEQ ID NOS: 1046
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 379
? LENGTH: 547
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(547)
? OTHER INFORMATION: n = A,T,C or G
US-09-834-975-379

Query Match
Best Local Similarity 3.4%; Score 21; DB 10; Length 547;
Pred. No. 100.0%; Score 21; DB 10; Length 547;
Pred. No. 8.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAAAAA 625
|||||
DB 527 TGNAAAAAAAAAAAAAAAAA 547

```

```
RESULT 18
US-09-783-590-7037
; Sequence 7037, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7037
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (36)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (122)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (133)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (185)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (408)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (409)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (418)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (428)
; OTHER INFORMATION: n equals a,t,g, or c
```

```
NAME/KEY: misc feature
LOCATION: (447)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (449)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (458)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (497)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (499)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (510)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (514)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (544)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (556)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (562)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (571)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (575)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-7037

Query Match
Best Local Similarity 100.0%; Pred. No. 8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 605 TGNAAAAAAAAAAAAA 625
Db 573 TGNAAAAAAAAAAAAA 593

RESULT 19
US-09-925-301-539
; Sequence 539, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 539
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1305)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1344)
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OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc-feature  
LOCATION: (1349)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-539

Query Match  
Best Local Similarity 3.4%; Score 21; DB 10; Length 1350;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAAA 625  
DB 1303 TGNAAAAAAAAAAAAAAA 1323

RESULT 20  
US-09-925-297-171  
Sequence 171, Application US/09925297  
Patent No. US20020081659A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA105  
CURRENT APPLICATION NUMBER: US/09/925,297  
PRIORITY FILING DATE: 2001-08-10  
PRIORITY FILING DATE: 2000-03-08  
PRIORITY FILING DATE: 2000-03-08  
PRIORITY FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 928  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 171  
LENGTH: 1402  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1370)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc-feature  
LOCATION: (1400)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-297-171

Query Match  
Best Local Similarity 3.4%; Score 21; DB 10; Length 1402;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAAAA 625  
DB 1368 TGNAAAAAAAAAAAAAAA 1388

RESULT 21  
US-09-783-590-2406/c  
Sequence 2406, Application US/09783590  
Patent No. US20020110850A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Haseltine, William A.  
APPLICANT: Li, Haodong  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: FO-16.2C1  
CURRENT APPLICATION NUMBER: US/09/783,590  
PRIORITY FILING DATE: 2000-02-15  
PRIORITY FILING DATE: 1995-04-12  
PRIORITY FILING DATE: 1994-11-21  
NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2406  
LENGTH: 58  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (34)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc-feature  
LOCATION: (41)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc-feature  
LOCATION: (47)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc-feature  
LOCATION: (52)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc-feature  
LOCATION: (58)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-2406

Query Match  
Best Local Similarity 3.2%; Score 20; DB 10; Length 58;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAAAA 625  
DB 35 GNAAAAAAAAAAAAAAAA 16

RESULT 22  
US-09-919-580-419/c  
Sequence 419, Application US/09919580  
Patent No. US20020110832A1  
GENERAL INFORMATION:  
APPLICANT: Pyle, Ruth  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: SECRETIST, HEATHER  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.552  
CURRENT APPLICATION NUMBER: US/09/919,580  
PRIORITY FILING DATE: 2001-07-30  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 419  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 54  
OTHER INFORMATION: n = A,T,C or G  
US-09-919-580-419

Query Match  
Best Local Similarity 3.2%; Score 20; DB 10; Length 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAAAA 625  
DB 55 GNAAAAAAAAAAAAAAAA 36

RESULT 23  
US-09-925-301-759/c  
Sequence 759, Application US/09925301  
Patent No. US20020052308A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA106

;; CURRENT APPLICATION NUMBER: US/09/925,301  
;; CURRENT FILING DATE: 2001-08-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/05882  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: 60/124,270  
;; NUMBER OF SEQ ID NOS: 1694  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 759  
;; LENGTH: 66  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (6)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (59)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (63)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (65)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: misc\_feature  
;; LOCATION: (66)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; US-09-925-301-759

Query Match 3.2%; Score 20; DB 10; Length 66;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAAAAAA 625  
|||||  
Db 60 GNAAAAAAAAAAAAAAAAAA 41

RESULT 24  
US-09-815-343-241/C  
;; Sequence 241, Application US/09815343  
;; Patent No. US2001005596A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Meagher, Madeleine  
;; APPLICANT: Xu, Jiangchun  
;; APPLICANT: King, Gordon E.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
;; FILE REFERENCE: 210121.504  
;; CURRENT APPLICATION NUMBER: US/09/815,343  
;; CURRENT FILING DATE: 2001-03-22  
;; NUMBER OF SEQ ID NOS: 1556  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 241  
;; LENGTH: 97  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..  
;; OTHER INFORMATION: n = A,T,C or G  
;; US-09-815-343-241

Query Match 3.2%; Score 20; DB 10; Length 97;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAAAAAA 625  
|||||  
Db 88 GNAAAAAAAAAAAAAAAAAA 69

RESULT 25  
US-09-895-828-248  
;; Sequence 248, Application US/09895828  
;; Patent No. US2002009012A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, Tonglong  
;; APPLICANT: McNeill, Patricia D.  
;; APPLICANT: Watanabe, Yoshihiro  
;; APPLICANT: Carter, Darriek  
;; APPLICANT: Henderson, Robert A.  
;; APPLICANT: Kalos, Michael D.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; FILE REFERENCE: 210121.539  
;; CURRENT APPLICATION NUMBER: US/09/895,828  
;; CURRENT FILING DATE: 2001-06-28  
;; NUMBER OF SEQ ID NOS: 473  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 248  
;; LENGTH: 217  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: 201  
;; OTHER INFORMATION: n = A,T,C or G  
;; US-09-895-828-248

Query Match 3.2%; Score 20; DB 10; Length 217;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 GTGNAAAAAAAAAAAAAAAAAA 623  
|||||  
Db 198 GTGNAAAAAAAAAAAAAAAAAA 217

RESULT 26  
US-10-046-935-291/C  
;; Sequence 291, Application US/10046935  
;; Patent No. US2002015601A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jiang, Yugu  
;; APPLICANT: Harlocker, Susan L.  
;; APPLICANT: Secrist, Heather  
;; APPLICANT: Wang, Aijun  
;; APPLICANT: Stolk, John A.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;; FILE REFERENCE: 210121.527C1  
;; CURRENT APPLICATION NUMBER: US/10/046,935  
;; CURRENT FILING DATE: 2002-01-15  
;; NUMBER OF SEQ ID NOS: 2239  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 291  
;; LENGTH: 226  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: 20, 57, 141, 184, 206  
;; OTHER INFORMATION: n = A,T,C or G  
;; US-10-046-935-291

Query Match 3.2%; Score 20; DB 9; Length 226;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 606 GNAAAAAAAAAAAAAAAAAA 625  
|||||  
Db 21 GNAAAAAAAAAAAAAAAAAA 2

RESULT 27  
US-10-040-916-46  
; Sequence 46, Application US/10040916  
; Patent No. US20020146769A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; McCoy, John  
; Lavallee, Edward  
; Racie, Lisa  
; Merberg, David  
; Treacy, Maurice  
; Evans, Cheryl  
; Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/040,916  
FILING DATE: 07-Jan-2002  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,029  
FILING DATE: 07-FEB-1997  
APPLICATION NUMBER: 08/686,878  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-10-040-916-46  
Query Match 3.2%; Score 20; DB 12; Length 265;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 606 GNAAAAAAAAAAAAAA 625  
DB 245 GNAAAAAAAAAAAAAA 264  
RESULT 28  
US-09-834-975-374/c  
; Sequence 374, Application US/09834975  
; Patent No. US20020110815A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; Applicant: Brown, Jeffrey  
; Applicant: Bolt, Andrew  
; Applicant: Van Hufel, Christophe  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS  
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

;; TITLE OF INVENTION: OF HUMAN CANCERS  
;; FILE REFERENCE: MRI-016B  
;; CURRENT APPLICATION NUMBER: US/09/834,975  
;; CURRENT FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/197,538  
;; PRIOR FILING DATE: 2000-04-14  
;; NUMBER OF SEQ ID NOS: 1046  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 374  
;; LENGTH: 291  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc-feature  
;; LOCATION: (1)...(291)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-834-975-374  
Query Match 3.2%; Score 20; DB 10; Length 291;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 605 TGNAAAAAAAAAAAAAA 624  
DB 41 TGNAAAAAAAAAAAAAA 22  
RESULT 29  
US-09-777-564-625/c  
; Sequence 625, Application US/09777564  
; Patent No. US2002022591A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; Applicant: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.493  
CURRENT APPLICATION NUMBER: US/09/777,564  
CURRENT FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 1730  
SOFTWARE: FastSeq for Window Version 4.0  
SEQ ID NO 625  
LENGTH: 451  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)...(451)  
OTHER INFORMATION: n = A,T,C or G  
US-09-777-564-625  
Query Match 3.2%; Score 20; DB 10; Length 451;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 606 GNAAAAAAAAAAAAAA 625  
DB 373 GNAAAAAAAAAAAAAA 354  
RESULT 30  
US-09-783-590-10830  
; Sequence 10830, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; Applicant: Haseltine, William A.  
; Applicant: Li, Haodong  
; Applicant: Rosen, Craig A.  
; Applicant: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: PO-16.2C1  
CURRENT APPLICATION NUMBER: US/09/783,590

CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/420,856  
PRIOR FILING DATE: 1995-04-12  
PRIOR APPLICATION NUMBER: 08/346,731  
PRIOR FILING DATE: 1994-11-21  
NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10830  
LENGTH: 496  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (161)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (182)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (209)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (210)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (216)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (237)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (278)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (279)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (283)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (289)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (304)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (310)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (318)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (321)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (357)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (364)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (392)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (396)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (404)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature

LOCATION: (416)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (419)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (441)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (445)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (447)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (448)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (461)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (493)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-10830  
Query Match 3.2%; Score 20; DB 10; Length 496;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 606 GNAAGAAAAAGAAAAAGAAAA 625  
DB 7 GNAAGAAAAAGAAAAAGAAAA 26  
RESULT 31  
US-09-925-301-819  
Sequence 819, Application US/09925301  
Patent No. US20020052308A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 819  
LENGTH: 648  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (369)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (518)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (544)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (547)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (565)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (584)  
OTHER INFORMATION: n equals a,t,g, or c

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; NAME/KEY: misc.feature
; LOCATION: (626)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-819

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Query Match
Best Local Similarity 3.2%; Score 20; DB 10; Length 648;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 606 GNAAAAAAAAAAAAAA 625
DB 625 GNAAAAAAAAAAAAAA 644

```

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RESULT 32
US-09-759-143-32/C
; Sequence 32, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-759-143-32

```

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Query Match
Best Local Similarity 3.2%; Score 20; DB 10; Length 789;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47

```

```

US-09-780-669-32/C
; Sequence 32, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.

```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurrell, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-780-669-32

```

```

Query Match
Best Local Similarity 3.2%; Score 20; DB 10; Length 789;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 606 GNAAAAAAAAAAAAAA 625
DB 66 GNAAAAAAAAAAAAAA 47

```

```

RESULT 34
US-09-030-606-32/C
; Sequence 32, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:

```

SEQUENCE CHARACTERISTICS:  
LENGTH: 789 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-030-606-32

Query Match 3.2%; Score 20; DB 10; Length 789;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 35  
US-09-822-827-32/C  
Sequence 32, Application US/09822827  
Patent No. US20020081680A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.534C1  
CURRENT APPLICATION NUMBER: US/09/822,827  
CURRENT FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 982  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-822-827-32

Query Match 3.2%; Score 20; DB 10; Length 789;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 36  
US-09-115-453-32/C  
Sequence 32, Application US/09115453B  
Patent No. US20020090372A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
FILE REFERENCE: 210121.427C4  
CURRENT APPLICATION NUMBER: US/09/115,453B  
CURRENT FILING DATE: 1998-07-14  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(789)  
OTHER INFORMATION: n = A,T,C or G  
US-09-115-453-32

Query Match 3.2%; Score 20; DB 10; Length 789;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 GNAAAAAAAAAAAAAA 625  
DB 66 GNAAAAAAAAAAAAAA 47

RESULT 37  
US-09-949-654-3/C  
Sequence 3, Application US/09949654  
Patent No. US20020127644A1  
GENERAL INFORMATION:  
APPLICANT: VAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
FILE REFERENCE: C1000817  
CURRENT APPLICATION NUMBER: US/09/949,654  
CURRENT FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: 60/231,572  
PRIOR FILING DATE: 2000-09-11  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 368004  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(368004)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-654-3

Query Match 3.2%; Score 20; DB 10; Length 368004;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 GAAAAACACAGCATGAGAAC 416  
DB 350891 GAAAAACACAGCATGAGAAC 350872

RESULT 38  
US-09-783-590-8086/C  
Sequence 8086, Application US/09783590  
Patent No. US20020110850A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Haseltine, William A.  
APPLICANT: Li, Haodong  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
FILE REFERENCE: PO-16.2C1  
CURRENT APPLICATION NUMBER: US/09/783,590  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 08/420,856  
PRIOR FILING DATE: 1995-04-12  
PRIOR APPLICATION NUMBER: 08/346,731  
PRIOR FILING DATE: 1994-11-21  
NUMBER OF SEQ ID NOS: 12485  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8086  
LENGTH: 51  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (10)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature



```
; LOCATION: (51)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-8086

Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 51 NAAAAAAAAAAAAAAAAAAAAA 33

RESULT 39
US-09-783-590-5881/c
; Sequence 5881, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5881
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-5881

Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 48 NAAAAAAAAAAAAAAAAAAAAA 30

RESULT 40
US-09-919-580-705/c
; Sequence 705, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 705
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: 34, 42, 46
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-705

Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 34 NAAAAAAAAAAAAAAAAAAAAA 16

RESULT 41
US-09-783-590-3220/c
; Sequence 3220, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3220
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3220

Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 53 NAAAAAAAAAAAAAAAAAAAAA 35

RESULT 42
US-09-919-580-171/c
; Sequence 171, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 56
; TYPE: DNA
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ORGANISM: Homo sapiens  
NAME/KEY: misc\_feature  
LOCATION: 49  
OTHER INFORMATION: n = A,T,C or G  
US-09-919-580-171

Query Match  
Best Local Similarity 100.0%; Score 19; DB 10; Length 56;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625  
DB 49 NAAAAAAAAAAAAAAAAAAAA 31

RESULT 43  
US-09-919-580-677/c  
Sequence 677, Application US/09919580  
Patent No. US20020110832A1  
GENERAL INFORMATION:  
APPLICANT: Pyle, Ruth  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: SECRET, HEATHER  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.552  
CURRENT APPLICATION NUMBER: US/09/919,580  
CURRENT FILING DATE: 2001-07-30  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 677  
LENGTH: 56  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 53  
OTHER INFORMATION: n = A,T,C or G  
US-09-919-580-677

Query Match  
Best Local Similarity 100.0%; Score 19; DB 10; Length 56;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625  
DB 53 NAAAAAAAAAAAAAAAAAAAA 35

RESULT 44  
US-09-919-580-713/c  
Sequence 713, Application US/09919580  
Patent No. US20020110832A1  
GENERAL INFORMATION:  
APPLICANT: Pyle, Ruth  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: SECRET, HEATHER  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.552  
CURRENT APPLICATION NUMBER: US/09/919,580  
CURRENT FILING DATE: 2001-07-30  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 713  
LENGTH: 56  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 35, 37, 42, 56  
OTHER INFORMATION: n = A,T,C or G

US-09-919-580-713

Query Match  
Best Local Similarity 100.0%; Score 19; DB 10; Length 56;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625  
DB 35 NAAAAAAAAAAAAAAAAAAAA 17

RESULT 45  
US-09-925-301-758/c  
Sequence 758, Application US/09925301  
Patent No. US20020052308A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 758  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (36)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (38)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (40)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (45)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (46)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-758

Query Match

Best Local Similarity 100.0%; Score 19; DB 10; Length 60;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625  
DB 36 NAAAAAAAAAAAAAAAAAAAA 18

Search completed: November 8, 2002, 02:06:25  
Job time : 100.162 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:02:33 ; Search time 1399.81 Seconds  
(Without alignments)  
11225.881 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
1 agtctctctgcagagact.....gnaaaaaaaaaaaaaa 625

Sequence: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Scoring table: Searched: 24791104 seqs, 12571243825 residues

Word size : 10

Total number of hits satisfying chosen parameters: 10637023

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main.\*  
1: /cgn2\_6/ptodata/1/pna/US06000\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06001\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US06002\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US06003\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US06004\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US06005\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US06006\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US06007\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US06008\_COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US06009\_COMB.seq.\*  
11: /cgn2\_6/ptodata/1/pna/US06010\_COMB.seq.\*  
12: /cgn2\_6/ptodata/1/pna/US06011\_COMB.seq.\*  
13: /cgn2\_6/ptodata/1/pna/US06012\_COMB.seq.\*  
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17: /cgn2\_6/ptodata/1/pna/US06016\_COMB.seq.\*  
18: /cgn2\_6/ptodata/1/pna/US06017\_COMB.seq.\*  
19: /cgn2\_6/ptodata/1/pna/US06018\_COMB.seq.\*  
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22: /cgn2\_6/ptodata/1/pna/US06021\_COMB.seq.\*  
23: /cgn2\_6/ptodata/1/pna/US06022\_COMB.seq.\*  
24: /cgn2\_6/ptodata/1/pna/US06023\_COMB.seq.\*  
25: /cgn2\_6/ptodata/1/pna/US06024\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US06025\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US06026\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US06027\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US06028\_COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US06029\_COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US06030\_COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US06031\_COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US06032\_COMB.seq.\*  
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36: /cgn2\_6/ptodata/1/pna/US06035\_COMB.seq.\*  
37: /cgn2\_6/ptodata/1/pna/US06036\_COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US06037\_COMB.seq.\*  
39: /cgn2\_6/ptodata/1/pna/US06038\_COMB.seq.\*  
40: /cgn2\_6/ptodata/1/pna/US06039\_COMB.seq.\*  
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Result	Score	Match	Length	ID	Description
1	625	100.0	625	1 PCT-US01-45395-210	Sequence 210, App
2	625	100.0	625	1 US-09-825-294-210	Sequence 210, App
3	625	100.0	625	3 US-09-867-701-10876	Sequence 10876, A
4	625	100.0	625	36 US-09-970-966-210	Sequence 210, App
5	625	100.0	625	42 US-10-212-677-210	Sequence 210, App
6	606	97.0	1897	1 PCT-US01-45395-214	Sequence 214, App
7	606	97.0	1897	31 US-09-825-294-214	Sequence 214, App
8	606	97.0	1897	36 US-09-970-966-214	Sequence 214, App
9	606	97.0	1897	42 US-10-212-677-214	Sequence 214, App
10	606	97.0	1897	70 US-10-212-677-214	Sequence 214, App
11	606	97.0	1897	70 US-10-212-677-214	Sequence 214, App
12	555	88.8	1608	1 PCT-US01-18569-111	Sequence 111, App
13	555	88.8	1608	43 US-10-264-049-111	Sequence 111, App
14	555	88.8	1832	42 US-10-108-260A-197	Sequence 197, App
15	555	88.8	1866	42 US-10-208-408-26	Sequence 26, App1
16	555	88.8	1866	73 US-60-295-262-26	Sequence 26, App1
17	555	88.8	1866	74 US-60-308-868-26	Sequence 26, App1
18	555	88.8	1917	17 US-09-371-168-7188	Sequence 7188, Ap
19	555	88.8	1917	25 US-09-644-873-9077	Sequence 9077, Ap
20	555	88.8	1917	25 US-09-652-109-9370	Sequence 9370, Ap
21	555	88.8	1917	25 US-09-652-121-6191	Sequence 6191, Ap
	555	88.8	1917	25 US-09-652-128-7518	Sequence 7518, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 555 88.8 1917 25 US-09-652-355-9112 Sequence 9112, Ap
23 555 88.8 1917 25 US-09-652-914-8473 Sequence 8473, Ap
24 555 88.8 1917 25 US-09-652-917-2477 Sequence 2477, Ap
25 555 88.8 1917 31 US-09-801-833-7188 Sequence 7188, Ap
26 555 88.8 1918 17 US-09-397-022-4454 Sequence 4454, Ap
27 555 88.8 1918 31 US-09-808-383-4454 Sequence 4454, Ap
28 555 88.8 1925 25 US-09-652-121-7293 Sequence 7293, Ap
29 555 88.8 1925 25 US-09-652-128-9375 Sequence 9375, Ap
30 555 88.8 1925 25 US-09-652-917-3346 Sequence 3346, Ap
31 555 88.8 1925 27 US-09-699-997-11085 Sequence 11085, A
32 555 88.8 1925 29 US-09-710-281-4458 Sequence 4458, Ap
33 555 88.8 1925 29 US-09-726-805-1608 Sequence 1608, Ap
34 555 88.8 1953 36 US-09-950-083-1914 Sequence 38, Appl
35 555 88.8 1953 36 US-09-950-083-1914 Sequence 1914, Ap
36 555 88.8 1953 40 US-10-105-299-2414 Sequence 2414, Ap
37 555 88.8 1956 1 PCT-US00-14973-23 Sequence 23, Appl
38 555 88.8 1956 36 US-09-950-083-1915 Sequence 1915, Ap
39 555 88.8 1956 40 US-10-105-299-2415 Sequence 2415, Ap
40 555 88.8 1967 1 PCT-US02-29964-16 Sequence 16, Appl
41 545 87.8 1890 23 US-09-611-523-203 Sequence 203, Appl
42 545 87.2 716 61 US-60-172-373-15734 Sequence 15734, A
43 486 77.8 1619 1 PCT-US01-45395-205 Sequence 205, Appl
44 486 77.8 1619 1 PCT-US01-45395-211 Sequence 211, Appl
45 486 77.8 1619 28 US-09-713-550-205 Sequence 205, Appl
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## ALIGNMENTS

```
RESULT 1
PCT-US01-45395-210
: Sequence 210, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
PCT-US01-45395-210
```

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Query Match 100.0% Score 625; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 6.3e-125;
Matches 625: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AGTTCTCTTTGAGAGAGACTGGCCGGGAGCGGAAAGACAAAGCGGCGCTGCACAAAGCG 60
|
|
|
DB 1 AGTTCTCTTTGAGAGAGACTGGCCGGGAGCGGAAAGACAAAGCGGCGCTGCACAAAGCG 60
|
|
|
QY 61 GGGCGTGTGGTGTGAGTGTGAGTGTGATGTACGCGCAGGCGCTTCTGTTGGCTGTGCTG 120
|
|
|
DB 61 GGGCGTGTGGTGTGAGTGTGAGTGTGATGTACGCGCAGGCGCTTCTGTTGGCTGTGCTG 120
|
|
|
QY 121 CAGCGACAGCGCGGACAGACAGCACTGTGACGAAACACCCCGGCAAACTGCTGCGAGAGAC 180
|
|
|
DB 121 CAGCGACAGCGCGGACAGACAGCACTGTGACGAAACACCCCGGCAAACTGCTGCGAGAGAC 180
|
|
|
QY 181 CGTGTACAGAGAGCGGGTGTATGACGAGCTGAGGTAGTAAAGAAACGTCTCGAGAGAGGAG 240
```

```
|||||
DB 181 CGTGTACAGAGAGCGGGTGTATGACGAGCTGAGTAAAGAAACGTCTCGAGAGAGGAG 240
|
|
|
QY 241 GAGGATCATGTACAGCGCGGAGAGTAGACCTGTCTCAGTGTCTGTTGGTTGGCCGAC 300
|
|
|
DB 241 GAGGATCATGTACAGCGCGGAGAGTAGACCTGTCTCAGTGTCTGTTGGTTGGCCGAC 300
|
|
|
QY 301 CATGATCTCTCCAAATCTGGTGGCATCCAGCATCCGCGCAATGTACAAACATGAGCC 360
|
|
|
DB 301 CATGATCTCTCCAAATCTGGTGGCATCCAGCATCCGCGCAATGTACAAACATGAGCC 360
|
|
|
QY 361 TGGGACAGACAGCAGAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGAACAG 420
|
|
|
DB 361 TGGGACAGACAGCAGAGAGAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGAACAG 420
|
|
|
QY 421 TAAATGAATTAACCAATTAATATTTAGCCCTGTCTGTCTGTCTACTGCCAGGAAT 480
|
|
|
DB 421 TAAATGAATTAACCAATTAATATTTAGCCCTGTCTGTCTGTCTACTGCCAGGAAT 480
|
|
|
QY 481 GGTACCAATTTTTCAGTGTGTGACTGTGACGCTTCTTTGCCAAGCAGAGAAATT 540
|
|
|
DB 481 GGTACCAATTTTTCAGTGTGTGACTGTGACGCTTCTTTGCCAAGCAGAGAAATT 540
|
|
|
QY 541 AACACTGTTTCAACCCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 600
|
|
|
DB 541 AACACTGTTTCAACCCCGGGGAGTGTGCTGTAAAGAAAGACATTAATGCTTTAG 600
|
|
|
QY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
|
|
|
DB 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
|
|
|
```

```
RESULT 2
US-09-825-294-210
: Sequence 210, Application US/09825294
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.4845
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 210
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (1)...(625)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210
```

```
Query Match 100.0% Score 625; DB 31; Length 625;
Best Local Similarity 100.0%; Pred. No. 6.3e-125;
Matches 625: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AGTTCTCTTTGAGAGAGACTGGCCGGGAGCGGAAAGACAAAGCGGCGCTGCACAAAGCG 60
|
|
|
DB 1 AGTTCTCTTTGAGAGAGACTGGCCGGGAGCGGAAAGACAAAGCGGCGCTGCACAAAGCG 60
|
|
|
QY 61 GGGCGTGTGGTGTGAGTGTGAGTGTGATGTACGCGCAGGCGCTTCTGTTGGCTGTGCTG 120
|
|
|
DB 61 GGGCGTGTGGTGTGAGTGTGAGTGTGATGTACGCGCAGGCGCTTCTGTTGGCTGTGCTG 120
|
|
|
QY 121 CAGCGACAGCGCGGACAGACAGCACTGTGACGAAACACCCCGGCAAACTGCTGCGAGAGAC 180
|
|
|
DB 121 CAGCGACAGCGCGGACAGACAGCACTGTGACGAAACACCCCGGCAAACTGCTGCGAGAGAC 180
|
|
|
```

Qy	181	CGTGCACGAGCGGGTTGATGACCCGAGCTGAGTAGAAAAAGCTCCGAGAAGGGAG	240
Dp	181	CGTGCACGAGCGGGTTGATGACCCGAGCTGAGTAGAAAAAGCTCCGAGAAGGGAG	240
Qy	241	GAGATCATGTAGCCCGGGAAGTAGACCTGTCAGTCTGCTTGGGTTTGGCCGAGC	300
Dp	241	GAGATCATGTAGCCCGGGAAGTAGACCTGTCAGTCTGCTTGGGTTTGGCCGAGC	300
Qy	301	CATGATCCTCCGAACTGCTTGGGSCATCCAGCATACGGCCAAATGTCAACAATCAGCC	360
Dp	301	CATGATCCTCCGAACTGCTTGGGSCATCCAGCATACGGCCAAATGTCAACAATCAGCC	360
Qy	361	TGGGCAGACAGCAGGAGGAGGAGACAGAGAAAAAACAACACATGAGAACACAG	420
Dp	361	TGGGCAGACAGCAGGAGGAGGAGACAGAGAAAAAACAACACATGAGAACACAG	420
Qy	421	TAAATGAATAAACCATTAATATTATTAAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT	480
Dp	421	TAAATGAATAAACCATTAATATTATTAAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT	480
Qy	481	GGTACCATTTTTTCAGTGTGGACTTACAGCCTCTTTGCCAACACAGACAGAAATT	540
Dp	481	GGTACCATTTTTTCAGTGTGGACTTACAGCCTCTTTGCCAACACAGACAGAAATT	540
Qy	541	AACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
Dp	541	AACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
Qy	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Dp	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	

```

RESULT 3
US-09-867-701-10876
: Sequence 10876, Application US/09867701
: GENERAL INFORMATION:
: APPLICANT: Agiate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlocker, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ ID NOS: 10912
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10876
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876

```

Query Match	100.0%	Score 625:	DB 33:	Length 625:
Best Local Similarity	100.0%	Pred. No. 6.3e-125:		
Matches	625:	Conservative	0:	Mismatches 0: Indels 0: Gaps 0:

QY	1	AGTTCCTCTTGACAGAGACTGCGCGCGGAGCCGCGAAGACAAACGGGCGGTGCACAAAGC	60
Db	1	AGTTCCTCTTGACAGAGACTGCGCGCGGAGCCGCGAAGACAAACGGGCGGTGCACAAAGC	60
QY	61	GCGCGTGTGCGGTGTGGAATGCCATGTACGCGCAGGCGCTTCTGTGGTGGCGTGTG	120
Db	61	GCGCGTGTGCGGTGTGGAATGCCATGTACGCGCAGGCGCTTCTGTGGTGTGCGTGTG	120
QY	121	CAGGCACAGGGGCGGACAGCAGCACTGCACGCAAAACCCGCGCAAACTGCTGCGAGGACAC	180
Db	121	CAGGCACAGGGGCGGACAGCAGCACTGCACGCAAAACCCGCGCAAACTGCTGCGAGGACAC	180

OY	181	CGGTACAGGAGGGGGTTGATGACCCGAGCTGAGGTACAAAAAGCTCTCCGAAAGGGAG	240
Db	181	CGTGTACGAGGGCGGGTTGATGATCCGAGCTGAGGTAGAAAAACGCTCTCCGAAAGGGAG	240
OY	241	GAGGATCATCTATACGCCCGGGAAGTATGAGACCTCTGTCACATCGCTGGTGGGTTGGCCGAGC	300
Db	241	GAGGATCATCTATACGCCCGGGAAGTATGAGACCTCTGTCACATCGCTGGTGGGTTGGCCGAGC	300
OY	301	CATGATCCTCCGAATCTTGGTTGGGCATTCACGATACGGCCATGTCAACAATCAGCCC	360
Db	301	CATGATCCTCCGAATCTTGGTTGGGCATTCACGATACGGCCATGTCAACAATCAGCCC	360
OY	361	TGGCGAGACACGACAGAGGAGGAGAGACAGAGAAAAAAGAAACACACATGAGAAACAG	420
Db	361	TGGCGAGACACGACAGAGGAGGAGAGACAGAGAAAAAAGAAACACACATGAGAAACAG	420
OY	421	TAAATGAATAAACCATTAATAATTTAGCCCTCTGTTCTGTGTACTGTGCCAGGAAT	480
Db	421	TAAATGAATAAACCATTAATAATTTAGCCCTCTGTTCTGTGTACTGTGCCAGGAAT	480
OY	481	GGTACCATTTTTCAGTGTGTGACTTACAGCTCTTTTCCCAACACAGACAGAAATT	540
Db	481	GGTACCATTTTTCAGTGTGTGACTTACAGCTCTTTTCCCAACACAGAGGAATTT	540
OY	541	AACACTGTTTCAAAACCCGGGGAGTGTGGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGAGTGTGGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
OY	601	ACAGTGNAAAAAAGAAAAAAGAAAAA 625	
Db	601	ACAGTGNAAAAAAGAAAAAAGAAAAA 625	

```

RESULT 4
US-09-970-966-210
; Sequence 210, Application US/09970966
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ. ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-210

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Query Match	100.0%	Score 625	DB 36	Length 625
Best Local Similarity	100.0%	Pred. No. 6.3e-125		
Matches 625	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	AGTTCTCCTTGAGAGGACTGGCGCCGGGAGCCGGAAGAGACAAGGGCGCTGCACAAAGCG	60		
Db 1	AGTTCTCCTTGAGAGGACTGGCGCCGGGAGCCGGAAGAGACAAGGGCGCTGCACAAAGCG	60		
QY 61	GGCGCTGTGCGGTGTGAGTGGCGCATGTACGGCGGAGCGCTTCTGCTGGTGGCGTGTG	120		
Db 61	GGCGCTGTGCGGTGTGAGTGGCGCATGTACGGCGGAGCGCTTCTGCTGGTGGCGTGTG	120		
QY 121	CAGGCACAGGGCGGACAGCAGCAGTGTGCACGAAACCCGGCGAAATGCTGTGGAGGACAC	180		
Db 121	CAGGCACAGGGCGGACAGCAGCAGTGTGCACGAAACCCGGCGAAATGCTGTGGAGGACAC	180		

```
QY 181 CGGTACAGAGGCGGTGATGACGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 240
    |||
Db 181 CGGTACAGAGGCGGTGATGACGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 240
QY 241 GAGGATCATGTACGCCGGAAGTAGGACCTGCTCAGTGTGCTTGGGTTGGCCGACG 300
    |||
Db 241 GAGGATCATGTACGCCGGAAGTAGGACCTGCTCAGTGTGCTTGGGTTGGCCGACG 300
QY 301 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTACAAATCAGCCC 360
    |||
Db 301 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTACAAATCAGCCC 360
QY 361 TGGGACAGACGACGAGGAGGAGACAGAGAAAAACACAGCATGAGACACAG 420
    |||
Db 361 TGGGACAGACGACGAGGAGGAGACAGAGAAAAACACAGCATGAGACACAG 420
QY 421 TAAATGAATAAACATTAATATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 480
    |||
Db 421 TAAATGAATAAACATTAATATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 480
QY 481 GGTACCAATTTTTCAGTGTGACACTTGACAGCTTCTTTTCCAGACAGAGAAATT 540
    |||
Db 481 GGTACCAATTTTTCAGTGTGACACTTGACAGCTTCTTTTCCAGACAGAGAAATT 540
QY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGCATTAAATGCTTTAG 600
    |||
Db 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGCATTAAATGCTTTAG 600
QY 601 ACAGTGNNAAAAAAGAAAAA 625
    |||
Db 601 ACAGTGNNAAAAAAGAAAAA 625
```

## RESULT 5

```
US-10-212-677-210
; Sequence 210, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jlangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-210
```

```
Query Match 100.0%; Score 625; DB 42; Length 625;
Best Local Similarity 100.0%; Pred. No. 6,3e-125;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCTTTGCAAGAGACTGGCGCCGAGCGGAAGACACAGGCGCTGCACAAAGCG 60
    |||
Db 1 AGTTCCTTTGCAAGAGACTGGCGCCGAGCGGAAGACACAGGCGCTGCACAAAGCG 60
QY 61 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGACAGGCGCTTCTGTGGTGGCGTGTG 120
    |||
Db 61 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGACAGGCGCTTCTGTGGTGGCGTGTG 120
QY 121 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCCCGAAGAACTGCTGCGAGGACAC 180
    |||
```

```
Db 121 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCCCGAAGAACTGCTGCGAGGACAC 180
    |||
QY 181 CGGTACAGAGGCGGTGATGACGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 240
    |||
Db 181 CGGTACAGAGGCGGTGATGACGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 240
QY 241 GAGGATCATGTACGCCGGAAGTAGGACCTGCTCAGTGTGCTTGGGTTGGCCGACG 300
    |||
Db 241 GAGGATCATGTACGCCGGAAGTAGGACCTGCTCAGTGTGCTTGGGTTGGCCGACG 300
QY 301 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTACAAATCAGCCC 360
    |||
Db 301 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTACAAATCAGCCC 360
QY 361 TGGGACAGACGACGAGGAGGAGACAGAGAAAAACACAGCATGAGACACAG 420
    |||
Db 361 TGGGACAGACGACGAGGAGGAGACAGAGAAAAACACAGCATGAGACACAG 420
QY 421 TAAATGAATAAACATTAATATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 480
    |||
Db 421 TAAATGAATAAACATTAATATTTAGCCCTCTGTCTGTCTTACTGGCCAGAAAT 480
QY 481 GGTACCAATTTTTCAGTGTGACACTTGACAGCTTCTTTTCCAGACAGAGAAATT 540
    |||
Db 481 GGTACCAATTTTTCAGTGTGACACTTGACAGCTTCTTTTCCAGACAGAGAAATT 540
QY 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGCATTAAATGCTTTAG 600
    |||
Db 541 AACACTGTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGCATTAAATGCTTTAG 600
QY 601 ACAGTGNNAAAAAAGAAAAA 625
    |||
Db 601 ACAGTGNNAAAAAAGAAAAA 625
```

## RESULT 6

```
PCT-US01-45395-214
; Sequence 214, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-214
```

```
Query Match 97.0%; Score 606; DB 1; Length 1897;
Best Local Similarity 100.0%; Pred. No. 5,3e-121;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCCTTTGCAAGAGACTGGCGCCGAGCGGAAGACACAGGCGCTGCACAAAGCG 60
    |||
Db 1271 AGTTCCTTTGCAAGAGACTGGCGCCGAGCGGAAGACACAGGCGCTGCACAAAGCG 1330
QY 61 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGACAGGCGCTTCTGTGGTGGCGTGTG 120
    |||
Db 1331 GGGCGTGTGGTGGTGGAGTGGCATGTACGGGACAGGCGCTTCTGTGGTGGCGTGTG 1390
QY 121 CAGCGACAGGCGGACAGACAGCACTGCACGAACACCCCGAAGAACTGCTGCGAGGACAC 180
    |||
```



```
OY 181 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGGAG 240
|
|
|
Db 1451 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGGAG 1510
OY 241 GAGGATCATGTACGCCCGGGAAGTAGAGCTCGTCCAGTGTGCTGGTTGGCCGACG 300
|
|
|
Db 1511 GAGGATCATGTACGCCCGGGAAGTAGAGCTCGTCCAGTGTGCTGGTTGGCCGACG 1570
OY 301 CATGATCTCCGAAATCTGTTGGGATCCAGCATACGAGCCAAATGTACACAATCAGCCC 360
|
|
|
Db 1571 CATGATCTCCGAAATCTGTTGGGATCCAGCATACGAGCCAAATGTACACAATCAGCCC 1630
OY 361 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAACACAGCATGAGAACACAG 420
|
|
|
Db 1631 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAACACAGCATGAGAACACAG 1690
OY 421 TAAATGAATAAACCATAAATATTATAGCCCTCTGTTCTGTCTACTGCGCAGGAAT 480
|
|
|
Db 1691 TAAATGAATAAACCATAAATATTATAGCCCTCTGTTCTGTCTACTGCGCAGGAAT 1750
OY 481 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTCTTTTGGCCACAAGAGAGAAATT 540
|
|
|
Db 1751 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTCTTTTGGCCACAAGAGAGAAATT 1810
OY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
|
|
|
Db 1811 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1870
OY 601 ACAGTG 606
|
|
|
Db 1871 ACAGTG 1876
```

RESULT 9  
US-10-212-677-214

```
; Sequence 214, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chenuault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-214
```

Query Match 97.0%; Score 606; DB 42; Length 1897;  
Best Local Similarity 100.0%; Pred. No. 5,3e-121;  
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 AGTTCTCTTGCAGAGAGCTGGCGCCGGAGACGGGAAGCAACGGCGCTGCACAAAGG 60
|
|
|
Db 1271 AGTTCTCTTGCAGAGAGCTGGCGCCGGAGACGGGAAGCAACGGCGCTGCACAAAGG 1330
OY 61 GGGCGTGTGGTGTGAGTGGCATGTACGGCAGCGCTTCTGCTGTTGGCTGCTG 120
|
|
|
Db 1331 GGGCGTGTGGTGTGAGTGGCATGTACGGCAGCGCTTCTGCTGTTGGCTGCTG 1390
OY 121 CAGCGACAGCGGCGACAGACAGCCTGCAAGAACACCCCGCAAACTGCTGCGAGGACAC 180
|
|
|
Db 1391 CAGCGACAGCGGCGACAGACAGCCTGCAAGAACACCCCGCAAACTGCTGCGAGGACAC 1450
OY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGGAG 240
|
|
|
```

```
Db 1451 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGGAG 1510
OY 241 GAGGATCATGTACGCCCGGGAAGTAGAGCTCGTCCAGTGTGCTGGTTGGCCGACG 300
|
|
|
Db 1511 GAGGATCATGTACGCCCGGGAAGTAGAGCTCGTCCAGTGTGCTGGTTGGCCGACG 1570
OY 301 CATGATCTCCGAAATCTGTTGGGATCCAGCATACGAGCCAAATGTACACAATCAGCCC 360
|
|
|
Db 1571 CATGATCTCCGAAATCTGTTGGGATCCAGCATACGAGCCAAATGTACACAATCAGCCC 1630
OY 361 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAACACAGCATGAGAACACAG 420
|
|
|
Db 1631 TGGGACAGACAGCAGCAGAGGAGAGACAGAAAAACACAGCATGAGAACACAG 1690
OY 421 TAAATGAATAAACCATAAATATTATAGCCCTCTGTTCTGTCTACTGCGCAGGAAT 480
|
|
|
Db 1691 TAAATGAATAAACCATAAATATTATAGCCCTCTGTTCTGTCTACTGCGCAGGAAT 1750
OY 481 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTCTTTTGGCCACAAGAGAGAAATT 540
|
|
|
Db 1751 GGTACCAATTTTTCAGTGTGTGACTTGACAGCTCTTTTGGCCACAAGAGAGAAATT 1810
OY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
|
|
|
Db 1811 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1870
OY 601 ACAGTG 606
|
|
|
Db 1871 ACAGTG 1876
```

RESULT 10  
US-60-261-974-9/C

```
; Sequence 9, Application US/60261974
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001096-PROV
; CURRENT APPLICATION NUMBER: US/60/261,974
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 43729
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(43729)
; OTHER INFORMATION: n = A,T,C or G
US-60-261-974-9
```

Query Match 97.0%; Score 606; DB 70; Length 43729;  
Best Local Similarity 100.0%; Pred. No. 2,2e-121;  
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 AGTTCTCTTGCAGAGAGCTGGCGCCGGAGACGGGAAGCAACGGCGCTGCACAAAGG 60
|
|
|
Db 41583 AGTTCTCTTGCAGAGAGCTGGCGCCGGAGACGGGAAGCAACGGCGCTGCACAAAGG 41524
OY 61 GGGCGTGTGGTGTGAGTGGCATGTACGGCAGCGCTTCTGCTGTTGGCTGCTG 120
|
|
|
Db 41523 GGGCGTGTGGTGTGAGTGGCATGTACGGCAGCGCTTCTGCTGTTGGCTGCTG 41464
OY 121 CAGCGACAGCGGCGACAGACAGCCTGCAAGAACACCCCGCAAACTGCTGCGAGGACAC 180
|
|
|
Db 41463 CAGCGACAGCGGCGACAGACAGCCTGCAAGAACACCCCGCAAACTGCTGCGAGGACAC 41404
OY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGGAG 240
|
|
|
Db 41403 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGCTCCGAGAGGGGAG 41344
```



```

QY 241 GAGGATCATGTACGCGCGGAGAGTAGACCTGCTGAGTCTGCTTGGGTTTGGCCGACG 300
    |||||||
Db 41343 GAGGATCATGTACGCGCGGAGAGTAGACCTGCTGAGTCTGCTTGGGTTTGGCCGACG 41284
QY 301 CATGATCTCTCGGAATCTGGTGGGATCCAGATACGGCCAAATGTACACAAATACGCC 360
    |||||||
Db 41283 CATGATCTCTCGGAATCTGGTGGGATCCAGATACGGCCAAATGTACACAAATACGCC 41224
QY 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||||||
Db 41223 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 41164
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGGCCAGAAAT 480
    |||||||
Db 41163 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGGCCAGAAAT 41104
QY 481 GGTACCAATTTTTCAGTGTGAGTGTGACCTCTTTTGCACACAGACAGAGAAATTT 540
    |||||||
Db 41103 GGTACCAATTTTTCAGTGTGAGTGTGACCTCTTTTGCACACAGACAGAGAAATTT 41044
QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGTTAAAGAAAGACATTAATGCTTTAG 600
    |||||||
Db 41043 AACACTGTTTCAAAACCCGGGGAGTGTGTTAAAGAAAGACATTAATGCTTTAG 40984
QY 601 ACAGTG 606
    |||||||
Db 40983 ACAGTG 40978

```

```

RESULT 11
PCT-US01-18569-111
: Sequence 111, Application PC/TUS0118569
: GENERAL INFORMATION:
: APPLICANT: Human Genome Sciences, Inc.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: P133PCT
: CURRENT APPLICATION NUMBER: PCT/US01/18569
: PRIORITY FILING DATE: 2001-06-07
: PRIOR APPLICATION NUMBER: 60/209,467
: PRIOR FILING DATE: 2000-06-07
: NUMBER OF SEQ ID NOS: 4360
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 111
: LENGTH: 1608
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (18)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (22)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (32)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (87)
: OTHER INFORMATION: n equals a,t,g, or c
PCT-US01-18569-111

```

```

Query Match      88.8%; Score 555; DB 1; Length 1608;
Best Local Similarity 99.8%; Pred. No. 4.6e-110;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGTTCTCTTGCAGAGACTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
    |||||||
Db 925 AGTTCTCTTGCAGAGACTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 984
QY 61 GCGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
    |||||||
Db 985 GCGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1044

```

```

QY 121 CAGCGACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
    |||||||
Db 1045 CAGCGACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1104
QY 181 CGTGTACAGAGAGCGGGTGTGATGACGAGTGAAGTGAAGAAAGAGTGTCCGAGAGAGAGAG 240
    |||||||
Db 1105 CGTGTACAGAGAGCGGGTGTGATGACGAGTGAAGTGAAGAAAGAGTGTCCGAGAGAGAGAG 1164
QY 241 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
    |||||||
Db 1165 GAGGATCATGTACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1224
QY 301 CATGATCTCTCGGAATCTGGTGGGATCCAGATACGGCCAAATGTACACAAATACGCC 360
    |||||||
Db 1225 CATGATCTCTCGGAATCTGGTGGGATCCAGATACGGCCAAATGTACACAAATACGCC 1284
QY 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||||||
Db 1285 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1344
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGGCCAGAAAT 480
    |||||||
Db 1345 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTCTGTCTTACTGGCCAGAAAT 1404
QY 481 GGTACCAATTTTTCAGTGTGAGTGTGACCTCTTTTGCACACAGACAGAGAAATTT 540
    |||||||
Db 1405 GGTACCAATTTTTCAGTGTGAGTGTGACCTCTTTTGCACACAGACAGAGAAATTT 1464
QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGTTAAAGAAAGACATTAATGCTTTAG 600
    |||||||
Db 1465 AACACTGTTTCAAAACCCGGGGAGTGTGTTAAAGAAAGACATTAATGCTTTAG 1524
QY 601 ACAGTG 606
    |||||||
Db 1525 ACAGTG 1530

```

```

RESULT 12
US-10-264-049-111
: Sequence 111, Application US/10264049
: GENERAL INFORMATION:
: APPLICANT: Biase et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P133P1
: CURRENT APPLICATION NUMBER: US/10/264,049
: PRIORITY FILING DATE: 2002-10-04
: PRIOR APPLICATION NUMBER: PCT/US01/18569
: PRIOR FILING DATE: 2001-06-07
: PRIOR APPLICATION NUMBER: US 60/209,467
: PRIOR FILING DATE: 2000-06-07
: NUMBER OF SEQ ID NOS: 4360
: SOFTWARE: PatentIn Ver. 3.1
: SEQ ID NO 111
: LENGTH: 1608
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (18)..(18)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (22)..(22)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (32)..(32)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (87)..(87)
: OTHER INFORMATION: n equals a,t,g, or c

```

```

QY 1 AGTTCTCTTGCAGAGACTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
    |||||||
Db 925 AGTTCTCTTGCAGAGACTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 984
QY 61 GCGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
    |||||||
Db 985 GCGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1044

```

US-10-264-049-111

Query Match	88.8%	Score 555;	DB 43;	length 1608;
Best Local Similarity	99.8%	Pred. No. 4.6e-110;		
Matches 605; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	AGTTTTCCTTTTGCAGAGACTGTGGCGCCGGGACCCGGAAGAGCAACGGGCGCTCTCACAAAGCG	60
Db	925	AGTTTTCCTTTTGCAGAGAGACTGGGGCCGGGACCCGGAAGAGCAACGGGCGCTCTCACAAAGCG	984
QY	61	GGGGCTGTGGTGTGTGGATGTGGGCATGTACGGGCGGAGGGGCTTCTGTGGTTGGGGTGTG	120
Db	985	GGGGCTGTGGTGTGTGGATGTGGGCATGTACGGGCGGAGGGGCTTCTGTGGTTGGCGTGTG	1044
QY	121	CAGCGACAGCGCGGCACACAGCACCTGTGCAGAACACCCGCCGMAACTGCTCGAGAGACAC	180
Db	1045	CAGCGACAGCGCGGCACACAGCACCTGTGCAGAACACCCGCCGMAACTGCTCGAGAGACAC	1104
QY	181	CGGTACAGAGAGGGGGGTATATGACGGAGCTGAGTGAAGAAAAAGTCCTCGAGAAAGGGAG	240
Db	1105	CGGTACAGAGAGGGGGGTATATGACGGAGCTGAGTGAAGAAAAAGTCCTCGAGAAAGGGAG	1164
QY	241	GAGGATCATGTACGCCCGCGGAAGTAGGAGCTGTGTCCAGTCTGTGGTTTGGCCGACG	300
Db	1165	GAGGATCATGTACGCCCGCGGAAGTAGGAGCTGTGTCCAGTCTGTGGTTTGGCCGACG	1224
QY	301	CATGATCTCTCCGAATCGTGGTGGGCATGTCCAGATACGGGCATGTGCACAAATCAGGCC	360
Db	1225	CATGATCTCTCCGAATCTGTTGGTGGGCATCCAGCATACGGGCATGTGCACAAATCAGGCC	1284
QY	361	TGGGCACACACGAGCAGAGAGGGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAG	420
Db	1285	TGGGCACACACGAGCAGAGAGGGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAG	1344
QY	421	TAAATGAATTAACACATTAATAATATTAGAGCCCTCTGTCTGTGTCTTACTGGCCAGAGAAAT	480
Db	1345	TAAATGAATTAACACATTAATAATAATTAGAGCCCTCTGTCTGTGTCTTACTGGCCAGAGAAAT	1404
QY	481	GGTACCAATTTTTCAGTGTGGTGGACTTGACAGCTTCTTTTGGCCAAAGCAAGAGAAATTT	540
Db	1405	GGTACCAATTTTTCAGTGTGGTGGACTTGACAGCTTCTTTTGGCCAAAGCAAGAGAAATTT	1464
QY	541	AACACTCTTTTCAAAACCCGGGGAGATTGGCTGTGTTTAAAGAAAGACCATTAATAGCTTTAG	600
Db	1465	AACACTCTTTTCAAAACCCGGGGAGATTGGCTGTGTTTAAAGAAAGACCATTAATAGCTTTAG	1524
QY	601	ACAAGTG 606	
Db	1525	ACAAGTG 1530	

RESULT 13  
US-10-108-260A-197  
; Sequence 197, Application US/10108260A

Query Match	88.8%	Score 555	DB 40	Length 1832
Best Local Similarity	99.8%	Pred.No. 4.4e-110		
Matches 605; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY 1 AGTTCTCTTGCAGAGGACTGGCCGCCGACGCGAAGAGCAACGGGGCTGCACAAAGCG 60

Db 1226 AGTTCTCTTCGAGAGGACTGCGCCGGGAGCCGAGAGCAACGGGCGCTTCACAAAGCG 1285

61 GGGCTGTCGGTGGTGAAGTCCCATGTACGGCAGCGCTTCTCGTGGTTGGCGTGTG 120

Db 1286 GGGCGTGTGGTGGAGTGGCGATGTACGCGCAGCGCTTCTCGTGGTTGGCGTCTG 1345

121 CAGCGACAGCGCGGACGACAGCACTGTGACGAACACCCGCCGAACCTGCTGGAGGACAC 180

Db 1346 CAGCCACAGCGCGGACGACAGCACCCTGCACGAACACCCCGCGAAACTGCTGCGAGGACAC 1405

181 CGTGTACAGGACGGGGTTGATGACCGAGCTAGAGGTAGAAAACTCTCCGAGAGAGGGAG 240

Db 1406 CGTGTACAGGAGCGGGTTCATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAACGGGAG 1465

[illegible]

Db 1466 GAGGACATGAACGCCCCGGAAGTAGGACCTCGTCCAGTCGTGCTTGGGTTGGCCCAAC 1523

[illegible][illegible]

Ph 1585 TGGGCGACACCAAGCAGAGGGAGGACAGAGAAAGAAAAACACAGCATGAGAACACAG 1645

421 TAAATGATAAACCATAAATATTTAGCCCCCTCTGTTCTGTGCTTACTGCCAGGAAT 480

Db 1646 TAAATGATATAAACCATTAATTTAGCCCCCTGTCTGTGCTTACTGGCCAGCAAT 1705

481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCACAGACAGAGAAATTT 540

D5 1706 GGTACCAATTTTCAGTGTGGACCTTGACACCTTCTTTTGGCCACAAGCAGAGAAATT 1765

541 AACACTGTTCAAAACCCGGGGGAGTTGGCTGCTTAAGAAGACCATTAATGCTTAG 600

Db 1766 AACACGTTCAAACCCGGGGAGTTGGCTGTCGTTAAAGAAAGACATTAAATGCTTTAG 1825

QY 601 ACAGTG 606  
|||||

Db 1826 A C A G T G 1831

US-10-208-408-26  
US-10-208-408-26  
; Sequence 26, Application US/10208408  
GENERAL INFORMATION.

```

; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 227484.13
US-10-208-408-26

```

```

Oy      1 AGTTCCTCCCTTGACAGAGACTGTGGCGCCGGGAGCGGAAAGCAACGGGGCGCTGCACAAACG 60
        |||||
Db      1141 AGTTCCTCCCTTGACAGAGACTGTGGCGCCGGGAGCGGAAAGCAACGGGGCGCTGCACAAACG 1200

```

QY	61	GGCGCTGTGGTGTGGAGTGGCCATGTACGGGAGCGCTTCGAGTTGGGGTGTG	120
Db	1201	GGCGCTGTGGTGTGGAGTGGCCATGTACGGGAGCGCTTCGAGTTGGGGTGTG	1260
QY	121	CAGCGACAGGGCGGACACACAGCACTTGCACGAACACCCGGCGAAACTGTCCGAGACAC	180
Db	1261	CAGCGACAGGGCGGACACACAGCACTTGCACGAACACCCGGCGAAACTGTCCGAGACAC	1320
QY	181	CGTGTACAGAGCGGGGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAAAGGAG	240
Db	1321	CGTGTACAGAGCGGGGTGATGACCGAGCTGAGGTAGAAAAAGCTCTCCGAGAAAGGAG	1380
QY	241	GAGGATCATGTACGGCCGGAAGAGGACCTGTCGACATCGGCTTGGGTTGGCCGACG	300
Db	1381	GAGGATCATGTACGGCCGGAAGAGGACCTGTCGACATCGGCTTGGGTTGGCCGACG	1440
QY	301	CATGATCCTCCGAATCTGTTGGGCATCCAGCATACCGCCAAATGTCAACAAATCAGCC	360
Db	1441	CATGATCCTCCGAATCTGTTGGGCATCCAGCATACCGCCAAATGTCAACAAATCAGCC	1500
QY	361	TGGCGCAACACGAGCGAGGAGAGACAGAGAAAGAAAAACACAGCATGAGAACACAG	420
Db	1501	TGGCGCAACACGAGCGAGGAGAGAGACAGAGAAAGAAAAACACAGCATGAGAACACAG	1560
QY	421	TAATGCAATAAAAACATATAAATTTATAGCCCTGTCTGTGCTTACTGGCCAGGAAT	480
Db	1561	TAATGCAATAAAAACATATAAATTTATAGCCCTGTCTGTGCTTACTGGCCAGGAAT	1620
QY	481	GGTACCAATTTTTCAGTGTGGAAGCTTGACAGCTTCTTTGCCACAAACAGAGAGAATTT	540
Db	1621	GGTACCAATTTTTCAGTGTGGAAGCTTGACAGCTTCTTTGCCACAAACAGAGAGAATTT	1680
QY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTTAATGCTTTAG	600
Db	1681	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTTAATGCTTTAG	1740
QY	601	ACAGTG 606	
Db	1741	ACAGTG 1746	

```

RESULT 15
US-60-295-262-26
: Sequence 26, Application US/60295262
: GENERAL INFORMATION:
: APPLICANT: Schebye, Xiao Min
: TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
: TITLE OF INVENTION: GAMMA ACONIST
: FILE REFERENCE: PA-0048 P
: CURRENT APPLICATION NUMBER: US/60/295,262
: CURRENT FILING DATE: 2001-06-01
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: PERL Program
: SEQ ID NO 26
: LENGTH: 1866
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No: 227484.13
US-60-295-262-26

```

Query Match	88.8%	Score 555	DB 733	Length 1866
Best Local Similarity	99.8%	Pred. No. 4.4e-110		
Matches 605	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	AGTTCCTTCAGAGGACTGGCGCCGGGACCCGGAAGACCAACGGGCGCTGCACAAAGCG	60	
Db	1141	AGTTCCTTCAGAGGACTGGCGCCGGGACCCGGAAGACCAACGGGCGCTGCACAAAGCG	1200	
OY	61	GGCGCTTCGGGTGCTGGAAGTGGGCAATGACGGCAGGCGCTTCGTGGTGGCTGCG	120	

Db	1201	GGCGCTGTGGTGTGGAGTGGCCATGTATACGCCAGGCGCTTTCGTTGGGTGTGTG	1260
OY	121	CAGCCACAGGCGGCACACACAGCACTTGCACAAACCCCGCGAAATCTGTCCAGAGAC	180
Db	1261	CAGCGCACAGCGGCACACAGCACTTGCACAAACCCCGCGAAATCTGTCCAGAGAC	1320
OY	181	CGTGTACAGAGAGGGGTGTGTACCGAGCTGAGGTGAAAAAGTCTCCGAAAGGGAG	240
Db	1321	CGTGTACAGAGAGGGGTGTGTACCGAGCTGAGGTGAAAAAGTCTCCGAAAGGGAG	1380
OY	241	GAGGATCATGTACGCCCGGAAGTAGACCTCTTCAAGTCGTGTGGTTTGCCGAC	300
Db	1381	GAGGATCATGTACGCCCGGAAGTAGACCTCTTCAAGTCGTGTGGTTTGCCGAC	1440
OY	301	CATTGATCTCCGATCTGGTTGGGCACTCCAGCATACGGCCAAATGTCAACAATCAGCCC	360
Db	1441	CATTGATCTCCGATCTGGTTGGGCACTCCAGCATACGGCCAAATGTCAACAATCAGCCC	1500
OY	361	TGGGACAGACGACGACGAGGAGGAGACACAGAAAAACACACCATGAGAACACAG	420
Db	1501	TGGGACAGACGACGACGAGGAGGAGACACAGAAAAACACACCATGAGAACACAG	1560
OY	421	TAAATGAATAAACCATAAATATTATAGCCCTCTGTCTGTCTTACTGCGCCAGAAAT	480
Db	1561	TAAATGAATAAACCATAAATATTATAGCCCTCTGTCTGTCTTACTGCGCCAGAAAT	1620
OY	481	GGTACCAATTTTTCAGTGTGGACCTTGACAGCTTCTTTGCCACAAAGCAGAGAAATTT	540
Db	1621	GGTACCAATTTTTCAGTGTGGACCTTGACAGCTTCTTTGCCACAAAGCAGAGAAATTT	1680
OY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGCATTAAATGCTTTAG	600
Db	1681	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGCATTAAATGCTTTAG	1740
OY	601	ACAGTG 606	
Db	1741	ACAGTG 1746	

```

RESULT 16
US-60-308-868-26
: Sequence 26, Application US/60308868
: GENERAL INFORMATION:
: APPLICANT: Schedye, Xiao Min
: TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
: FILE REFERENCE: PA-0048-1 P
: CURRENT APPLICATION NUMBER: US/60/308,868
: CURRENT FILING DATE: 2001-07-30
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PERL Program
: SEQ ID NO 26
: LENGTH: 1866
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 227484.13
: US-60-308-868-26

```

Query Match	88.8%	Score 555	DB 74	Length 1866
Best Local Similarity	99.8%	Pred. No. 4	4E-110	
Matches 605	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	AGTTCCTCTGTCAGAGGACTGGCGCCGGGAGCGCGAAGACAAACGGCGCTGCACAAAGCG	60	
Db	1141	AGTTCCTCTGTCAGAGGACTGGCGCCGGGAGCGCGAAGACAAACGGCGCTGCACAAAGCG	1200	
QY	61	GGCGCTGTGCGTGTGTGAGTGCACATGTACGCGCAGGCGCTCTCGTGTGCGCTGCGT	120	
Db	1201	GGCGCTGTGCGTGTGTGAGTGCACATGTACGCGCAGGCGCTCTCGTGTGCGCTGCGT	1260	
QY	121	CAGGACAGCGGGCAGCAGCAGCACTGCACGAAACCGCGCGAANCTGCTGGAGACAC	180	

Db 1261 CAGCGACAGGCGGACAGACAGACCTGACAGAAACCCCGCAAACTGCTGCGAGACAC 1320  
Qy 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTGTCGAGAAAGGGAG 240  
Db 1321 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTGTCGAGAAAGGGAG 1380  
Qy 241 GAGGATCATGTACGCGCCGGAAGTAGACCTGTCAGTCGTCGTTGGCTTGGCCGACG 300  
Db 1381 GAGGATCATGTACGCGCCGGAAGTAGACCTGTCAGTCGTCGTTGGCTTGGCCGACG 1440  
Qy 301 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCACAAATCAGCCC 360  
Db 1441 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCACAAATCAGCCC 1500  
Qy 361 TGGGACAGACAGACGAGGAGGAGACAGAAAAAACAACGATGAGAACACAG 420  
Db 1501 TGGGACAGACAGACGAGGAGGAGACAGAAAAAACAACGATGAGAACACAG 1560  
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTGTTGCTGCTTACTGCGCAGGAAT 480  
Db 1561 TAAATGAATAAACATTAATATTTAGCCCTGTTGCTGCTTACTGCGCAGGAAT 1620  
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAGACAGAAATTT 540  
Db 1621 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAGACAGAAATTT 1680  
Qy 541 AACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTAG 600  
Db 1681 AACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTAG 1740  
Qy 601 ACAAGT 606  
Db 1741 ACAAGT 1746

RESULT 17  
US-09-371-168-7188  
; Sequence 7188, Application US/09371168  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, M. Alexandra  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
; FILE REFERENCE: HUMAN BRAIN LIBRARY  
; CURRENT APPLICATION NUMBER: US/09/371,168  
; EARLIER FILING DATE: 1999-08-10  
; EARLIER APPLICATION NUMBER: 60/095,907  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/103,145  
; NUMBER OF SEQ ID NOS: 8285  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 7188  
; LENGTH: 1917  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-371-168-7188

Query Match 88.8%; Score 555; DB 17; Length 1917;  
Best Local Similarity 99.8%; Pred. No. 4.4e-110;  
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCTCTTGCAGAGAGACTGGCGCGGAGACGGAAGACAGCGGCGCTGCACAAAGC 60  
Db 1286 AGTTCTCTTGCAGAGAGACTGGCGCGGAGACGGAAGACAGCGGCGCTGCACAAAGC 1345  
Qy 61 GCGCGTGTGCTGTGAGTGGCGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTCTG 120  
Db 1346 GCGCGTGTGCTGTGAGTGGCGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTCTG 1405  
Qy 121 CAGCGACAGGCGGACAGACAGACCTGACAGAAACACCGCGCAAACTGCTGCGAGGAC 180  
Db 1406 CAGCGACAGGCGGACAGACAGACCTGACAGAAACACCGCGCAAACTGCTGCGAGGAC 1465

Qy 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTGTCGAGAAAGGGAG 240  
Db 1466 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTGTCGAGAAAGGGAG 1525  
Qy 241 GAGGATCATGTACGCGCCGGAAGTAGACCTGTCAGTCGTCGTTGGCTTGGCCGACG 300  
Db 1526 GAGGATCATGTACGCGCCGGAAGTAGACCTGTCAGTCGTCGTTGGCTTGGCCGACG 1585  
Qy 301 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCACAAATCAGCCC 360  
Db 1586 CATGATCTCCGAATCTGTTGGGATCCAGCATACGCGCAATGTCACAAATCAGCCC 1645  
Qy 361 TGGGACAGACAGACGAGGAGGAGACAGAAAAAACAACGATGAGAACACAG 420  
Db 1646 TGGGACAGACAGACGAGGAGGAGACAGAAAAAACAACGATGAGAACACAG 1705  
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTGTTGCTGCTTACTGCGCAGGAAT 480  
Db 1706 TAAATGAATAAACATTAATATTTAGCCCTGTTGCTGCTTACTGCGCAGGAAT 1765  
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAGACAGAAATTT 540  
Db 1766 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGGCCACAGACAGAAATTT 1825  
Qy 541 AACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTAG 600  
Db 1826 AACACGTGTTCAAAACCCGGGGAGTGGCTGTGTTAAGAAAGACATTAATGCTTTAG 1885  
Qy 601 ACAAGT 606  
Db 1886 ACAAGT 1891

RESULT 18  
US-09-644-873-9077  
; Sequence 9077, Application US/09644873  
; GENERAL INFORMATION:  
; APPLICANT: Siles-Santiago, Immaculada  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600,1169-001  
; CURRENT APPLICATION NUMBER: US/09/644,873  
; EARLIER FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: 60/151,064  
; EARLIER FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 11286  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 9077  
; LENGTH: 1917  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-644-873-9077

Query Match 88.8%; Score 555; DB 25; Length 1917;  
Best Local Similarity 99.8%; Pred. No. 4.4e-110;  
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCTCTTGCAGAGAGACTGGCGCGGAGACGGAAGACAGCGGCGCTGCACAAAGC 60  
Db 1286 AGTTCTCTTGCAGAGAGACTGGCGCGGAGACGGAAGACAGCGGCGCTGCACAAAGC 1345  
Qy 61 GCGCGTGTGCTGTGAGTGGCGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTCTG 120  
Db 1346 GCGCGTGTGCTGTGAGTGGCGCATGTACGCGCAGGCGCTTCTGCTGTTGGCGTCTG 1405  
Qy 121 CAGCGACAGGCGGACAGACAGACCTGACAGAAACACCGCGCAAACTGCTGCGAGGAC 180  
Db 1406 CAGCGACAGGCGGACAGACAGACCTGACAGAAACACCGCGCAAACTGCTGCGAGGAC 1465  
Qy 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTGTCGAGAAAGGGAG 240  
Db 1466 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGTAGAAAAAGCTGTCGAGAAAGGGAG 1525

QY 241 GAGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTGTGCTTGGTTGGCCGACG 300  
| | | | |  
Db 1526 GAGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTGTGCTTGGTTGGCCGACG 1585  
QY 301 CATGATCTCCGAATCTGTGGGCTATCAGCCATACGCGCAATGTACAAATCAGCCC 360  
| | | | |  
Db 1586 CATGATCTCCGAATCTGTGGGCTATCAGCCATACGCGCAATGTACAAATCAGCCC 1645  
QY 361 TGGGACAGACGAGAGGAGAGAGACAGAAAGAAAACAGAGCTGAGAACACAG 420  
| | | | |  
Db 1646 TGGGACAGACGAGAGGAGAGAGAGACAGAAAGAAAACAGAGCTGAGAACACAG 1705  
QY 421 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTTACTGCGCAGGAAT 480  
| | | | |  
Db 1706 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTTACTGCGCAGGAAT 1765  
QY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGCAAGAAATTT 540  
| | | | |  
Db 1766 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGCAAGAAATTT 1825  
QY 541 AACACTGTTTCAAAACCGGGGAGTGTGCTGTAAAGAAAGACCATTAATGCTTTAG 600  
| | | | |  
Db 1826 AACACTGTTTCAAAACCGGGGAGTGTGCTGTAAAGAAAGACCATTAATGCTTTAG 1885  
QY 601 ACAGTG 606  
| | | | |  
Db 1886 ACAGTG 1891

RESULT 19  
US-09-652-109-9370  
; Sequence 9370, Application us/09652109  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1180-001  
; CURRENT APPLICATION NUMBER: US/09/652.109  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR FILING DATE: 1999-08-30  
; NUMBER OF SEQ ID NOS: 10105  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9370  
; LENGTH: 1917  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-109-9370

Query Match 88.8%; Score 555; DB 25; Length 1917;  
Best Local Similarity 99.8%; Pred. No. 4.4e-110;  
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGTTCTCCTTGCAGAGACTGGCGCGGAGCGCAAGACGAGGCGCTGCACAAAGCG 60  
| | | | |  
Db 1286 AGTTCTCCTTGCAGAGACTGGCGCGGAGCGCAAGACGAGGCGCTGCACAAAGCG 1345  
QY 61 GGGCGTGTGCGTGTGAGTGCAGTATGACGCGAGGCGCTTCGCTGCTGGCTGCTG 120  
| | | | |  
Db 1346 GGGCGTGTGCGTGTGAGTGCAGTATGACGCGAGGCGCTTCGCTGCTGGCTGCTG 1405  
QY 121 CAGCGACAGCGCGCAGACAGACCTGCAGCAACACCGCGGAAATCTCTCGAGAGAC 180  
| | | | |  
Db 1406 CAGCGACAGCGCGCAGACAGACCTGCAGCAACACCGCGGAAATCTCTCGAGAGAC 1465  
QY 181 CGGTACAGAGAGGGGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAGGAG 240  
| | | | |  
Db 1466 CGGTACAGAGAGGGGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAGGAG 1525  
QY 241 GAGGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTGTGCTTGGTTGGCCGACG 300  
| | | | |  
Db 1526 GAGGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTGTGCTTGGTTGGCCGACG 1585

QY 301 CATGATCTCCGAATCTGTGGGCTATCAGCCATACGCGCAATGTACAAATCAGCCC 360  
| | | | |  
Db 1586 CATGATCTCCGAATCTGTGGGCTATCAGCCATACGCGCAATGTACAAATCAGCCC 1645  
QY 361 TGGGACAGACGAGAGGAGAGACAGAGAAAGAAAACAGAGCTGAGAACACAG 420  
| | | | |  
Db 1646 TGGGACAGACGAGAGGAGAGAGACAGAGAAAGAAAACAGAGCTGAGAACACAG 1705  
QY 421 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTTACTGCGCAGGAAT 480  
| | | | |  
Db 1706 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTTACTGCGCAGGAAT 1765  
QY 481 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGCAAGAAATTT 540  
| | | | |  
Db 1766 GGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAAAGCAAGAAATTT 1825  
QY 541 AACACTGTTTCAAAACCGGGGAGTGTGCTGTAAAGAAAGACCATTAATGCTTTAG 600  
| | | | |  
Db 1826 AACACTGTTTCAAAACCGGGGAGTGTGCTGTAAAGAAAGACCATTAATGCTTTAG 1885  
QY 601 ACAGTG 606  
| | | | |  
Db 1886 ACAGTG 1891

RESULT 20  
US-09-652-121-6191  
; Sequence 6191, Application us/09652121  
; GENERAL INFORMATION:  
; APPLICANT: Distefano, Peter  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1188-001  
; CURRENT APPLICATION NUMBER: US/09/652.121  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR FILING DATE: 1999-08-30  
; NUMBER OF SEQ ID NOS: 7615  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6191  
; LENGTH: 1917  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-121-6191

Query Match 88.8%; Score 555; DB 25; Length 1917;  
Best Local Similarity 99.8%; Pred. No. 4.4e-110;  
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGTTCTCCTTGCAGAGACTGGCGCGGAGCGCAAGACGAGGCGCTGCACAAAGCG 60  
| | | | |  
Db 1286 AGTTCTCCTTGCAGAGACTGGCGCGGAGCGCAAGACGAGGCGCTGCACAAAGCG 1345  
QY 61 GGGCGTGTGCGTGTGAGTGCAGTATGACGCGAGGCGCTTCGCTGCTGGCTGCTG 120  
| | | | |  
Db 1346 GGGCGTGTGCGTGTGAGTGCAGTATGACGCGAGGCGCTTCGCTGCTGGCTGCTG 1405  
QY 121 CAGCGACAGCGCGCAGACAGACCTGCAGCAACACCGCGGAAATCTCTCGAGAGAC 180  
| | | | |  
Db 1406 CAGCGACAGCGCGCAGACAGACCTGCAGCAACACCGCGGAAATCTCTCGAGAGAC 1465  
QY 181 CGGTACAGAGAGGGGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAGGAG 240  
| | | | |  
Db 1466 CGGTACAGAGAGGGGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAGAGGAG 1525  
QY 241 GAGGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTGTGCTTGGTTGGCCGACG 300  
| | | | |  
Db 1526 GAGGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTGTGCTTGGTTGGCCGACG 1585  
QY 301 CATGATCTCCGAATCTGTGGGCTATCAGCCATACGCGCAATGTACAAATCAGCCC 360  
| | | | |  
Db 1586 CATGATCTCCGAATCTGTGGGCTATCAGCCATACGCGCAATGTACAAATCAGCCC 1645



Db 1706 TAAATTAATTAACCATTAATAATTTAGCCCTCTGTTGCTTACTGGCCAGGAAT 1765  
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 540  
Db 1766 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 1825  
Qy 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACATTAAATGCTTTAG 600  
Db 1826 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACATTAAATGCTTTAG 1885  
Qy 601 ACAGTG 606  
Db 1886 ACAGTG 1891

## RESULT 23

US-09-652-914-8473  
; Sequence 8473, Application US/09652914  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1193-001  
; CURRENT APPLICATION NUMBER: US/09/652,914  
; PRIOR FILING DATE: 2000-08-31  
; NUMBER OF SEQ ID NOS: 9677  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8473  
; LENGTH: 1917  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-914-8473

Query Match 88.8% Score 555; DB 25; Length 1917;  
Best Local Similarity 99.8% Pred. No. 4,4e-110;  
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCCTCTTGCAGAGACTGGCCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 60  
Db 1286 AGTTCCTCTTGCAGAGACTGGCCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 1345  
Qy 61 GCGCCTGTGCGTGGTGGAGTGCATGTACGCGCAGCGCTTCTGCTGGTGGCGTGTG 120  
Db 1346 GCGCCTGTGCGTGGTGGAGTGCATGTACGCGCAGCGCTTCTGCTGGTGGCGTGTG 1405  
Qy 121 CAGGACAGCGCGGAGCAGACACCTGACAGAACCCGCGCAACTGCTGGAGAGACAC 180  
Db 1406 CAGGACAGCGCGGAGCAGACACCTGACAGAACCCGCGCAACTGCTGGAGAGACAC 1465  
Qy 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAACGTCGCGAAGAGGAG 240  
Db 1466 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAACGTCGCGAAGAGGAG 1525  
Qy 241 GAGGATATGTACCCCGGAGAGTAGACCTGTCAGTCGCTGCTGGGTTGGCCGACG 300  
Db 1526 GAGGATATGTACCCCGGAGAGTAGACCTGTCAGTCGCTGCTGGGTTGGCCGACG 1585  
Qy 301 CATGATCTCTCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATCAGCCC 360  
Db 1586 CATGATCTCTCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATCAGCCC 1645  
Qy 361 TGGGACAGACAG 420  
Db 1646 TGGGACAGACAG 1705  
Qy 421 TAAATGAATTAACCATTAATAATTTAGCCCTCTGTTGCTTACTGGCCAGGAAT 480  
Db 1706 TAAATGAATTAACCATTAATAATTTAGCCCTCTGTTGCTTACTGGCCAGGAAT 1765  
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 540  
Db 1766 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 1825

Db 1766 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 1825  
Qy 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACATTAAATGCTTTAG 600  
Db 1826 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAGAAAGACATTAAATGCTTTAG 1885  
Qy 601 ACAGTG 606  
Db 1886 ACAGTG 1891

## RESULT 24

US-09-652-917-2477  
; Sequence 2477, Application US/09652917  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1170-001  
; CURRENT APPLICATION NUMBER: US/09/652,917  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 3855  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2477  
; LENGTH: 1917  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-917-2477

Query Match 88.8% Score 555; DB 25; Length 1917;  
Best Local Similarity 99.8% Pred. No. 4,4e-110;  
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGTTCCTCTTGCAGAGACTGGCCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 60  
Db 1286 AGTTCCTCTTGCAGAGACTGGCCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCG 1345  
Qy 61 GCGCCTGTGCGTGGTGGAGTGCATGTACGCGCAGCGCTTCTGCTGGTGGCGTGTG 120  
Db 1346 GCGCCTGTGCGTGGTGGAGTGCATGTACGCGCAGCGCTTCTGCTGGTGGCGTGTG 1405  
Qy 121 CAGGACAGCGCGGAGCAGACACCTGACAGAACCCGCGCAACTGCTGGAGAGACAC 180  
Db 1406 CAGGACAGCGCGGAGCAGACACCTGACAGAACCCGCGCAACTGCTGGAGAGACAC 1465  
Qy 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAACGTCGCGAAGAGGAG 240  
Db 1466 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAACGTCGCGAAGAGGAG 1525  
Qy 241 GAGGATATGTACCCCGGAGAGTAGACCTGTCAGTCGCTGCTGGGTTGGCCGACG 300  
Db 1526 GAGGATATGTACCCCGGAGAGTAGACCTGTCAGTCGCTGCTGGGTTGGCCGACG 1585  
Qy 301 CATGATCTCTCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATCAGCCC 360  
Db 1586 CATGATCTCTCGAATCTGGTGGGATCCAGCATACGGCAATGTACAAACATCAGCCC 1645  
Qy 361 TGGGACAGACAG 420  
Db 1646 TGGGACAGACAG 1705  
Qy 421 TAAATGAATTAACCATTAATAATTTAGCCCTCTGTTGCTTACTGGCCAGGAAT 480  
Db 1706 TAAATGAATTAACCATTAATAATTTAGCCCTCTGTTGCTTACTGGCCAGGAAT 1765  
Qy 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 540  
Db 1766 GGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCACAGAAGAGAAATTT 1825





QY 481 GGTACCAATTTTTCAGTGTGACTTGCACAGCTTCTTTTCCACAAGACAAGAAATT 540  
 |||||||  
 Db 1767 GGTACCAATTTTTCAGTGTGACTTGCACAGCTTCTTTTCCACAAGACAAGAAATT 1826  
 QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600  
 |||||||  
 Db 1827 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1886  
 QY 601 ACACTG 606  
 |||||||  
 Db 1887 ACACTG 1892

RESULT 27  
 ; Sequence 4454, Application US/09808383  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geating, David P.  
 ; APPLICANT: Holtzman, Douglas A.  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
 ; FILE REFERENCE: 1600.1046-002  
 ; CURRENT APPLICATION NUMBER: US/09/808.383  
 ; CURRENT FILING DATE: 2001-03-13  
 ; PRIOR APPLICATION NUMBER: US 09/397,022  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: US 60/100,465  
 ; PRIOR FILING DATE: 1998-09-15  
 ; PRIOR APPLICATION NUMBER: US 60/106,443  
 ; PRIOR FILING DATE: 1998-10-30  
 ; PRIOR APPLICATION NUMBER: US 60/107,257  
 ; PRIOR FILING DATE: 1998-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/126,906  
 ; PRIOR FILING DATE: 1999-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/132,099  
 ; PRIOR FILING DATE: 1999-04-30  
 ; NUMBER OF SEQ ID NOS: 5775  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 4454  
 ; LENGTH: 1918  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-808-383-4454

Query Match 88.8%; Score 555; DB 31; Length 1918;  
 Best Local Similarity 99.8%; Pred. No. 4.4e-110;  
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGTTCCTCTTGCAGAGACTGGCCGGGAGCGGAAGACAAGGCGCTGCACAAAGCG 60  
 |||||||  
 Db 1287 AGTTCCTCTTGCAGAGACTGGCCGGGAGCGGAAGACAAGGCGCTGCACAAAGCG 1346  
 QY 61 GGGCCTGCGGTGGTGGAGTGCATGTAACGGGAGCGCTTCTGTGGTTGGCTGCTG 120  
 |||||||  
 Db 1347 GGGCCTGCGGTGGTGGAGTGCATGTAACGGGAGCGCTTCTGTGGTTGGCTGCTG 1406  
 QY 121 CAGCGACAGGCGGAGCAGACACCTGCAAGACAACCCGCCAAATGCTGGAGAGAC 180  
 |||||||  
 Db 1407 CAGCGACAGGCGGAGCAGACACCTGCAAGACAACCCGCCAAATGCTGGAGAGAC 1466  
 QY 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAAAGGGAG 240  
 |||||||  
 Db 1467 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAAAGGGAG 1526  
 QY 241 GAGGATCATGTAGCGCCGGAAGTGGAGCTGCTCAGTCTGCTGGTTGGCGCAGC 300  
 |||||||  
 Db 1527 GAGGATCATGTAGCGCCGGAAGTGGAGCTGCTCAGTCTGCTGGTTGGCGCAGC 1586  
 QY 301 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGGCAATGTACAAACATCAGGCC 360  
 |||||||  
 Db 1587 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGGCAATGTACAAACATCAGGCC 1646

QY 361 TGGCAGACACAGCAGAGGAGAGAGACAGAAAAAGAAACACAGCATGAGAACAG 420  
 |||||||  
 Db 1647 TGGCAGACACAGCAGAGGAGAGAGACAGAAAAAGAAACACAGCATGAGAACAG 1706  
 QY 421 TAAATGAATAAACAATATAATATTAGCCCTCTGTTCTGTGCTTACTGCGCAGAAAT 480  
 |||||||  
 Db 1707 TAAATGAATAAACAATATAATATTAGCCCTCTGTTCTGTGCTTACTGCGCAGAAAT 1766  
 QY 481 GGTACCAATTTTTCAGTGTGACTTGCACAGCTTCTTTTCCACAAGACAAGAAATT 540  
 |||||||  
 Db 1767 GGTACCAATTTTTCAGTGTGACTTGCACAGCTTCTTTTCCACAAGACAAGAAATT 1826  
 QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600  
 |||||||  
 Db 1827 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 1886  
 QY 601 ACACTG 606  
 |||||||  
 Db 1887 ACACTG 1892

RESULT 28  
 ; Sequence 7293, Application US/09652121  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Distefano, Peter  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
 ; FILE REFERENCE: 1600.1188-001  
 ; CURRENT APPLICATION NUMBER: US/09/652.121  
 ; CURRENT FILING DATE: 2000-08-30  
 ; PRIOR APPLICATION NUMBER: 60/151,129  
 ; PRIOR FILING DATE: 1999-08-30  
 ; NUMBER OF SEQ ID NOS: 7615  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 7293  
 ; LENGTH: 1925  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-652-121-7293

Query Match 88.8%; Score 555; DB 25; Length 1925;  
 Best Local Similarity 99.8%; Pred. No. 4.4e-110;  
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGTTCCTCTTGCAGAGACTGGCCCGGAGCGGAAGACAAGGCGCTGCACAAAGCG 60  
 |||||||  
 Db 636 AGTTCCTCTTGCAGAGACTGGCCCGGAGCGGAAGACAAGGCGCTGCACAAAGCG 577  
 QY 61 GGGCCTGCGGTGGTGGAGTGCATGTAACGGGAGCGCTTCTGTGGTTGGCTGCTG 120  
 |||||||  
 Db 576 GGGCCTGCGGTGGTGGAGTGCATGTAACGGGAGCGCTTCTGTGGTTGGCTGCTG 517  
 QY 121 CAGCGACAGGCGGAGCAGACACCTGCAAGACAACCCGCCAAATGCTGGAGAGAC 180  
 |||||||  
 Db 516 CAGCGACAGGCGGAGCAGACACCTGCAAGACAACCCGCCAAATGCTGGAGAGAC 457  
 QY 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAAAGGGAG 240  
 |||||||  
 Db 456 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTAAAGAAAGCTCTCCGAAAGGGAG 397  
 QY 241 GAGGATCATGTAGCGCCGGAAGTGGAGCTGCTCAGTCTGCTGGTTGGCGCAGC 300  
 |||||||  
 Db 396 GAGGATCATGTAGCGCCGGAAGTGGAGCTGCTCAGTCTGCTGGTTGGCGCAGC 337  
 QY 301 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGGCAATGTACAAACATCAGGCC 360  
 |||||||  
 Db 336 CATGATCCTCCGAATCTGTTGGGATCCAGCATACGGCAATGTACAAACATCAGGCC 277  
 QY 361 TGGGACAGACAGCAGAGGAGAGAGACAGAAAAAGAAACACAGCATGAGAACAG 420  
 |||||||  
 Db 276 TGGGACAGACAGCAGAGGAGAGAGACAGAAAAAGAAACACAGCATGAGAACAG 217

QY 421 TAAATGAATAAACATTAATATTATTTAGCCCTGTCTGTCTACTGTCCAGGAAAT 480  
| | | | |  
DB 216 TAAATTAATTAATTAATTAATTAATTTAGCCCTGTCTGTCTACTGTCCAGGAAAT 157  
| | | | |  
QY 481 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGGCCACAAGAGAGAAATTT 540  
| | | | |  
DB 156 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGGCCACAAGAGAGAAATTT 97  
| | | | |  
QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600  
| | | | |  
DB 96 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 37  
| | | | |  
QY 601 ACACTG 606  
| | | | |  
DB 36 ACACTG 31

## RESULT 29

US-09-652-128-9375/c  
; Sequence 9375, Application US/09652128  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1171-001  
; CURRENT APPLICATION NUMBER: US/09/652,128  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/151,133  
; NUMBER OF SEQ ID NOS: 10265  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 9375  
; LENGTH: 1925  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-128-9375

Query Match 88.8%; Score 555; DB 25; Length 1925;  
Best Local Similarity 99.8%; Pred. No. 4.4e-110;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGGAGAGAGACTGGCCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 60  
| | | | |  
DB 636 AGTTCTCTTGGAGAGAGACTGGCCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 577  
| | | | |  
QY 61 GGGCGTGTGGGTGTGAGTGGCATGTACGCGCAGGCGCTTCTGTGTTGGCGTGTG 120  
| | | | |  
DB 576 GGGCGTGTGGGTGTGAGTGGCATGTACGCGCAGGCGCTTCTGTGTTGGCGTGTG 517  
| | | | |  
QY 121 CAGCGACAGGCGGAGCAGACAGCACTGACAGAAACACCGCGGCAACTGTGCGAGGACAC 180  
| | | | |  
DB 516 CAGCGACAGGCGGAGCAGACAGCACTGACAGAAACACCGCGGCAACTGTGCGAGGACAC 457  
| | | | |  
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAACGTCGAGAAAGGGAG 240  
| | | | |  
DB 456 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAACGTCGAGAAAGGGAG 397  
| | | | |  
QY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTGTGTTGGGTTGGCCGACG 300  
| | | | |  
DB 396 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTGTGTTGGGTTGGCCGACG 337  
| | | | |  
QY 301 CATGATCTCTCCGAATCTGTTGGGCAATCCAGCATGCGCAATGTACAAACATTCAGCCC 360  
| | | | |  
DB 336 CATGATCTCTCCGAATCTGTTGGGCAATCCAGCATGCGCAATGTACAAACATTCAGCCC 277  
| | | | |  
QY 361 TGGGCGACAGCAGGAGGAGAGAGACAGAGAAAACACAGCATGAGAACACAG 420  
| | | | |  
DB 276 TGGGCGACAGCAGGAGGAGAGAGACAGAGAAAACACAGCATGAGAACACAG 217  
| | | | |  
QY 421 TAAATGAATTAATTAATTAATTTAGCCCTGTCTGTCTACTGTCCAGGAAAT 480  
| | | | |  
DB 216 TAAATGAATTAATTAATTAATTTAGCCCTGTCTGTCTACTGTCCAGGAAAT 157  
| | | | |

QY 481 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGGCCACAAGAGAGAAATTT 540  
| | | | |  
DB 156 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGGCCACAAGAGAGAAATTT 97  
| | | | |  
QY 541 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600  
| | | | |  
DB 96 AACACTGTTTCAAAACCCGGGGAGTGTGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 37  
| | | | |  
QY 601 ACACTG 606  
| | | | |  
DB 36 ACACTG 31

## RESULT 30

US-09-652-917-3346/c  
; Sequence 3346, Application US/09652917  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Distefero, Peter  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; FILE REFERENCE: 1600.1170-001  
; CURRENT APPLICATION NUMBER: US/09/652,917  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/151,422  
; NUMBER OF SEQ ID NOS: 3855  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3346  
; LENGTH: 1925  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-652-917-3346

Query Match 88.8%; Score 555; DB 25; Length 1925;  
Best Local Similarity 99.8%; Pred. No. 4.4e-110;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGGAGAGAGACTGGCCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 60  
| | | | |  
DB 636 AGTTCTCTTGGAGAGAGACTGGCCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 577  
| | | | |  
QY 61 GGGCGTGTGGGTGTGAGTGGCATGTACGCGCAGGCGCTTCTGTGTTGGCGTGTG 120  
| | | | |  
DB 576 GGGCGTGTGGGTGTGAGTGGCATGTACGCGCAGGCGCTTCTGTGTTGGCGTGTG 517  
| | | | |  
QY 121 CAGCGACAGGCGGAGCAGACAGCACTGACAGAAACACCGCGGCAACTGTGCGAGGACAC 180  
| | | | |  
DB 516 CAGCGACAGGCGGAGCAGACAGCACTGACAGAAACACCGCGGCAACTGTGCGAGGACAC 457  
| | | | |  
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAACGTCGAGAAAGGGAG 240  
| | | | |  
DB 456 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTAGAAAACGTCGAGAAAGGGAG 397  
| | | | |  
QY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTGTGTTGGGTTGGCCGACG 300  
| | | | |  
DB 396 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTGTGTTGGGTTGGCCGACG 337  
| | | | |  
QY 301 CATGATCTCTCCGAATCTGTTGGGCAATCCAGCATGCGCAATGTACAAACATTCAGCCC 360  
| | | | |  
DB 336 CATGATCTCTCCGAATCTGTTGGGCAATCCAGCATGCGCAATGTACAAACATTCAGCCC 277  
| | | | |  
QY 361 TGGGCGACAGCAGGAGGAGAGAGACAGAGAAAACACAGCATGAGAACACAG 420  
| | | | |  
DB 276 TGGGCGACAGCAGGAGGAGAGAGACAGAGAAAACACAGCATGAGAACACAG 217  
| | | | |  
QY 421 TAAATGAATTAATTAATTAATTTAGCCCTGTCTGTCTACTGTCCAGGAAAT 480  
| | | | |  
DB 216 TAAATGAATTAATTAATTAATTTAGCCCTGTCTGTCTACTGTCCAGGAAAT 157  
| | | | |  
QY 481 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTCTTTTGGCCACAAGAGAGAAATTT 540  
| | | | |



```

Db      96 AACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 37
      601 ACAGTG 606
      36 ACAGTG 31

```

## RESULT 33

```

US-09-726-805-1608/c
; Sequence 1608, Application US/09726805
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600, 2017-001
; CURRENT APPLICATION NUMBER: US/09/726,805
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,140
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 2158
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1608
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-805-1608

```

Query Match 88.8%; Score 555; DB 29; Length 1925;

Best Local Similarity 99.8%; Pred. No. 4,4e-110; Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 AGTTCCTCTTGACAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60
      636 AGTTCCTCTTGACAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 577
QY      61 GCGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
      576 GCGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 517
QY      121 CAGCGACAGCGCGGACAGACACACCTGACAGAAACCCCGCCCAACTGCTGCGAGACAC 180
      516 CAGCGACAGCGCGGACAGACACACCTGACAGAAACCCCGCCCAACTGCTGCGAGACAC 457
QY      181 CGGTACAGAGAGCGGGTGTGACGAGCTGAGTGAAGAAAGCTGCTCCGAGAGAGGAG 240
      456 CGGTACAGAGAGCGGGTGTGACGAGCTGAGTGAAGAAAGCTGCTCCGAGAGAGGAG 397
QY      241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGTGGTGGTGG 300
      396 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGTGGTGGTGG 337
QY      301 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCCATGTACAAACATTCAGCCC 360
      336 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCCATGTACAAACATTCAGCCC 277
QY      361 TGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
      276 TGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 217
QY      421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 480
      216 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 157
QY      481 GGTACCAATTTTCACTGTTGACCTTGACAGCTTCTTTTCCCAAGCAAGAGAGATTT 540
      156 GGTACCAATTTTCACTGTTGACCTTGACAGCTTCTTTTCCCAAGCAAGAGAGATTT 97
QY      541 AACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
      96 AACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 37

```

```

QY      601 ACAGTG 606
      36 ACAGTG 31

```

## RESULT 34

```

PCT-US00-09066-38/c
; Sequence 38, Application PC/TUS0009066
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P549PCT
; CURRENT APPLICATION NUMBER: PCT/US00/09066
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,694
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/176,931
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 1953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1362)
; OTHER INFORMATION: n equals a,t,g, or c
PCT-US00-09066-38

```

Query Match 88.8%; Score 555; DB 1; Length 1953;

Best Local Similarity 99.8%; Pred. No. 4,3e-110; Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 AGTTCCTCTTGACAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 60
      684 AGTTCCTCTTGACAGAGACTGGCGCCGGAGCGGAAGACAGCGGCGCTGCACAAAGCG 625
QY      61 GCGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
      624 GCGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 565
QY      121 CAGCGACAGCGCGGACAGACACCTGACAGAAACCCCGCCCAACTGCTGCGAGACAC 180
      564 CAGCGACAGCGCGGACAGACACCTGACAGAAACCCCGCCCAACTGCTGCGAGACAC 505
QY      181 CGGTACAGAGAGCGGGTGTGACGAGCTGAGTGAAGAAAGCTGCTCCGAGAGAGGAG 240
      504 CGGTACAGAGAGCGGGTGTGACGAGCTGAGTGAAGAAAGCTGCTCCGAGAGAGGAG 445
QY      241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGTGGTGGTGG 300
      444 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGTGGTGGTGG 385
QY      301 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCCATGTACAAACATTCAGCCC 360
      384 CATGATCTCCGAATCTGGTGGGATCCAGCATACGGCCATGTACAAACATTCAGCCC 325
QY      361 TGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
      324 TGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 265
QY      421 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 480
      264 TAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 205
QY      481 GGTACCAATTTTCACTGTTGACCTTGACAGCTTCTTTTCCCAAGCAAGAGAGATTT 540
      204 GGTACCAATTTTCACTGTTGACCTTGACAGCTTCTTTTCCCAAGCAAGAGAGATTT 145
QY      541 AACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 600
      144 AACACTGTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCTTTAG 85

```

QY 601 ACAGTG 606  
 |||||  
 Db 84 ACAGTG 79

RESULT 35  
 US-09-950-083-1914/c  
 ; Sequence 1914, Application US/09950083  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, et. al  
 ; TITLE OF INVENTION: Human Secreted Proteins  
 ; FILE REFERENCE: PS805  
 ; CURRENT APPLICATION NUMBER: US/09/950, 083  
 ; CURRENT FILING DATE: 2001-09-12  
 ; PRIOR APPLICATION NUMBER: 60/278,650  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 09/833,245  
 ; PRIOR FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: PCT/US01/11988  
 ; PRIOR FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06043  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06012  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06058  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06044  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06059  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06042  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06014  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06013  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06049  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06057  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06824  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06765  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06792  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06830  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06782  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06822  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06791  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06828  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06823  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/06781  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07505  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07440  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07506  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07507  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07535  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07525  
 ; PRIOR FILING DATE: 2000-03-22

;; PRIOR APPLICATION NUMBER: PCT/US00/07534  
 ;; PRIOR FILING DATE: 2000-03-22  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07483  
 ;; PRIOR FILING DATE: 2000-03-22  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07526  
 ;; PRIOR FILING DATE: 2000-03-22  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07527  
 ;; PRIOR FILING DATE: 2000-03-22  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07661  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07579  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07723  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07724  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14929  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07722  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07578  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07726  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07677  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/07725  
 ;; PRIOR FILING DATE: 2000-03-23  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/09070  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/08982  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/08983  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/09067  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/09066  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/09068  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/08981  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/08980  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/09071  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/09069  
 ;; PRIOR FILING DATE: 2000-04-06  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/15136  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14926  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14963  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/15135  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14934  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14933  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/15137  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14928  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14973  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/14964  
 ;; PRIOR FILING DATE: 2000-06-01  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/26376  
 ;; PRIOR FILING DATE: 2000-09-26  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/26371  
 ;; PRIOR FILING DATE: 2000-09-26  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/26324



OY	121	CAGCAGACGGGCGGACGACACACTGTGCAGACAACC	GCGGAATCTGTGCGAGGACAC	180
Dd	564	CAGCGACAGCGGCGCACGACACACTTGCACGACAACC	GCGGAATCTGTGCGAGGACAC	505
OY	181	CGTGTCACGAGACGGGTTGATGACCCGAGCTGAGGTA	AAAAAAGCOTCCGAGAAGGGAG	240
Dd	504	CGTGTCACGAGAGCGGGTTGATGACCCGAGCTGAGGTA	AAAAAAGCOTCCGAGAAGGGAG	445
OY	241	GAGGATCATGTAACGCCGGAATGAGAACCTGTCACGT	CGCTGGGCTTTGGCCGAGC	300
Dd	444	GAGGATCATGTAACGCCGGAATGAGAACCTGTCACGT	CGCTGGGCTTTGGCCGAGC	385
OY	301	CATGATCTCCGAAATCTGTGTGGGCATTCACAGATAC	GCCCAATGTCCAACAATCAAGCCC	360
Dd	384	CATGATCTCCGAAATCTGTGTGGGCATTCACAGATAC	GCCCAATGTCCAACAATCAAGCCC	325
OY	361	TGGGACAGACAGGACGAGGAGGAGACAGAAAATAA	AAAAAACACACACATGAGAACACAG	420
Dd	324	TGGGACAGACAGGACGAGGAGGAGACAGAAAATAA	AAAAAACACACACATGAGAACACAG	265
OY	421	TAAATGAATAAACCATPAAAAATATTATTTAGCCCC	CTGTCTGTGCTTACTGCGCAGAAAT	480
Dd	264	TAAATRAATAAACCATPAAAAATATTATTTAGCCCC	CTGTCTGTGCTTACTGCGCAGAAAT	205
OY	481	GGTACCAATTTTTTTCAGTGTGTGCATTTGACAGCT	CTTTTGGCCACAGCAAGAGAAATTT	540
Dd	204	GGTACCAATTTTTTTCAGTGTGTGCATTTGACAGCT	CTTTTGGCCACAGCAAGAGAAATTT	145
OY	541	AACACTGTTTCAAACCCGGGCGAGATTGGCTGTGTT	AAAGAAAGCACATPAAATGCTTTAG	600
Dd	144	AACACTGTTTCAAACCCGGGCGAGATTGGCTGTGTT	AAAGAAAGCACATPAAATGCTTTAG	85
OY	601	ACACGTG	606	
Dd	84	ACAGTG	79	

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RESULT 37
PCT-US00-14973-23/c
Sequence 23, Application PC/TUS0014973
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PS559PCt
CURRENT APPLICATION NUMBER: PCT/US00/14973
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,630
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 23
LENGTH: 1956
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1362)
OTHER INFORMATION: n equals a,t,g, or c
PCT-US00-14973-23

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Query Match	88.8%	Score 555	DB 1	Length 1956
Best Local Similarity	99.8%	Pred. No. 4.3e-110		
Matches 605; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	AGTTCCTCTTGCACAGACACTGGCCCGGAGCGCCAAAGACAAACGCG	60
Dd	684	AGTTCCTCTTGCACAGACACTGGCCCGGAGCGCCAAAGACAAACGCG	6255
QY	61	GGCGGTGCGGTGGAGAGTGGCATAGCCGAGAGCGCTTCTGCTGGTGGCGCTG	120
Dd	624	GGCGGTGCGGTGGAGAGTGGCATAGCCGAGAGCGCTTCTGCTGGTGGCGCTG	5655
QY	121	CAGCGACAGCGCGGACGACACACACTTGCACGACATACCCGCCGAAACTGTTCCGAGGACAC	180

Db	564	CAGCGACAGGGCGGACGACACACACTGTGAGCAACACCCGGCGAAACTGTGCGAGGACAC	505
OY	131	CGTGTACAGGAGCGGGTTGATGACCCGAGCTGAGTAGAAAAAGCTTCCGAGAAAGGGAG	240
Db	504	CGTGTACAGGAGCGGGTTGATGACCCGAGCTGAGGTTAGAAAAACGTCGCGAGAAAGGGAG	445
OY	241	GAGGATCATGTACGCGCGGGAATGAGAGCTGTGACCTGCTGCTGGGTTTGGCGCGAGC	300
Db	444	GAGGATCATGTACGCGCGGGAATGAGAGCTGTGACCTGCTGCTGGGTTTGGCGCGAGC	385
OY	301	CATGATCCTCCGAATCTGTGTGGGCATTCACAGCATACGCGCAATGTCAACAATACAGCCC	366
Db	384	CATGATCCTCCGAATCTGTGTGGGCATTCACAGCATACGCGCAATGTCAACAATACAGCCC	325
OY	361	TGGCGACAGCAGCAGGAGGGAGAGACAGAGAAAAAACAACACAGCATGAGAACACAG	420
Db	324	TGGCGACAGCAGCAGGAGGGAGAGAGACAGAGAAAAAACAACACAGCATGAGAACACAG	265
OY	421	TAAATGATTAATAACCATTAATATTTAGCCCCCTGTGTCTGTACTGTGACCGAGAAAT	480
Db	264	TAAATGATTAATAACCATTAATATTTAGCCCCCTGTGTCTGTACTGTGACCGAGAAAT	205
OY	481	GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTGCGACACAGAGAGAAATTT	540
Db	204	GGTACCAATTTTTCAGTGTGTGACTTGACAGCTTCTTTGCGACACAGAGAGAAATTT	145
OY	541	AACACTGTTTCAAAACCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATATGCTTTAG	600
Db	144	AACACTGTTTCAAAACCGGGGGAGTTGGCTGTGTTAAAGAAAGACATTAATATGCTTTAG	85
OY	601	ACAGTG 606	
Db	84	ACAGTG 79	

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38      RESULT 38
39      US-09-950-083-1915/C
40      Sequence 1915, Application US/09950083
41      GENERAL INFORMATION:
42      APPLICANT: Rosen, et. al
43      TITLE OF INVENTION: Human Secreted Proteins
44      FILE REFERENCE: PS805
45      CURRENT APPLICATION NUMBER: US/09/950,083
46      CURRENT FILING DATE: 2001-09-12
47      PRIOR APPLICATION NUMBER: 60/278,650
48      PRIOR FILING DATE: 2001-03-27
49      PRIOR APPLICATION NUMBER: 09/833,245
50      PRIOR FILING DATE: 2001-04-12
51      PRIOR APPLICATION NUMBER: PCT/US01/11988
52      PRIOR FILING DATE: 2001-04-12
53      PRIOR APPLICATION NUMBER: PCT/US00/06043
54      PRIOR FILING DATE: 2000-03-09
55      PRIOR APPLICATION NUMBER: PCT/US00/06012
56      PRIOR FILING DATE: 2000-03-09
57      PRIOR APPLICATION NUMBER: PCT/US00/06058
58      PRIOR FILING DATE: 2000-03-09
59      PRIOR APPLICATION NUMBER: PCT/US00/06044
60      PRIOR FILING DATE: 2000-03-09
61      PRIOR APPLICATION NUMBER: PCT/US00/06059
62      PRIOR FILING DATE: 2000-03-09
63      PRIOR APPLICATION NUMBER: PCT/US00/06042
64      PRIOR FILING DATE: 2000-03-09
65      PRIOR APPLICATION NUMBER: PCT/US00/06014
66      PRIOR FILING DATE: 2000-03-09
67      PRIOR APPLICATION NUMBER: PCT/US00/06013
68      PRIOR FILING DATE: 2000-03-09
69      PRIOR APPLICATION NUMBER: PCT/US00/06049
70      PRIOR FILING DATE: 2000-03-09
71      PRIOR APPLICATION NUMBER: PCT/US00/06057
72      PRIOR FILING DATE: 2000-03-09
73      PRIOR APPLICATION NUMBER: PCT/US00/06824
74      PRIOR FILING DATE: 2000-03-16

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OY	127	CAGGCGGAGACACAGCACTCGCAAGAACCCGCGAAATCGTGGAGAGAACCGCTGA	186
Db	1410	CAGCGCGACACAGCACTCGCAAGAACCCGCGAAATCGTGGAGAGAACCGCTGA	1469
OY	187	CAGGAGCGGCTTGATGACCCAGCTGAGGTGAGAAAACTCTCCGAGAAAGGGAGAGAGAT	246
Db	1470	CAGGAGCGGCTTGATGACCCAGCTGAGGTGAGAAAACTCTCCGAGAAAGGGAGAGAGAT	1529
OY	247	CATGATGCCCGGGAAGTAAAGAACCTCGTCCAGTGTGCTGTGGTTTGTGGCCGACCATGAT	306
Db	1530	CATGATGCCCGGGAAGTAAAGAACCTCGTCCAGTGTGCTGTGGTTTGTGGCCGACCATGAT	1588
OY	307	CCTCCGAATCTGTGTGGGCATATCCAGCATAGCGGCATATGCACAAACATAGACCCCTGGCA	366
Db	1590	CCTCCGAATCTGTGTGGGCATATCCAGCATAGCGGCATATGCACAAACATAGACCCCTGGCA	1648
OY	367	GACACGACGAGGAGGAGACACAGAAAAAGAAACACAGCATGAGAACACATGAATG	426
Db	1650	GACACGACGAGGAGGAGACACAGAAAAAGAAACACAGCATGAGAACACATGAATGA	1709
OY	427	AATAAAAACATAAAAATTTTAGCCCGCTGTGCTACTCGGCGAGAAATGTATCC	486
Db	1710	AATAAAAACATAAAAATTTTAGCCCGCTGTGCTACTCGGCGAGAAATGTATCC	1769
OY	487	AATTTTCAGTTGACCTTGACAGCTTCTTTTCCACAGCAGAGAGAAATTTAACT	546
Db	1770	AATTTTCAGTTGACCTTGACAGCTTCTTTTCCACAGCAGAGAGAAATTTAACT	1829
OY	547	GTTTCAAAACCGGGGGAGTGGCTGTGTTAAGAAAGACCATTAATGCTTTAGACATG	606
Db	1830	GTTTCAAAACCGGGGGAGTGGCTGTGTTAAGAAAGACCATTAATGCTTTAGACATG	1889

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RESULT 42
US-60-172-373-15734
: Sequence 15734, Application US/60172373
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: FILE REFERENCE: GX-0006 P
: CURRENT APPLICATION NUMBER: US/60/172,373
: CURRENT FILING DATE: 1999-12-16
: NUMBER OF SEQ ID NOS: 25,772
: SOFTWARE: PERL Program
: SEQ ID NO 15734
: LENGTH: 716
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 227484.3c
: US-60-172-373-15734

```

[illegible]

Db	181	ACCGGGTTGATGACGACGAGCTGAGGTAGAAAAACCTCTCCGAGAAAGGGAGGAGGATCATG	240
QY	251	TACGGCCGGAAAGTAAAGACTGTGTCCAGTCGAGCTGGGTTTGGCCGAGCCATGATCTC	310
Db	241	TACGGCCGGAAAGTAAAGACTGTGTCCAGTCGAGCTGGGTTTGGCCGAGCCATGATCTC	300
QY	311	CGAATCTGGTTGGGCGATCCAGCATACGGCCAAATGTCAACAATCAGCCCTGGGCGACA	370
Db	301	CGAATCTGGTTGGGCGATCCAGCATACGGCCAAATGTCAACAATCAGCCCTGGGCGACA	360
QY	371	CGAGCAGGAGGAGAGACAGAGAAAAGAAAAACACAGCATGAGAAACAGCTAAATGATA	430
Db	361	CGAGCAGGAGGAGAGACAGAGAAAAGAAAAACACAGCATGAGAAACAGCTAAATGATA	420
QY	431	AAACATATAAATATTATGACCCCTCTGTTCTGTCTTACTGCGCCAGAAATGATACCAATT	490
Db	421	AAACATATAAATATTATGACCCCTCTGTTCTGTCTTACTGCGCCAGAAATGATACCAATT	480
QY	491	TTTCAGTTGTGACCTGACACCTCTTTTGGCCAAACAGCAGAGAAATTTAAACACGTGT	550
Db	481	TTTCAGTTGTGACCTGACACCTCTTTTGGCCAAACAGCAGAGAAATTTAAACACGTGT	540
QY	551	CAAAACCCGGGGAGCTGGCTGTGTTAAGAAAGCAATTTAAATGCTTTATACAGTG	606
Db	541	CAAAACCCGGGGAGCTGGCTGTGTTAAGAAAGCAATTTAAATGCTTTATACAGTG	596

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RESULT 43
PCT-US01-45395-205
: Sequence 205. Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.48401PC
: CURRENT APPLICATION NUMBER: PCT/US01/45395
: CURRENT FILING DATE: 2001-11-13
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 205
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US01-45395-205

```

Query Match	77.8%	Score 486	DB 1	Length 1619
Best Local Similarity	99.8%	Pred. No. 2.7e-95		
Matches	606	Conservative	0	Mismatches 0; Indels 1; Gaps 1;
QY	1	AGTTCCTCTTCAGAGAGACTGGCCCGGAGCCGCAAGAGCAACGGCCCTGCACAAACG	60	
Db	992	AGTTCCTCTTCAGAGAGACTGGCCCGGAGCCGCAAGAGCAACGGCCCTGCACAAACG	1051	
QY	61	GGCGTGTCCGCTGGTGGAGTGGCATTGTACGGCAGCGCTTCTGTGAGTGGCGTCTG	120	
Db	1052	GGCGTGTCCGCTGGTGGAGTGGCATTGTACGGCAGCGCTTCTGTGAGTGGCGTCTG	1111	
QY	121	CAGGCACAGGGGGCGACGACAGACC -TGCAGAAACACCGCGGAAACATCCCGAGGACA	179	
Db	1112	CAGGCACAGGGGGCGACGACAGACCTTTCACAGAAACACCGCGGAAACATCCCGAGGACA	1171	
QY	180	CCGTGTACAGAGAGCGGGTGTGATGACCCGAGCTGAGGTAGAAAAAGCTCTCCAGAGAGGGA	239	
Db	1172	CCGTGTACAGAGAGCGGGTGTGATGACCCGAGCTGAGGTAGAAAAAGCTCTCCAGAGAGGGA	1231	
QY	240	GGAGGATATGTAGCCCGGAAATGGAACCTGTCCAAGTCGTGGGTTTGGCCGAG	299	

```

Db 1232 GGAGGATCATGTACGCCGGAAGTAGACCTGTCAGTCTGCTGGGTTGGCCGAG 1291
QY 300 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCC 1351
QY 360 CTGGGACAGACAGCAGAGGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 1352 CTGGGACAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 420 GTAATGATATAAACCATAAATATTTAGCCCTCTGTTCTGTCTGTCTGTCTGTCTGTCT 479
Db 1412 GTAATGATATAAACCATAAATATTTAGCCCTCTGTTCTGTCTGTCTGTCTGTCTGTCT 1471
QY 480 TGTGACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCACAGAGAGAGAGAT 539
Db 1472 TGTGACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCACAGAGAGAGAT 1531
QY 540 TAACACTGTTTCAACCCCGGGGAGTGGCTGTGTTAAGAAAGCATTAAATGCTTTA 599
Db 1532 TAACACTGTTTCAACCCCGGGGAGTGGCTGTGTTAAGAAAGCATTAAATGCTTTA 1591
QY 600 GACAGTG 606
Db 1592 GACAGTG 1598

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RESULT 44
PCT-US01-45395-211
; Sequence 211, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-211

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```

Query Match 77.8%; Score 486; DB 1; Length 1619;
Best Local Similarity 99.8%; Pred. No. 2.7e-95;
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 AGTTCTCTTCGAGAGAGACTGGCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 60
Db 992 AGTTCTCTTCGAGAGAGACTGGCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 1051
QY 61 GCGCGTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
Db 1052 GCGCGTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
QY 121 CAGCGACAGAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 179
Db 1112 CAGCGACAGAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1171
QY 180 CCGTGTACAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 239
Db 1172 CCGTGTACAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1231
QY 240 GGAGGATCATGTACGCCGGAAGTAGAGCTGTCCAGTGTGCTGTGGTTGGCCGAG 299
Db 1232 GGAGGATCATGTACGCCGGAAGTAGAGCTGTCCAGTGTGCTGTGGTTGGCCGAG 1291

```

```

QY 300 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCC 1351
QY 360 CTGGGACAGACAGCAGAGGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 1352 CTGGGACAGACAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 420 GTAATGATATAAACCATAAATATTTAGCCCTCTGTTCTGTCTGTCTGTCTGTCTGTCT 479
Db 1412 GTAATGATATAAACCATAAATATTTAGCCCTCTGTTCTGTCTGTCTGTCTGTCTGTCT 1471
QY 480 TGTGACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCACAGAGAGAGAT 539
Db 1472 TGTGACCAATTTTCACTGTTGAGCTTGACAGCTTCTTTTCCACAGAGAGAGAT 1531
QY 540 TAACACTGTTTCAACCCCGGGGAGTGGCTGTGTTAAGAAAGCATTAAATGCTTTA 599
Db 1532 TAACACTGTTTCAACCCCGGGGAGTGGCTGTGTTAAGAAAGCATTAAATGCTTTA 1591
QY 600 GACAGTG 606
Db 1592 GACAGTG 1598

```

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RESULT 45
US-09-713-550-205
; Sequence 205, Application US/09713550
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713.550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-713-550-205

```

```

Query Match 77.8%; Score 486; DB 28; Length 1619;
Best Local Similarity 99.8%; Pred. No. 2.7e-95;
Matches 606; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 AGTTCTCTTCGAGAGAGACTGGCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 60
Db 992 AGTTCTCTTCGAGAGAGACTGGCGCGGAGCGGAGAGCAACGGGCGCTGCACAAAGCG 1051
QY 61 GCGCGTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
Db 1052 GCGCGTGTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
QY 121 CAGCGACAGAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 179
Db 1112 CAGCGACAGAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1171
QY 180 CCGTGTACAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 239
Db 1172 CCGTGTACAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1231
QY 240 GGAGGATCATGTACGCCGGAAGTAGAGCTGTCCAGTGTGCTGTGGTTGGCCGAG 299
Db 1232 GGAGGATCATGTACGCCGGAAGTAGAGCTGTCCAGTGTGCTGTGGTTGGCCGAG 1291
QY 300 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCC 359
Db 1292 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCC 1351

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187

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 18:16:33 ; Search time 17.4612 Seconds  
(without alignments)  
3937.596 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agtctccttcgagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 193892 seqs, 55004114 residues

Word size : 10

Total number of hits satisfying chosen parameters: 43951

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Pending Patents\_MN\_New:\*  
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3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
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7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	62.9	1524	6 US-10-230-437-15	Sequence 15, Appl
2	3	3.5	1329	6 US-10-264-237-1044	Sequence 1044, Ap
3	22	3.5	2049	6 US-10-264-237-1380	Sequence 1380, Ap
4	21	3.4	2062	6 US-10-264-237-464	Sequence 464, App
5	21	3.4	2176	6 US-09-721-456-3	Sequence 0, Appl
6	20	3.2	457	6 US-10-240-425-208	Sequence 208, App
7	19	3.0	163	5 US-09-513-999C-21763	Sequence 21763, A
8	19	3.0	496	6 US-10-131-813A-533	Sequence 533, App
9	19	3.0	496	6 US-10-131-819A-533	Sequence 533, App
10	19	3.0	496	6 US-10-131-823A-533	Sequence 533, App
11	19	3.0	496	6 US-10-131-824A-533	Sequence 533, App
12	19	3.0	496	6 US-10-131-826A-533	Sequence 533, App
13	19	3.0	496	6 US-10-131-829A-533	Sequence 533, App
14	19	3.0	496	6 US-10-125-926A-533	Sequence 533, App
15	19	3.0	496	6 US-10-127-829A-533	Sequence 533, App
16	19	3.0	496	6 US-10-127-831A-533	Sequence 533, App
17	19	3.0	496	6 US-10-127-835A-533	Sequence 533, App
18	19	3.0	496	6 US-10-127-837A-533	Sequence 533, App
19	19	3.0	496	6 US-10-127-842A-533	Sequence 533, App
20	19	3.0	496	6 US-10-127-850A-533	Sequence 533, App
21	19	3.0	496	6 US-10-127-901A-533	Sequence 533, App
22	19	3.0	496	6 US-10-128-889A-533	Sequence 533, App
23	19	3.0	496	6 US-10-131-830A-533	Sequence 533, App
24	19	3.0	496	6 US-10-131-833A-533	Sequence 533, App
25	19	3.0	496	6 US-10-131-837A-533	Sequence 533, App
26	19	3.0	496	6 US-10-125-930A-533	Sequence 533, App

27	19	3.0	496	6 US-10-127-825A-533	Sequence 533, App
28	19	3.0	496	6 US-10-127-838B-533	Sequence 533, App
29	19	3.0	496	6 US-10-127-843A-533	Sequence 533, App
30	19	3.0	496	6 US-10-127-849A-533	Sequence 533, App
31	19	3.0	496	6 US-10-128-664A-533	Sequence 533, App
32	19	3.0	496	6 US-10-128-685A-533	Sequence 533, App
33	19	3.0	496	6 US-10-128-686A-533	Sequence 533, App
34	19	3.0	496	6 US-10-128-687A-533	Sequence 533, App
35	19	3.0	496	6 US-10-128-688A-533	Sequence 533, App
36	19	3.0	496	6 US-10-128-689A-533	Sequence 533, App
37	19	3.0	496	6 US-10-131-821A-533	Sequence 533, App
38	19	3.0	496	6 US-10-131-822A-533	Sequence 533, App
39	19	3.0	496	6 US-10-137-872A-533	Sequence 533, App
40	19	3.0	531	4 US-08-250-795A-19	Sequence 19, Appl
41	19	3.0	692	4 US-10-264-237-662	Sequence 662, App
42	19	3.0	1330	6 US-10-264-237-1069	Sequence 1069, Ap
43	19	3.0	2069	6 US-10-264-237-447	Sequence 447, App
44	19	3.0	3196	6 US-10-264-237-1221	Sequence 1221, Ap
45	19	3.0	15832	6 US-10-240-453-117	Sequence 117, App

ALIGNMENTS

```

RESULT 1
US-10-230-437-15
; Sequence 15, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P35301C94
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-15
Query Match      62.9%; Score 393; DB 6; Length 1524;

```

Best Local Similarity 100.0%; Pred. No. 9 3e-177;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGTTCCTCTTGAGAGAGACTGGCGCGGAGCCGGAAGAGACGGCGCTGCACAAAGCG 60
    |||||||
DB 1132 ACTTCTCCTTGAGAGAGACTGGCGCGGAGCCGGAAGAGACGGCGCTGCACAAAGCG 1191
QY 61 GCGCTGTGGTGGTGGATGGCGATGTACGGCGAGGGCTTCTGCTGGTTGGCGTGTG 120
    |||||||
DB 1192 GCGCTGTGGTGGTGGATGGCGATGTACGGCGAGGGCTTCTGCTGGTTGGCGTGTG 1251
QY 121 CAGCGACAGCGCGAGCAGACAGCAGCTGCAGAAACCCCGGAACTGCTGGAGAGACAC 180
    |||||||
DB 1252 CAGCGACAGCGCGAGCAGACAGCAGCAGCAACCCCGGAACTGCTGGAGAGACAC 1311
QY 181 CGTGTACAGAGCGGGTGTATGACGAGCTGAGAGTGAAGAAACGCTCCGAGAGGGAG 240
    |||||||
DB 1312 CGTGTACAGAGCGGGTGTATGACGAGCTGAGAGTGAAGAAACGCTCCGAGAGGGAG 1371
QY 241 GAGGATCATGTACCGCCGGAAGTAGACCTGCTCAGTGTGGTTGGCGCAGC 300
    |||||||
DB 1372 GAGGATCATGTACCGCCGGAAGTAGACCTGCTCAGTGTGGTTGGCGCAGC 1431
QY 301 CATGATCTCCGAATCTGGTTGGGCAATCCAGCATAGGCCAATGTCAACAATCAGCCC 360
    |||||||
DB 1432 CATGATCTCCGAATCTGGTTGGGCAATCCAGCATAGGCCAATGTCAACAATCAGCCC 1491
QY 361 TGGGACAGACGACGAGAGAGGAGAGACAGAGA 393
    |||||||
DB 1492 TGGGACAGACGAGAGAGGAGAGAGACAGAGA 1524
```

RESULT 2  
US-10-264-237-1044

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; Sequence 1044, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1044
; LENGTH: 1329
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1297)..(1297)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1044
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Query Match 3.5%; Score 22; DB 6; Length 1329;  
Best Local Similarity 100.0%; Pred. No. 0.099;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 604 GTGNAAAAAAAAAAAAAAAAAAAAA 625
    |||||||
DB 1294 GTGNAAAAAAAAAAAAAAAAAAAAA 1315
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RESULT 3  
US-10-264-237-1380/C

```
; Sequence 1380, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
```

CURRENT APPLICATION NUMBER: US/10/264,237  
CURRENT FILING DATE: 2002-10-04

```
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1380
; LENGTH: 2049
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (322)..(322)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1819)..(1819)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2021)..(2021)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1380
```

Query Match 3.5%; Score 22; DB 6; Length 2049;  
Best Local Similarity 100.0%; Pred. No. 0.097;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 604 GTGNAAAAAAAAAAAAAAAAAAAAA 625
    |||||||
DB 325 GTGNAAAAAAAAAAAAAAAAAAAAA 304
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RESULT 4  
US-10-264-237-464

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; Sequence 464, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 464
; LENGTH: 2062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1998)..(1998)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-464
```

Query Match 3.4%; Score 21; DB 6; Length 2062;



Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAA 625  
DB 1996 TGNAAAAAAAAAAAAA 2016

## RESULT 5

US-09-721-456-3

Sequence 0, Application US/09721456

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-Nov-2000

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-Nov-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-Oct-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: /note= "clone 712562"

SEQUENCE CHARACTERISTICS:

LENGTH: 2176 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: -

LOCATION: 1..2176

SEQUENCE DESCRIPTION: SEQ ID NO: 3;

US-09-721-456-3

## Query Match

Best Local Similarity 3.4%; Score 21; DB 5; Length 2176;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 TGNAAAAAAAAAAAAA 625

DB 2148 TGNAAAAAAAAAAAAA 2168

## RESULT 6

US-10-240-425-208

Sequence 208, Application US/10240425

GENERAL INFORMATION:

APPLICANT: Williams, Amanda

APPLICANT: Boland, Joseph F.

APPLICANT: Lord, Reginald V.

APPLICANT: Alvarez, Chris

APPLICANT: Wetzel, Jon C.

APPLICANT: Scherf, Uwe

APPLICANT: Vockley, Joseph G.

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue

FILE REFERENCE: 44921-5026

CURRENT APPLICATION NUMBER: US/10/240,425

CURRENT FILING DATE: 2002-09-30

PRIOR APPLICATION NUMBER: PCT/US01/09847

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/193,446

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 1588

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 208

LENGTH: 457

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. AA631399

US-10-240-425-208

## Query Match

Best Local Similarity 3.2%; Score 20; DB 6; Length 457;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 GAAAAACACAGCATGAGAAC 416

DB 334 GAAAAACACAGCATGAGAAC 353

## RESULT 7

US-09-513-999C-21763

Sequence 21763, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclet, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59 US2 REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 21763

LENGTH: 163

TYPE: DNA

ORGANISM: Homo sapiens

```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 134
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 135
; OTHER INFORMATION: n-a, g, c or t
US-09-513-999C-21763

Query Match      3.0%; Score 19; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 135 NAAAAAAAAAAAAAAAAAAAA 153

RESULT 8
US-10-131-813A-533
; Sequence 533, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C139
; CURRENT APPLICATION NUMBER: US/10/131, 813A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-813A-533

Query Match      3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 9
US-10-131-819A-533
; Sequence 533, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C134
; CURRENT APPLICATION NUMBER: US/10/131, 819A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-819A-533

Query Match      3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
```

Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625  
 |||  
 Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 10  
 US-10-131-823A-533  
 ; Sequence 533, Application US/10131823A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: Deforge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P330R1C143  
 ; CURRENT APPLICATION NUMBER: US/10/131,823A  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: 60/049911  
 ; PRIOR FILING DATE: 1997-06-18  
 ; PRIOR APPLICATION NUMBER: 60/056974  
 ; PRIOR FILING DATE: 1997-08-26  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059115  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059122  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059184  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059352  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/059588  
 ; PRIOR FILING DATE: 1997-09-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 533  
 ; LENGTH: 496  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: 396  
 ; OTHER INFORMATION: unknown base  
 US-10-131-823A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625  
 |||  
 Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 11  
 US-10-131-824A-533  
 ; Sequence 533, Application US/10131824A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: Deforge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P330R1C126  
 ; CURRENT APPLICATION NUMBER: US/10/131,824A  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: 60/049911  
 ; PRIOR FILING DATE: 1997-06-18  
 ; PRIOR APPLICATION NUMBER: 60/056974  
 ; PRIOR FILING DATE: 1997-08-26  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059115  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059117  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059122  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059184  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059352  
 ; PRIOR FILING DATE: 1997-09-19  
 ; PRIOR APPLICATION NUMBER: 60/059588  
 ; PRIOR FILING DATE: 1997-09-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 533  
 ; LENGTH: 496  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: 396  
 ; OTHER INFORMATION: unknown base  
 US-10-131-824A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625  
 |||  
 Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 12  
 US-10-131-826A-533  
 ; Sequence 533, Application US/10131826A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

```

: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Geritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C128
: CURRENT APPLICATION NUMBER: US/10/131,826A
: PRIOR FILING DATE: 1997-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: LENGTH: 496
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
: US-10-131-826A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 13
: Sequence 533, Application US/10131829A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Geritsen, Mary E.

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: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,829A
: PRIOR FILING DATE: 2002-04-27
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: LENGTH: 496
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
: US-10-131-829A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 14
: Sequence 533, Application US/10125926A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Geritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.

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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C80
CURRENT APPLICATION NUMBER: US/10/125,926A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 533
LENGTH: 496
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 396
OTHER INFORMATION: unknown base
US-10-125-926A-533

Query Match
Best Local Similarity 3.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 15
US-10-127-829A-533
Sequence 533, Application US/10127829A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvarioff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILE REFERENCE: P3330R1C85
CURRENT APPLICATION NUMBER: US/10/127,829A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 533
LENGTH: 496
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 396
OTHER INFORMATION: unknown base
US-10-127-829A-533

Query Match
Best Local Similarity 3.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 16
US-10-127-831A-533
Sequence 533, Application US/10127831A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvarioff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C107
CURRENT APPLICATION NUMBER: US/10/127,831A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
```

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; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-831A-533
```

```
Query Match 3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414
```

```
RESULT 17
US-10-127-835A-533
```

```
; Sequence 533, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C102
; CURRENT APPLICATION NUMBER: US/10/127, 835A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
```

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-835A-533
```

```
Query Match 3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414
```

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RESULT 18
US-10-127-837A-533
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```
; Sequence 533, Application US/10127837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C96
; CURRENT APPLICATION NUMBER: US/10/127, 837A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-837A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 19
US-10-127-842A-533
; Sequence 533, Application US/10127842A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C100
; CURRENT APPLICATION NUMBER: US/10/127, 842A
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-842A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 20
US-10-127-850A-533
; Sequence 533, Application US/10127850A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C110
; CURRENT APPLICATION NUMBER: US/10/127, 850A
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
```

NAME/KEY: unsure  
LOCATION: 396  
OTHER INFORMATION: unknown base  
US-10-127-850A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 21  
US-10-127-901A-533  
Sequence 533, Application US/10127901A

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C86  
CURRENT APPLICATION NUMBER: US/10/127,901A  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See file Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 533  
LENGTH: 496  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 396  
OTHER INFORMATION: unknown base  
US-10-127-901A-533

Query Match 3.0%; Score 19; DB 6; Length 496;

Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 607 NAAAAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 22  
US-10-128-689A-533  
Sequence 533, Application US/10128689A

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C17  
CURRENT APPLICATION NUMBER: US/10/128,689A  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See file Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 533  
LENGTH: 496  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 396  
OTHER INFORMATION: unknown base  
US-10-128-689A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAAAAA 414



```

RESULT 23
US-10-131-830A-533
; Sequence 533, Application US/10131830A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; APPLICANT: Matanabe, Colin K
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C137
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/059974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-830A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 24
US-10-131-833A-533
; Sequence 533, Application US/10131833A
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; APPLICANT: Matanabe, Colin K
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C142
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-131-833A-533

Query Match
Best Local Similarity 100.0%; Score 19; DB 6; Length 496;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 25
US-10-131-837A-533
; Sequence 533, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C131
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-131-837A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 26
US-10-125-930A-533
; Sequence 533, Application US/10125930A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Defoige, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C78
; CURRENT APPLICATION NUMBER: US/10/125,930A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-125-930A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 27
US-10-127-825A-533
; Sequence 533, Application US/10127825A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Defoige, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C84
; CURRENT APPLICATION NUMBER: US/10/127,825A
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-825A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 28
US-10-127-838B-533
; Sequence 533, Application US/10127838B
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C98
; CURRENT APPLICATION NUMBER: US/10/127,838B
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
```

```

; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-127-838B-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 29
US-10-127-843A-533
; Sequence 533, Application US/10127843A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C99
; CURRENT APPLICATION NUMBER: US/10/127,843A
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
```

```
;; PRIOR APPLICATION NUMBER: 60/059117
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059122
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO: 533
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-127-843A-533
```

```
Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414
```

```
RESULT 30
US-10-127-849A-533
; Sequence 533, Application US/10127849A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C103
; CURRENT APPLICATION NUMBER: US/10/127, 849A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-19
```

```
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO: 533
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo Sapien
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-127-849A-533
```

```
Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 607 NAAAAAAAAAAAAAAAAAAAA 625
Db 396 NAAAAAAAAAAAAAAAAAAAA 414
```

```
RESULT 31
US-10-128-684A-533
; Sequence 533, Application US/10128684A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C118
; CURRENT APPLICATION NUMBER: US/10/128, 684A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
```

Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 533  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 396  
; OTHER INFORMATION: unknown base  
US-10-128-684A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 32  
US-10-128-685A-533  
; Sequence 533, Application US/10128685A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OR INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C116  
; CURRENT APPLICATION NUMBER: US/10/128, 685A  
; PRIOR FILING DATE: 2002-04-23  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 533  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Homo Sapien

FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 396  
; OTHER INFORMATION: unknown base  
US-10-128-685A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 33  
US-10-128-686A-533  
; Sequence 533, Application US/10128686A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OR INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C119  
; CURRENT APPLICATION NUMBER: US/10/128, 686A  
; PRIOR FILING DATE: 2002-04-23  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 533  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 396  
; OTHER INFORMATION: unknown base  
US-10-128-686A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625  
|||||  
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 34  
US-10-128-690A-533

; Sequence 533, Application US/10128690A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Mei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C122

; CURRENT APPLICATION NUMBER: US/10/128,690A

; PRIOR FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533

; LENGTH: 496

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 396

; OTHER INFORMATION: unknown base

US-10-128-690A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625  
|||||

DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 35  
US-10-128-693A-533

; Sequence 533, Application US/10128693A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Mei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C120

; CURRENT APPLICATION NUMBER: US/10/128,693A

; PRIOR FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533

; LENGTH: 496

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 396

; OTHER INFORMATION: unknown base

US-10-128-693A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625  
|||||  
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 36  
US-10-131-821A-533  
; Sequence 533, Application US/10131821A

```

: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Mei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zhenli
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,821A
: PRIOR FILING DATE: 2002-04-23
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: LENGTH: 496
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
US-10-131-821A-533

Query Match      3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 37
US-10-131-836A-533
: Sequence 533, Application US/10131836A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Mei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zhenli
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C138
: CURRENT APPLICATION NUMBER: US/10/131,821A
: PRIOR FILING DATE: 2002-04-23
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: LENGTH: 496
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
US-10-131-821A-533

Query Match      3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 607 NAAAAAAAAAAAAAAAAAAAA 625
DB 396 NAAAAAAAAAAAAAAAAAAAA 414

```

```

: APPLICANT: Gao,Wei-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Audrey
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas,Daniel
: APPLICANT: Watanabe,Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang,Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C135
: CURRENT APPLICATION NUMBER: US/10/131,836A
: PRIOR FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 533
: LENGTH: 496
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 396
: OTHER INFORMATION: unknown base
US-10-131-836A-533

Query Match          3.0%; Score 19; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 607 NAAAAAAAAAAAAAAAAAAAA 625
      ||||||||||||||||||
Db 396 NAAAAAAAAAAAAAAAAAAAA 414

RESULT 38
US-10-137-872A-533
: Sequence 533, Application US/10137872A
: GENERAL INFORMATION:
: APPLICANT: Baker,Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao,Wei-Qiang
: APPLICANT: Gerritsen,Mary E.
: APPLICANT: Goddard,Audrey
: APPLICANT: Godowski,Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood,Steven

```

APPLICANT: Smith,Victoria  
APPLICANT: Stewart,Timothy A.  
APPLICANT: Tumas,Daniel  
APPLICANT: Watanabe,Colin K  
APPLICANT: Wood,William  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C150  
CURRENT APPLICATION NUMBER: US/10/137,872A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 533  
LENGTH: 496  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 396  
OTHER INFORMATION: unknown base  
US-10-137-872A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 39  
US-10-137-873A-533  
Sequence 533, Application US/10137873A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Mei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C149  
CURRENT APPLICATION NUMBER: US/10/137,873A  
CURRENT FILING DATE: 2002-04-23  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 533  
LENGTH: 496  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 396  
OTHER INFORMATION: unknown base  
US-10-137-873A-533

Query Match 3.0%; Score 19; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 NAAAAAAAAAAAAAAAAA 625  
Db 396 NAAAAAAAAAAAAAAAAA 414

RESULT 40  
US-08-250-795A-19  
Sequence 19, Application US/08250795A  
GENERAL INFORMATION:  
APPLICANT: Berlin, Vivian  
APPLICANT: Chiu, Isabel  
TITLE OF INVENTION: Immunosuppressant Target Proteins  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ROPES & GRAY  
STREET: 1 International Place  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/250,795A  
FILING DATE: 27-May-1994  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709



```

? REFERENCE/DOCKET NUMBER: APBI-P01-0036
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 951-7000
? TELEFAX: (617) 951-7050
? INFORMATION FOR SEQ ID NO: 19:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 531 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-250-795A-19

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Query Match	3.0%	Score 19	DB 4	Length 531
Best Local Similarity	100.0%	Pred. No. 2.7		
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	607	AAAAAAAAAAAAAAAAAA	625
Db	492	AAAAAAAAAAAAAAAAAA	510

RESULT 41  
US-10-264-237-662

APPLICANT: Blirise et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PA13191

; CURRENT APPLICATION NUMBER: US/10/264,237  
 ; CURRENT FILING DATE: 2002-10-04  
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450  
 ; PRIOR FILING DATE: 2001-05-18

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; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIT ver 3.1

```

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; SEQ ID NO 662
; LENGTH: 692
; TYPE: DNA
; ORGANISM: H

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: n e

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: n equals a.t.d. or c

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (651)..(651)
; OTHER INFORMATION: n equals a.t.d. or c

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (684)..(684)
; OTHER INFORMATION: n equals a,t,g, or c

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (692)..(692)
; OTHER INFORMATION: n equals a.t.d. or c
;

```

```

US-10-204-23/-062
Query Match          3.0%;  score 19;  DB 6;  length 692
Best Local Similarity 100.0%;  Pred, No. 2.7:

```

QY	607	AAAAAAAAAAAAAAAAAA	625
Db	651	AAAAAAAAAAAAAAAAAA	669

```

RESULT 42 237-1069
US-10-264-237-1069
; Sequence 1069, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1331P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1069
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1265)..(1265)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1069

```

Query Match	3.0%	Score 19	DB 6	Length 1330
Best Local Similarity	100.0%	Pred. No. 2.6		
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	607	NAAAAAAAAAAAAAAAAAAA	625
Db	1265	AAAAAAAAAAAAAAAAAAAAA	1283

RESULT 43  
US-10-264-237-447  
Sequence 447

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; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILING REFERENCE: 0433101

```

; CURRENT APPLICATION NUMBER: US/10/264,237  
 ; CURRENT FILING DATE: 2002-10-04  
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450  
 ; PRIORITY DATE: 2001-05-18

```

; PRIOR APPLICATION NUMBER: US 60/205,513
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIT ver 3.1

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; SEQ ID NO 447
; LENGTH: 2065
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2046) .. (2046)
; OTHER INFORMATION: n equal s a t c or c

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Query Match	3.0%	Score 19;	DB 6;	length 2069;
Best local	100.0%	pred NO	2.5%	
Stimilarity				

QY	607	NAAAAAAAAAAAAAAAAA	625
Db	2046	NAAAAAAAAAAAAAAAAA	206

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RESULT 44
US-10-264-237-1221
; Sequence 1221, Application US/10264233
; GENERAL INFORMATION:
; APPLICANT: Birse et al.

```

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PA131P1  
CURRENT APPLICATION NUMBER: US/10/264,237  
CURRENT FILING DATE: 2002-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/16450  
PRIOR FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: US 60/205,515  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 2876  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 1221  
LENGTH: 3196  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (668)..(668)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (3170)..(3170)  
OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-1221

Query Match 3.0%; Score 19; DB 6; Length 3196;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625  
Db 3170 NAAAAAAAAAAAAAAAAA 3188

RESULT 45  
US-10-240-453-117/c  
Sequence 117, Application US/10240453  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA  
TITLE OF INVENTION: Transcription  
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated  
FILE REFERENCE: 5013.1009  
CURRENT APPLICATION NUMBER: US/10/240,453  
CURRENT FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: PCT/EP01/03973  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 350  
SEQ ID NO 117  
LENGTH: 15832  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (791, 2400, 3281, 4994, 5001..5002, 5006, 5012, 5016, 5024)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (5221, 5244, 6508, 12917, 12968, 12987..12988, 13055)  
US-10-240-453-117

Query Match 3.0%; Score 19; DB 6; Length 15832;

Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 607 NAAAAAAAAAAAAAAAAA 625  
Db 791 NAAAAAAAAAAAAAAAAA 773

Search completed: November 8, 2002, 02:02:48  
Job time : 48.4612 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 17:54:48 ; Search time 837.445 seconds

(without alignments)  
12086.984 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agtctccttcgacagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 10

Total number of hits satisfying chosen parameters: 10588158

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :  
1: em\_estb:\*  
2: em\_estm:\*  
3: em\_estln:\*  
4: em\_estlu:\*  
5: em\_estlv:\*  
6: em\_estlp:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	88.8	702	14	B0006545
2	546	87.4	678	9	A1936826
3	546	87.4	666	12	BF439382
4	537	85.9	537	12	BF594242
5	529	84.6	616	9	A1990500
6	526	84.2	627	13	BM669397

7	525	84.0	696	13	BM547680
8	516	82.6	649	12	AM590950
9	499	79.8	551	12	BE858216
10	489	78.2	540	12	BF936932
11	471	75.4	530	12	BF726459
12	462	73.9	527	10	AM338938
13	459	73.4	515	9	A1336858
14	442	70.7	690	10	AM149665
15	437	69.9	500	10	AM075598
16	425	68.0	591	9	A1884686
17	425	68.0	676	10	BE385990
18	423	67.7	467	9	A1150931
19	421	67.4	538	13	BM667957
20	415	66.4	537	9	A1018769
21	396	63.4	396	9	AA613995
22	393	62.9	452	9	A1391683
23	390	62.4	396	9	A1499630
24	390	62.4	534	10	BE350014
25	380	60.8	456	9	A1765236
26	369	59.0	381	12	BF054837
27	368	58.9	371	12	BF054680
28	365	58.4	378	9	A1742092
29	347	55.5	432	10	AM087372
30	339	54.2	759	12	BF126050
31	339	54.2	843	12	BF125134
32	338	54.1	387	9	A1272281
33	332	53.1	454	10	AM191974
34	315	50.4	480	9	A1423162
35	314	50.2	337	9	AA665640
36	314	50.2	354	9	AA970361
37	314	50.2	373	9	AA075710
38	314	50.2	412	9	AA084249
39	312	49.9	312	12	BF726644
40	307	49.1	349	9	AA173739
41	307	49.1	408	12	BG057775
42	298	47.7	420	9	A1566797
43	294	47.0	475	9	A1363261
44	282	45.1	888	14	BQ689771
45	272	43.5	402	10	AM128849

## ALIGNMENTS

RESULT 1  
B0006545/c 702 bp mRNA linear EST 26-MAR-2002  
LOCUS  
DEFINITION  
IMAGE:5846228 3', mRNA sequence.  
ACCESSION  
B0006545  
VERSION  
B0006545.1 GI:19731445  
KEYWORDS  
EST.  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (Bases 1 to 702)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue procurement: Dr. Jose Mercuende  
CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Seq primer: M13 FORWARD  
POLA=yes.  
FEATURES  
Location/Qualifiers  
I..702

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846228"
/clone_lib="NCI CGAP E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dt)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG_LIB=UI-H-E11
TAG_TISSUE=Chondrosarcoma
TAG_SEQ=ACACTTGCAC"
BASE COUNT      137 a      200 c      163 g      202 t
ORIGIN

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Query Match      88.8%; Score 555; DB 14; Length 702;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGTTCCTTCGACGAGGACGCGCGCGGAGAGCAAGCGCGCGTGCACAAACG 60
DB 625 AGTTCCTTCGACGAGGACGCGCGCGGAGAGCAAGCGCGCGTGCACAAACG 566
QY 61 GCGGCTGTGCGTGGAGAGTGCATGTACGCGCAGCGCTTCTCGTGTGGCGTCTG 120
DB 565 GCGGCTGTGCGTGGAGAGTGCATGTACGCGCAGCGCTTCTCGTGTGGCGTCTG 506
QY 121 CAGCGACAGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGAC 180
DB 505 CAGCGACAGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGAC 446
QY 181 CGGTACAGGAGGCGGTGTGACCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 240
DB 445 CGGTACAGGAGGCGGTGTGACCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 386
QY 241 GAGGATCATGTACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 385 GAGGATCATGTACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 326
QY 301 CATGATCTCTCCGAACTCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 360
DB 325 CATGATCTCTCCGAACTCTGTTGGGATCCAGCATACGCGCAATGTCAACAATCAGCC 266
QY 361 TGGGACAGACGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 265 TGGGACAGACGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 206
QY 421 TAAATGAATAAATTAATATTTAGCCCTCTGTTCTGTGTCTACTGTGCGCAGAAAT 480
DB 205 TAAATGAATAAATTAATATTTAGCCCTCTGTTCTGTGTCTACTGTGCGCAGAAAT 146
QY 481 GGTACCAATTTTTCAGTGTGAGTGTACAGCTCTTTTGGCAACAAGAGAGAAATTT 540
DB 145 GGTACCAATTTTTCAGTGTGAGTGTACAGCTCTTTTGGCAACAAGAGAGAAATTT 86
QY 541 AACACTGTTTCAACCGCGGGAGTGTGGCTGTGTTAAAGAAAGACCAATTAATCTTTAG 600
DB 85 AACACTGTTTCAACCGCGGGAGTGTGGCTGTGTTAAAGAAAGACCAATTAATCTTTAG 26
QY 601 ACAAGT 606
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DB 25 ACAAGT 20

RESULT 2  
AI936826/c  
LOCUS  
DEFINITION  
AI936826  
wp69h10.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2467075 3'  
Similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GPR39.; mRNA SEQUENCE.

ACCESSION  
AI936826  
VERSION  
AI936826.1 GI:5675696  
KEYWORDS  
EST.  
SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
1 (bases 1 to 678)  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
CONTACT: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.

JOURNAL  
COMMENT  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
Insert length: 1143 Std Error: 0.00  
Seq. primer: -400P from Gibco  
High quality sequence stop: 454.  
Location/Qualifiers

#### FEATURES

source

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1..678
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2467075"
/clone_lib="NCI CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/notes="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer (5'
TGTTCACCAATCTGAAGTGGAGCGCGGCGCATACGATTTTGTGTGTGTGTGTGT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

```

BASE COUNT 133 a 199 c 161 g 182 t 3 others

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Query Match      87.4%; Score 546; DB 9; Length 678;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 10 TGCAGAGAGCTGGCGCGGAGCGGAGAGCAACGCGCGCTGCAACAAAGCGCGCTGTG 69
DB 597 TGCAGAGAGCTGGCGCGGAGCGGAGAGCAACGCGCGCTGCAACAAAGCGCGCTGTG 538
QY 70 GGTGTGAGTGGCGCATGTACGCGCAGGCGCTTCTCGTGTGGCGTGTGCTACGACGAC 129
DB 537 GGTGTGAGTGGCGCATGTACGCGCAGGCGCTTCTCGTGTGGCGTGTGCTACGACGAC 478
QY 130 GCGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 189
DB 477 GCGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 418
QY 190 GAGCGGGTGTATGACCGAGCTGAGTGAAGGAGGAGGAGGAGGAGGAGGATCAT 249

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Db 417 GAGGGGTTGATGACCGAGCTGAGTACAGAAAACGCTCCGAGGAGGAGGATCAT 358  
 250 GTACGCCGGAAGTAGAGACTGTCAGTCCGTCGTTGGTTGGCCGAGCCATGATCT 309  
 Db 357 GTACGCCGGAAGTAGAGACTGTCAGTCCGTCGTTGGTTGGCCGAGCCATGATCT 298  
 QY 310 CCGAATCTGTTGGGATCCAGCATACGCCAATGTCAACAAATCAGCCCTGGCAGAC 369  
 Db 297 CCGAATCTGTTGGGATCCAGCATACGCCAATGTCAACAAATCAGCCCTGGCAGAC 238  
 QY 370 ACGAGCAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAGTAATGAT 429  
 Db 237 ACGAGCAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAGTAATGAT 178  
 QY 430 AAAACCTAAATATTTAGCCCTCTGTTGCTTACTGGCCGAGAAATGTATCAT 489  
 Db 177 AAAACCTAAATATTTAGCCCTCTGTTGCTTACTGGCCGAGAAATGTATCAT 118  
 QY 490 TTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACACAGCAGAGAAATTTAAGCTGT 549  
 Db 117 TTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACACAGCAGAGAAATTTAAGCTGT 58  
 QY 550 TCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGCACTTAATGCTTTAGACAGTG 606  
 Db 57 TCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGCACTTAATGCTTTAGACAGTG 1

RESULT 3  
 BF439382/c 696 bp mRNA linear EST 30-MAR-2001  
 LOCUS nab63906.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3272627.3, similar to SW:GP39\_HUMAN O43194 PUTATIVE G  
 PROTEIN-COUPLED RECEPTOR GPR39. ;, mRNA sequence.

ACCESSION BF439382  
 VERSION BF439382.1 GI:11451899  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 696)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@lml.gov) for further information.  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 459.

FEATURES  
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 1. 696  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3272627"  
 /clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled: Vector: pUT73D-Pac (Pharmacia) with  
 a modified polylinker. Site\_1: Not I. Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized  
 libraries were mixed, and ss circles were made in vitro.  
 Following HAP purification, this DNA was used as tracer in  
 a subtractive hybridization reaction. The driver was  
 PCR-amplified cDNAs from pools of 5,000 clones made from  
 the same 5 libraries. The pools consisted of the following  
 libraries and clones: Soares NBHSF pool 1:  
 309384-310919, 323208-323895 Soares NB2HP pool 1:  
 145032-147335, 147720-148103, 148872-149255, 15002 -  
 150407, 151176-152327 Soares NB2HF-9W pool 1:  
 758280-760583, 772104-774407 Soares NBHPA pool 1:  
 304776-306311, 320136-322823, 326280-326663 Soares NBHOT

BASE COUNT 138 a 202 c 164 g 192 t  
 ORIGIN  
 pool 1: 723720-726407, 739080-740999 subtraction by Bento  
 Soares and M. Fatima Bonaldo.

Query Match 87.4%; Score 546; DB 12; Length 696;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCAGAGACTGCGCGGGAGCGGGAAGAGACAGGCGCTGACAAACCGCGCTGTC 69  
 Db 603 TGCAGAGACTGCGCGGGAGCGGGAAGAGACAGGCGCTGACAAACCGCGCTGTC 544  
 QY 70 GGTGGTGGAGTGGCCATGTATGACCCGAGCCGCTTCTGTTGGGCTGTCGAGCAGAC 129  
 Db 543 GGTGGTGGAGTGGCCATGTATGACCCGAGCCGCTTCTGTTGGGCTGTCGAGCAGAC 484  
 QY 130 GCGGACAGCAGCAGCTGACAGAACCCGCGAATGCTGCGAGACACCGTGTACAG 189  
 Db 483 GCGGACAGCAGCAGCTGACAGAACCCGCGAATGCTGCGAGACACCGTGTACAG 424  
 QY 190 GAGCGGTTGATGACGAGCTGAGGTGAGAAACGCTCCGAGAAAGGAGAGAGATCAT 249  
 Db 423 GAGCGGTTGATGACGAGCTGAGGTGAGAAACGCTCCGAGAAAGGAGAGAGATCAT 364  
 QY 250 GTACGCCGGAAGTAGAGACTGTCAGTCCGTCGTTGGGTTGGCCGAGCCATGATCT 309  
 Db 363 GTACGCCGGAAGTAGAGACTGTCAGTCCGTCGTTGGGTTGGCCGAGCCATGATCT 304  
 QY 310 CCGAATCTGTTGGGATCCAGCATACGCCAATGTCAACAAATCAGCCCTGGCAGAC 369  
 Db 303 CCGAATCTGTTGGGATCCAGCATACGCCAATGTCAACAAATCAGCCCTGGCAGAC 244  
 QY 370 ACGAGCAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAGTAATGAT 429  
 Db 243 ACGAGCAGGAGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAGTAATGAT 184  
 QY 430 AAAACCTAAATATTTAGCCCTCTGTTGCTTACTGGCCGAGAAATGTATCAT 489  
 Db 183 AAAACCTAAATATTTAGCCCTCTGTTGCTTACTGGCCGAGAAATGTATCAT 124  
 QY 490 TTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACACAGCAGAGAAATTTAAGCTGT 549  
 Db 123 TTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACACAGCAGAGAAATTTAAGCTGT 64  
 QY 550 TCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGCACTTAATGCTTTAGACAGTG 606  
 Db 63 TCAACCCGGGGGAGTGGCTGTGTTAAAGAAAGCACTTAATGCTTTAGACAGTG 7

RESULT 4  
 BF594242/c 537 bp mRNA linear EST 12-DEC-2000  
 LOCUS 7n10d03.x1 NCI-CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:3564316.3,  
 DEFINITION similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39. ;, mRNA sequence.  
 ACCESSION BF594242  
 VERSION BF594242.1 GI:11686566  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 537)  
 AUTHORS NCI-MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfield M.D.,  
 Ph.D.



QY 327 TCCAGCATAGCGCCATGTCACAAACATCAGCCCTGGCGACACAGAGAGAGAGAG 386  
 DB 281 TCCAGCATAGCGCCATGTCACAAACATCAGCCCTGGCGACACAGAGAGAGAGAG 222  
 QY 387 ACAGAGAAAAGAAAACACAGCATGAGAACACACTTAATGATTAACCAATTAATATT 446  
 DB 221 ACAGAGAAAAGAAAACACAGCATGAGAACACACTTAATGATTAACCAATTAATATT 162  
 QY 447 AGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 506  
 DB 161 AGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 102  
 QY 507 GACAGCT 566  
 DB 101 GACAGCT 42  
 QY 567 GCGTGTCTTAAGAAAGAACCATTAATGCTTTAGACAGTG 606  
 DB 41 GCGTGTCTTAAGAAAGAACCATTAATGCTTTAGACAGTG 2

RESULT 6  
 BM669397/c 627 bp mRNA linear EST 27-FEB-2002  
 LOCUS UI-E-DWI-and-c-11-0-UI.s1 UI-E-DWI Homo sapiens cDNA clone  
 DEFINITION  
 ACCESSION BM669397 GI:18979294  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 627)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT

Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.reagen.com).  
 Seq primer: M13 Forward  
 Polya-Tes.

FEATURES  
 source

Location/Qualifiers  
 1..627  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="UI-E-DWI-and-c-11-0-UI"  
 /clone\_1ib="UI-E-DWI"  
 /tissue\_type="adult"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pRT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-E-DWI is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT73-Pac vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)<sub>18</sub> tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).  
 TAG-LIB-UI-E-DWI  
 TAG-Tissue-human lens  
 TAG-SEQ-CGATTAGCGA"  
 BASE COUNT 118 a 180 c 145 g 183 t 1 others  
 ORIGIN

Query Match 84.2%; Score 526; DB 13; Length 627;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 576; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 ACGGAGAGACAGAGGCGCTGCACAAAGCGGCGCTGCTGTGTGAGTGCAGTGA 89  
 DB 596 ACGGAGAGACAGAGGCGCTGCACAAAGCGGCGCTGCTGTGTGAGTGCAGTGA 537  
 QY 90 CGCGCAGCGCTTCTGCTGT 149  
 DB 536 CGCGCAGCGCTTCTGCTGT 477  
 QY 150 CGAACCACCGCGGAACTGCTGCGAGACACCGTGTACAGAGCGGCTTGTGACCGAGC 209  
 DB 476 CGAACCACCGCGGAACTGCTGCGAGACACCGTGTACAGAGCGGCTTGTGACCGAGC 417  
 QY 210 TGAGGTAGAAAACGCTCCGAGAAAGGAGAGAGATATGTAGCCCGGAATGAGACC 269  
 DB 416 TGAGGTAGAAAACGCTCCGAGAAAGGAGAGAGATATGTAGCCCGGAATGAGACC 357  
 QY 270 TCGTCCAGTCTGCTGT 329  
 DB 356 TCGTCCAGTCTGCTGT 297  
 QY 330 AGCATYACGGCCATGTGACAAATCAGCCCTGGGACACAGACAGAGAGAGAGACA 389  
 DB 296 AGCATYACGGCCATGTGACAAATCAGCCCTGGGACACAGACAGAGAGAGAGACA 237  
 QY 390 GAGAAAAGAAAACACAGCATGAGACACAGTAATGATTAATGATTAATGATTTTATG 449  
 DB 236 GAGAAAAGAAAACACAGCATGAGACACAGTAATGATTAATGATTAATGATTTTATG 177  
 QY 450 CCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 509  
 DB 176 CCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 117  
 QY 510 AGCTTCTTTTGGCCACAGAGAGAGAAATTTAACACTGTTTCAAAACCCGGGAGATTGGC 569  
 DB 116 AGCTTCTTTTGGCCACAGAGAGAGAAATTTAACACTGTTTCAAAACCCGGGAGATTGGC 57  
 QY 570 TGTGTAAAGAAAGACCATTAATGCTTTAGACAGTG 606  
 DB 56 TGTGTAAAGAAAGACCATTAATGCTTTAGACAGTG 20

RESULT 7  
 BM547680 696 bp mRNA linear EST 20-FEB-2002  
 LOCUS AGENCOURT\_5507108 NIH\_MGC\_124 Homo sapiens cDNA clone IMAGE:5727798  
 DEFINITION  
 ACCESSION BM547680 GI:18781656  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 696)  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov  
 Tissue Procurement: Invitrogen  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: L1M12722 row: h column: 07  
 High quality sequence stop: 641.  
 Location/Qualifiers

## FEATURES

source

1.696  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:572798"  
 /clone\_lib="NIH\_MGC\_124"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-Sport6; Site\_1: EcorV  
 (destroyed); Site\_2: NotI; RNA source male hippocampus,  
 age 27. Library is oligo-dT primed and directionally  
 cloned (EcorV site is destroyed upon cloning). Average  
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 012."  
 BASE COUNT 188 a 160 c 197 g 134 t 17 others  
 ORIGIN

Query Match 84.0%; Score 525; DB 13; Length 696;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCTTCAAGAGACTGGCGGCGGACGGAAGCAAGGGCGCTGCACAAACG 60  
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 DB 65 AGTCTCTTCAAGAGAGACTGGCGGCGGACGGAAGCAAGGGCGCTGCACAAACG 124  
 |||||||  
 QY 61 GGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120  
 |||||||  
 DB 125 GGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 184  
 |||||||  
 QY 121 CAGGACAGGGGCGGACAGACACCTGCAGCAACACCGCGGAACTCTCGAGAGAC 180  
 |||||||  
 DB 185 CAGGACAGGGGCGGACAGACACCTGCAGCAACACCGCGGAACTCTCGAGAGAC 244  
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 QY 181 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGTCCTCGAGAGAGG 240  
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 DB 245 CGTGTACAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGTCCTCGAGAGAGG 304  
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 QY 241 GAGGATCATGTACGCGCGGAGTAGACCTGCTCCAGTCGTCGTTGGGTTGGCGGACG 300  
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 DB 305 GAGGATCATGTACGCGCGGAGTAGACCTGCTCCAGTCGTCGTTGGGTTGGCGGACG 364  
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 QY 301 CATGATCTCCGAATCTGTTGGGATCCAGATACGGCCAAATGTACAAATCAGCCC 360  
 |||||||  
 DB 365 CATGATCTCCGAATCTGTTGGGATCCAGATACGGCCAAATGTACAAATCAGCCC 424  
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 QY 361 TGGGACAGACGAG 420  
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 DB 425 TGGGACAGACGAG 484  
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 QY 421 TAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
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 DB 485 TAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 544  
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 QY 481 GGTACCAATTTTTCAGTGTGGAGCTTGAACGCTCTTTTGGCCACAAGCAGAGAAATT 540  
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 DB 545 GGTACCAATTTTTCAGTGTGGAGCTTGAACGCTCTTTTGGCCACAAGCAGAGAAATT 604  
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 QY 541 AACACTGTTTCAACCCGGGGAGTTGGCTGTGTTA 576  
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 DB 605 AACACTGTTTCAACCCGGGGAGTTGGCTGTGTTA 640  
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RESULT 8  
 AM590950/c  
 LOCUS

AM590950 649 bp mRNA linear EST 22-MAR-2000  
 hg51e12.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2949166 3'

DEFINITION  
 similar to SW:GP39.HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39.; mRNA sequence.

ACCESSION  
 AM590950  
 VERSION  
 AM590950.1 GI:7278094  
 EST.

KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 649)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS  
 TITLE  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

COMMENT  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[image.lnl.gov/image/html/lresources.shtml](http://image.lnl.gov/image/html/lresources.shtml)

Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 457.

## FEATURES

source

1.649  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2949166"  
 /clone\_lib="NCI CGAP-GC6"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
 from the normalized library NCI-CGAP-GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonoids  
 1257096-1258631, 1469064-1470983, and 1475392-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo.  
 BASE COUNT 132 a 189 c 155 g 173 t  
 ORIGIN

Query Match 82.6%; Score 516; DB 10; Length 649;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 566; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 CAAGGGGCGCTGCACAAAGCGGGCGCTGCGGTGGAGAGTCCGATGACGAGCGG 99  
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 DB 568 CAAGGGGCGCTGCACAAAGCGGGCGCTGCGGTGGAGAGTCCGATGACGAGCGG 509  
 |||||||  
 QY 100 CTTCTCGTGGTGGCGGTGCTGCAGGACAGGCGGAGCAGACACCTGCAGACACCGG 159  
 |||||||  
 DB 508 CTTCTCGTGGTGGCGGTGCTGCAGGACAGGCGGAGCAGACACCTGCAGACACCGG 449  
 |||||||  
 QY 160 CCGAAATCTGCTCGAGAGACACCGTGTACAGAGCGGGTGTGATGACCGAGCTAGGTAGA 219  
 |||||||  
 DB 448 CCGAAATCTGCTCGAGAGACACCGTGTACAGAGCGGGTGTGATGACCGAGCTAGGTAGA 389  
 |||||||  
 QY 220 AAAGCTCTCGAAGAGGAGAGAGATCATGTACGCGCGGAGTGAAGACTGTCTCAGTGC 279  
 |||||||  
 DB 388 AAAGCTCTCGAAGAGGAGAGAGATCATGTACGCGCGGAGTGAAGACTGTCTCAGTGC 329  
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QY 280 GTGCTGGGTTGGCCCGAGCCATGATCCTCCGAATCTGTTGGGATCCAGCATACGCG 339  
|||||  
Db 328 GTGCTGGGTTGGCCCGAGCCATGATCCTCCGAATCTGTTGGGATCCAGCATACGCG 269  
QY 340 CAATGTACACATCAGCCCTGGGAGACACGAGAGAGAGAGAGAGAGAGAGAGAG 399  
Db 268 CAATGTACACATCAGCCCTGGGAGACACGAGAGAGAGAGAGAGAGAGAGAGAG 209  
QY 400 AACACAGCATGAGAACAGTAATGATTAATGATTAATGATTAATGATTAATGATTA 459  
Db 208 AACACAGCATGAGAACAGTAATGATTAATGATTAATGATTAATGATTAATGATTA 149  
QY 460 TGTGCTTACTGGCCAGAGAAATGTACCAATTTTTCAGTTGGACTTGACAGCTTCTTT 519  
Db 148 TGTGCTTACTGGCCAGAGAAATGTACCAATTTTTCAGTTGGACTTGACAGCTTCTTT 89  
QY 520 GCCACAAGCAAGAGAGAAATTAACATGTTTCAAAACCCGGGGAGTTGGCTGTAAAG 579  
Db 88 GCCACAAGCAAGAGAGAAATTAACATGTTTCAAAACCCGGGGAGTTGGCTGTAAAG 29  
QY 580 AAGACCATTAATGCTTTAGACAGTG 606  
Db 28 AAGACCATTAATGCTTTAGACAGTG 2  
RESULT 9  
BE858216/c 551 bp mRNA linear EST 29-SEP-2000  
LOCUS 7919g07.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:3305972.3  
DEFINITION similar to SW:GP33\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GPR33. ; mRNA sequence.  
ACCESSION BE858216 GI:10372861  
VERSION BE858216  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 551)  
NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL, send email to:  
infoimage.lnl.gov  
Seq primer: -40UP from GIBCO  
High quality sequence stop: 490.  
location/Qualifiers  
FEATURES  
SOURCE  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3306972"  
/clone\_id="NCI\_CGAP\_Brn23"  
/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10b"  
/note="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAGTGGAGCGCGCATATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.

BASE COUNT 110 a 161 c 128 g 152 t  
ORIGIN  
Query Match 79.8%; Score 499; DB 12; Length 551;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 57 AGCGGGCGCTGTGGTGGAGTGGCATGATGCGCAGAGCGGTTTCGNGTGGGCT 116  
Db 551 AGCGGGCGCTGTGGTGGAGTGGCATGATGCGCAGAGCGGTTTCGNGTGGGCT 492  
QY 117 GCTGACGCGACAGCGCGGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 176  
Db 491 GCTGACGCGACAGCGCGGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 432  
QY 177 ACACCGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAACGTCCTCCGAAGG 236  
Db 431 ACACCGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAAACGTCCTCCGAAGG 372  
QY 237 GGAGGAGATCATGTATGACCGCGGAGTACGCTGCTGAGTGGCTGGGTTGGCGG 296  
Db 371 GGAGGAGATCATGTATGACCGCGGAGTACGCTGCTGAGTGGCTGGGTTGGCGG 312  
QY 297 CAGCCATGATCTCCGATCTGTTGGCATCCAGCATACGCCCATGTCAACAATCA 356  
Db 311 CAGCCATGATCTCCGATCTGTTGGCATCCAGCATACGCCCATGTCAACAATCA 252  
QY 357 GCCCTGGCGACACGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416  
Db 251 GCCCTGGCGACACGACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192  
QY 417 ACAGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 476  
Db 191 ACAGTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 132  
QY 477 AAATGATCAATTTTTCAGTGTGACCTGACAGCTTCTTTTCCACACAGAGAGAG 536  
Db 131 AAATGATCAATTTTTCAGTGTGACCTGACAGCTTCTTTTCCACACAGAGAGAG 72  
QY 537 ATTTACACGCTTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAACATTAATGCT 596  
Db 71 ATTTACACGCTTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAACATTAATGCT 12  
QY 597 TTAGACAGTG 606  
Db 11 TTAGACAGTG 2  
RESULT 10  
BF939693/c 540 bp mRNA linear EST 22-JAN-2001  
LOCUS nacc8b12.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:3440591.3  
DEFINITION similar to SW:GP33\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GPR33. ; mRNA sequence.  
ACCESSION BF939693  
VERSION BF939693  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 540)  
NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.



QY 436 ATAAATATTAGCCCTCTGTTCTGCTTACTGCGCAGAGAAATGTACCAATTTTCA 495  
 DB 301 ATAAATATTAGCCCTCTGTTCTGCTTACTGCGCAGAGAAATGTACCAATTTTCA 360  
 QY 496 GTGTGACTTGACAGCTTCTTTTGCACAGAGAGAAATTTAACAAGTTTCAAC 555  
 DB 361 GTTGTGACTTGACAGCTTCTTTTGCACAGAGAGAAATTTAACAAGTTTCAAC 420  
 QY 556 CCGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGT 606  
 DB 421 CCGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGT 471

RESULT 12 527 bp mRNA linear EST 31-JAN-2000  
 AM338938  
 LOCUS ha68h04.x1 NCI\_CGAP\_Pan1 Homo sapiens CDNA clone IMAGE:2878903 3'  
 DEFINITION similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39. ; mRNA sequence.

ACCESSION AM338938.1 GI:6835564  
 VERSION EST  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 527)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Life Technologies catalog #: 11548-013  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.lnl.gov/bdrp/image/image.html

FEATURES  
 source  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 420.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2878903"  
 /clone\_id="NCI\_CGAP\_Pan1"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B"  
 /note="Organ: Pancreas; Vector: PCMV-SPORT6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

BASE COUNT 103 a 143 c 120 g 161 t  
 ORIGIN

Query Match 73.9% Score 462; DB 10; Length 527;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 94 CAGGCGCTTCTGCTGTTGGCGTGCAGCAGCAGCGCAGCAGCAGCAGCAGCAG 153  
 DB 527 CAGGCGCTTCTGCTGTTGGCGTGCAGCAGCAGCGCAGCAGCAGCAGCAGCAG 468  
 QY 154 CACCGCGCGAACTGCTGCGAGACACCGGTGTACAGAGCGGTTGATGACCGAGCTGAG 213  
 DB 467 CACCGCGCGAACTGCTGCGAGACACCGGTGTACAGAGCGGTTGATGACCGAGCTGAG 408  
 QY 214 GTAGAAAACGCTTCGAGAGAGGAGAGATCATGTACGCCGCGAGTAGAGCTCGT 273  
 DB 407 GTAGAAAACGCTTCGAGAGAGGAGAGATCATGTACGCCGCGAGTAGAGCTCGT 348

QY 274 CCAGTGTGCTGGTGGTTGGCCGACGACCATGATCCTCCGATTCGTGTGGCATCCAGCA 333  
 DB 347 CCAGTGTGCTGGTGGTTGGCCGACGACCATGATCCTCCGATTCGTGTGGCATCCAGCA 288  
 QY 334 TACGGCAATGTACAAACATTCAGCCCTGGGCGACACGAGCAGAGAGAGAGACAGAGA 393  
 DB 287 TACGGCAATGTACAAACATTCAGCCCTGGGCGACACGAGCAGAGAGAGAGACAGAGA 228  
 QY 394 AAGAAAAACACAGCATGTAGACACACTTAATGTAATTAACCATTAATTTAGCCCT 453  
 DB 227 AAGAAAAACACAGCATGTAGACACACTTAATGTAATTAACCATTAATTTAGCCCT 168  
 QY 454 CTGCTGTGCTTACTGCGCCAGGAAATGTACCAATTTTCACTGTGTGACTGACACT 513  
 DB 167 CTGCTGTGCTTACTGCGCCAGGAAATGTACCAATTTTCACTGTGTGACTGACACT 108  
 QY 514 TCTTTTGGCCCAAGCAAGAGAGAAATTTAACAAGTTTCAACCCGGGAGTTGGCTGTG 573  
 DB 107 TCTTTTGGCCCAAGCAAGAGAGAAATTTAACAAGTTTCAACCCGGGAGTTGGCTGTG 48  
 QY 574 TTAAGAAAGACCATTAATGCTTTAGACAGT 606  
 DB 47 TTAAGAAAGACCATTAATGCTTTAGACAGT 15

RESULT 13 515 bp mRNA linear EST 15-FEB-1999  
 A1336858  
 LOCUS qx86g11.x1 NCI\_CGAP\_G66 Homo sapiens CDNA clone IMAGE:2009444 3'  
 DEFINITION similar to SW:NTRI\_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ; mRNA  
 sequence.

ACCESSION A1336858  
 VERSION A1336858  
 KEYWORDS  
 SOURCE EST  
 ORGANISM human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 515)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.lnl.gov/bdrp/image/image.html  
 Insert length: 1161 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 444.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2009444"  
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 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA  
 from the normalized library NCI\_CGAP\_G64 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).

FEATURES  
 source

BASE COUNT 103 a 142 c 119 g 151 t  
 ORIGIN

Query Match 73.4%; Score 459; DB 9; Length 515;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

97 GCGCTCTCTGTTGGTGGCTGCGAGCAGAGCGGCGGACAGACACCTGCGACAGAAC 156  
 515 GCGCTCTCTGTTGGTGGCTGCGAGCAGAGCGGCGGACAGACACCTGCGACAGAAC 456  
 157 CCGCGAAACCTGCTGCGAGACACCGCTGTACAGAGAGCGGCTTGTATGACCGAGCTGAGTA 216  
 455 CCGCGAAACCTGCTGCGAGACACCGCTGTACAGAGAGCGGCTTGTATGACCGAGCTGAGTA 396  
 217 GAAAAACGCTCTGCGAGAGAGGAGGATCATGTACGCCCGGAACTAGAGACCTGCTCCA 276  
 395 GAAAAACGCTCTGCGAGAGAGGAGGATCATGTACGCCCGGAACTAGAGACCTGCTCCA 336  
 277 GTCGTCTGTTGGGTTGGCGCGACCGCATGATCCGCAATCTGTTGGCATCCAGCATAC 336  
 335 GTCGTCTGTTGGGTTGGCGCGACCGCATGATCCGCAATCTGTTGGCATCCAGCATAC 276  
 337 GCCCAATGTACACACATCATGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAGAA 396  
 275 GGCCTAATGTACACACATCATGCCCTGGGCGACAGCAGAGAGAGAGAGAGAGAGAA 216  
 397 GAAAAACGAGATGAGAACACATTAATGAATTAATTAATTAATTAATTAATTAATTAAT 456  
 215 GAAAAACGAGATGAGAACACATTAATGAATTAATTAATTAATTAATTAATTAATTAAT 156  
 457 TTTCTGTCTTACTGGCGCAGAGAAATGTTACCAATTTTTCAGTGTGAGCTGACAGCTTC 516  
 155 TTTCTGTCTTACTGGCGCAGAGAAATGTTACCAATTTTTCAGTGTGAGCTGACAGCTTC 96  
 517 TTTGCCACAGCAGAGAGAGAAATTAACACTGTTTCAACCCGGGGAGTTGGCTGTGTA 576  
 95 TTTGCCACAGCAGAGAGAGAAATTAACACTGTTTCAACCCGGGGAGTTGGCTGTGTA 36  
 577 AAGAAAGACCATTAATGCTTTAGACAGTG 606  
 35 AAGAAAGACCATTAATGCTTTAGACAGTG 6

RESULT 14  
 AM149665/c  
 LOCUS  
 DEFINITION x140h05.x1 NCI\_CGAP\_Brn50 Homo sapiens cDNA clone IMAGE:2620569 3'  
 similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39.; mRNA sequence.  
 ACCESSION AM149665  
 VERSION AM149665.1 GI:6197561  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 690)  
 AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BTGAIP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMW at:  
 www-bio.lnlnl.gov/bdrp/image/image.html

FEATURES  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2620569"  
 /clone\_11b="NCI\_CGAP\_Brn50"  
 /tissue\_type="medulloblastoma"  
 /lab\_host="DH10B (phage resistant)"  
 /note="Organ: brain; Vector: Vector: p773D-Pac (Pharmacia) with a  
 modified polylinker; 1st strand cDNA was prepared from  
 medulloblastoma tumor tissue, and was then primed with a  
 Not I - 01190(OT) primer. Double-stranded cDNA was ligated  
 to Eco RI adaptors (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of the modified  
 p773 vector. This library is normalized. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 142 a 196 c 160 g 191 t  
 ORIGIN

Query Match 70.7%; Score 442; DB 10; Length 690;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 592; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

12 CAGAGACTGGCGCGCGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 71  
 607 CAGAGAGCTGGCGCGCGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548  
 72 TGGTGAGTGGCGCATGTACGCGAGCGGCTTCGCTGTTGGCGCTGCTGACGAGCAGC 131  
 547 TGGTGAGTGGCGCATGTACGCGAGCGGCTTCGCTGTTGGCGCTGCTGACGAGCAGC 488  
 132 GCGAGCAGACACCTGTCACAGAACACCCGCCGAACTGTGCGAGACACCGTGTACAGGA 191  
 487 GCGAGCAGACACCTGTCACAGAACACCCGCCGAACTGTGCGAGACACCGTGTACAGGA 428  
 192 GCGGCTGATGACCGGAGCTGAGGTAGAAACAGTCTCCGAGAAAGGAGAGAGATATAT 251  
 427 GCGGCTGATGACCGGAGCTGAGGTAGAAACAGTCTCCGAGAAAGGAGAGATATAT 368  
 252 ACGCCCGAAGTAGAGACCTGTCAGTCTGCTTGGGTTGGCGGAGCATGATCTCTCC 311  
 367 ACGCCCGAAGTAGAGACCTGTCAGTCTGCTTGGGTTGGCGGAGCATGATCTCTCC 308  
 312 GAATCTGTTGGGATTCAGCATATGCGGCAATGTCACAAACATTCAGCCCTGGGAGACAC 371  
 307 GAATCTGTTGGGATTCAGCATATGCGGCAATGTCACAAACATTCAGCCCTGGGAGACAC 248  
 372 GAGCAGAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGACAGACATTAATGAATTA 431  
 247 GAGCAGAGAGAGAGAGACAGAGAAAGAAACACAGCATGAGACAGACATTAATGAATTA 188  
 432 AACCATTAATTAATTAAGCCCTCTGTTCTGCTTACTGGCCAGGAAATGATACCAATTT 491  
 187 AACCATTAATTAATTAAGCCCTCTGTTCTGCTTACTGGCCAGGAAATGATACCAATTT 128  
 492 TTTCACTGTTGGACCTTGACAGCTTCTTTTGGCCACAAGCAGAGAGAAATTAACACTGTTTC 551  
 127 TTTCACTGTTGGACCTTGACAGCTTCTTTTGGCCACAAGCAGAGAGAAATTAACACTGTTTC 68  
 552 AAACCCGGGGAGTTGGCTGCTTAAAGAAAGACATTAATGCTTTAGACAGTG 606  
 67 AAACCCGGGGAGTTGGCTGCTTAAAGAAAGACATTAATGCTTTAGACAGTG 13

RESULT 15  
 AM075598/c  
 LOCUS  
 DEFINITION x140h07.x1 NCI\_CGAP\_K1413 Homo sapiens cDNA clone IMAGE:2577252 3'  
 similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR

GPR39.1, mRNA sequence.  
 ACCESSION AM075598  
 VERSION AM075598.1 GI:6030596  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 500)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
 Genome Sequencing Center  
 Clone distribution: NCI-CCGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrip/image/image.html

Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 413.  
 Location/Qualifiers  
 source 1..500  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2577252"  
 /clone\_1lb="NCI CGAP Kid13"  
 /tissue.type="NCI pooled Wilms' tumors, one primary and one  
 metastatic to brain"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: PCMV-SPORE6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies."

BASE COUNT 99 a 139 c 114 g 148 t  
 ORIGIN  
 Query Match 69.9%; Score 437; DB 10; Length 500;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 119 TGCAGCGACAGGGGGGCGACAGACCTGCGACGACCCCGCAACTGCTGCGAGGAC 178  
 |||||||  
 DB 490 TGCAGCGACAGGGGGGCGACAGACCTGCGACGACCCCGCAACTGCTGCGAGGAC 431  
 |||||||  
 QY 179 ACCGTGTACAGAGCGGGGTTGATGACGAGCTGAGGTAGAAAACGTCCTCGAGAAAGGG 238  
 |||||||  
 DB 430 ACCGTGTACAGAGCGGGGTTGATGACGAGCTGAGGTAGAAAACGTCCTCGAGAAAGGG 371  
 |||||||  
 QY 239 AGGAGATCATGTACGCCCGGAGTAGAGACCTGCTCAGTGTGCTTGGGTTGGCCGCA 298  
 |||||||  
 DB 370 AGGAGATCATGTACGCCCGGAGTAGAGACCTGCTCAGTGTGCTTGGGTTGGCCGCA 311  
 |||||||  
 QY 299 GCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCAAATGTCAACAATCAGC 358  
 |||||||  
 DB 310 GCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCAAATGTCAACAATCAGC 251  
 |||||||  
 QY 359 CCTGGGACAGACAG 418  
 |||||||  
 DB 250 CCTGGGACAGACAG 191  
 |||||||  
 QY 419 AGTAATGAATAAAACATATAATATTAGCCCTCTGCTGTGCTTACTGCGCCAGAA 478  
 |||||||  
 DB 190 AGTAATGAATAAAACATATAATATTAGCCCTCTGCTGTGCTTACTGCGCCAGAA 131  
 |||||||  
 QY 479 ATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAGCAAGAGAGAA 538  
 |||||||  
 DB 130 ATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTTGCACAGCAAGAGAGAA 71  
 |||||||

QY 539 TTACACTGTTTCAACCCCGGGAGCTGGCTGTGTTAAAGAAAGACATTAAATGCTT 598  
 |||||||  
 DB 70 TTACACTGTTTCAACCCCGGGAGCTGGCTGTGTTAAAGAAAGACATTAAATGCTT 11  
 |||||||  
 QY 599 AGACAGTG 606  
 |||||||  
 DB 10 AGACAGTG 3  
 |||||||

RESULT 16  
 A1884686 591 bp mRNA linear EST 07-MAR-2000  
 LOCUS w1834d07.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2431501 3'  
 DEFINITION similar to SW:GPR39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39.1, mRNA sequence.  
 ACCESSION A1884686  
 VERSION A1884686  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 591)  
 NCI/MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrip/image/image.html  
 Insert Length: 1462 Std Error: 0.00  
 Seq primer: -40UP from Glibco  
 High quality sequence stop: 444.  
 Location/Qualifiers  
 source 1..591  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2431501"  
 /clone\_1lb="NCI CGAP Brn25"  
 /tissue.type="anaplastic oligodendroglioma"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGGAGCGCGCGCATAGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT73 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT 109 a 179 c 147 g 155 t 1 others  
 ORIGIN  
 Query Match 68.0%; Score 425; DB 9; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTCAGAGACTGGCGCGGAGCGGAGCAAGCAAGCGGCGTCAACAAACG 60  
 |||||||  
 DB 447 AGTTCTCCTTCAGAGACTGGCGCGGAGCGGAGCAAGCAAGCGGCGTCAACAAACG 388  
 |||||||  
 QY 61 GCGCGTGTGCGGTGAGATGCGCATGTACGCGCAGCGCTTCTCGTGTGGGTGCGTCTG 120  
 |||||||

Db	387	GGCGCTGTCGGTGGTGAGTGCAGTCATGACCGCAGCGCTTCTTCGTTGGCGTGTG	328
Qy	121	CAGGCACAGGCGGCGACGACACACACTCTCAGACGACACCCCGCGAATCTGCTGCAGGACAC	180
Db	327	CAGGACACGGGCGGAGACACACACTCTCAGAACACCCCGCGAAACTGCTGCAGGACAC	268
Qy	181	CGTGCACGAGGCGGGTTGATGATCCGAGCTGAGGTTACAAAAGCTCTCCGAGAGGGGAG	240
Db	267	CGTGCACGAGGCGGGTTGATGATCCGAGCTGAGGTTACAAAAGCTCTCCGAGAGGGGAG	208
Qy	241	GAGGATCATGTACGCCCGCGGAAGTGTAGACCTCGTCTCAGTCTGGTGTGGGTTGGCCGACG	300
Db	207	GAGGATCATGTACGCCCGCGGAAGTGTAGACCTCGTCTCAGTCTGGTGTGGGTTGGCCGACG	148
Qy	301	CATGATCTCTCCGAATCTGTGTGGGCATTCAGCATACGGCCATGTCTCAACAATCAAGCCC	360
Db	147	CATGATCTCTCCGAATCTGTGTGGGCATTCAGCATACGGCCATGTCTCAACAATCAAGCCC	88
Qy	361	TGGGCACACACAGACAGGAGGAGGAGACACAGAAAAAGAAAAACACAGCATGACACACAG	420
Db	87	TGGGCACACACAGACAGGAGGAGGAGACACAGAAAAAGAAAAACACAGCATGACACACAG	28
Qy	421	TAAAT 425	
Db	27	TAAAT 23	

RESULT 17	LOCUS	DEFINITION	ACCSSION VERSION
BE385990	676 bp mRNA	EST 21-JUL-2000	
	601227636p1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:3617696 5',		
	mRNA sequence.		
	BE385890		
	BE38590.1 GI:9331355		

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 676)
REFERENCE	NIH-MGC <a href="http://mgc.ncbi.nlm.nih.gov/">http://mgc.ncbi.nlm.nih.gov/</a> .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	

## FEATURES

### Location/Qualifiers

**source**

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:361766"
/clone_id="NH_MGC-20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB1; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT
168 a 172 c 199 g 137 t

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Query Match

68.0%; Score 425; DB 10; Length 676;

Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	AGTTCTCCTTGACAGAGGAACTGGCGCCGGGACGCGAAGACCAACGGGGCGTTGCAACAAAGCG	60
Db	163	AGTTCTCCTTGACAGAGGAACTGGCGCCGGGACGCGAAGACCAACGGGGCGTTGCAACAAAGCG	222
OY	61	GGCGCTGTGCGGTGATGGAGTGGCGCATGTACGGCAGGGCGCTTCTGCTGGTGGCGTGTG	120
Db	223	GGCGCTGTGCGGTGATGGAGTGGCGCATGTACGGCAGGGCGCTTCTGCTGGTGGCGTGTG	282
OY	121	CAGCGACAGCGCGGACAGCAGCAGCAGCAACACCCGCGCAAACTGCTGGGAGAGCAC	180
Db	283	CAGCGACAGCGCGGACAGCAGCAGCAGCAACACCCGCGCAAACTGCTGGGAGAGCAC	342
OY	181	CGTGTACAGAGAGCGGGTTGATGATCAGCAGACTGTAGTATGAAAAACGTCCTCGAAGAGGGAG	240
Db	343	CGTGTACAGAGAGCGGGTTGATGATCAGCAGACTGTAGTATGAAAAACGTCCTCGAAGAGGGAG	402
OY	241	GAGGATCATGTATACGCCCGGAGAGTAGGACCTGCTCCAGTCTGCTTGGGTTGGCCGACG	300
Db	403	GAGGATCATGTATACGCCCGGAGAGTAGGACCTGCTCCAGTCTGCTTGGGTTGGCCGACG	462
OY	301	CATGATTCCTCCGAATCTGTTGGGATCCAGATACGGGCAATGTACAAACAATCAGGCC	360
Db	463	CATGATTCCTCCGAATCTGTTGGGATCCAGATACGGGCAATGTACAAACAATCAGGCC	522
OY	361	TGGGCAGACAGCAGCAGGAGGAGAGAGACAGAAAAAGAAAAACACAGCATGTGAACACAG	420
Db	523	TGGGCAGACAGCAGCAGGAGGAGAGAGACAGAAAAAGAAAAACACAGCATGTGAACACAG	582
OY	421	TAAAT 425	
Db	583	TAAAT 587	

RESULT	18
A1150931/c	
LOCUS	
DEFINITION	467 bp mRNA linear EST 26-OCT-1998
	gb53c04.x1 NC1 CGAP Brn2 Homo sapiens cDNA clone IMAGE:1703814.3 ' , mRNA similar to SM:NTR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ' , mRNA sequence.
ACCESSION	A1150931
VERSION	A1150931.1 GI:3679400
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

JOURNAL  
COMMENT  
REFERENCE 1 (bases 1 to 467)  
AUTHORS NCI/NIHDS-CGAP  
TITLE http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: [www.bio.linn.gov/bdrrp/image/image.html](http://www.bio.linn.gov/bdrrp/image/image.html)  
Insert length: 1149 Std Error: 0.00  
Seq primer: ~40m13 fwd. Er from Amersham  
High quality sequence stop: 425.  
Location/Qualifiers  
1. .467

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/organism="Homo sapiens"  
/db_xref="taxon:9606"
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Db      131 AGTGTGGACCTTGACAGCTTTTGGCCACAGAACAGAGATTTACACTGTTTCAAA 72
QY      555 CCGGGGGAGTTGGCTGTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTG 606
Db      71  CCGGGGGAGTTGGCTGTGTGTTAAGAAAGACCATTAATGCTTTAGACAGTG 20

RESULT 20
LOCUS   A1018769/c 537 bp mRNA linear EST 27-AUG-1998
DEFINITION ov32e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639038
            3' similar to SW:NTNL_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;
            mRNA sequence.
ACCESSION A1018769
VERSION   A1018769.1 GI:3232567
KEYWORDS EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 537)
           NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
           Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
           , Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CCAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www.bio.llnl.gov/bbrp/image/image.html
           Insert Length: 1394 Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 452.
           Location/Qualifiers
FEATURES
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                   /db_xref="taxon:9606"
                   /clone_image="1639038"
                   /clone_lib="Soares_testis_NHT"
                   /sex="male"
                   /lab_host="DH10B"
                   /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                   polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                   was prepared from mRNA obtained from Clontech Laboratories
                   , Inc., and primed with a Not I - oligo(dT) primer [5'
                   TGTTCACATCTGAGTGGAGCGCGCCGCCCAATTTTTTTTTTTT 3'].
                   Double-stranded cDNA was ligated to Eco RI adaptors
                   (Pharmacia), digested with Not I and cloned into the Not I
                   and Eco RI sites of the modified pT7T3 vector. Library
                   went through one round of normalization to Col5, and was
                   constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      105 a 147 c 126 g 159 t
ORIGIN
Query Match      66.4%; Score 415; DB 9; Length 537;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 515; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      84 CATGTACGGGCGAGGCGCTCTGTGTTGGCGTGCAGCGACAGGCGGCACACAGCA 143
Db      537 CATGTACGGGCGAGGCGCTCTGTGTTGGCGTGCAGCGACAGGCGGCACACAGCA 478
QY      144 CCGTGCAGAACCCCGCAAACTGCTGCAGAGACACCGTGTACAGAGCGGGTGTATGA 203
Db      477 CCGTGCAGAACCCCGCAAACTGCTGCAGAGACACCGTGTACAGAGCGGGTGTATGA 418
QY      204 CCGAGCTGAGGTAGAAAAGCTCCGAGAGAGGAGAGAGATCATGTACGCCGGAAGT 263
Db      417 CCGAGCTGAGGTAGAAAAGCTCCGAGAGAGGAGAGAGATCATGTACGCCGGAAGT 358

```

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QY      264 AGGACCTCGTCCAGTCGTGCTGGTTGGCCGACACCCAGCAGTCCGGAATCGGTGG 323
Db      357 AGGACCTCGTCCAGTCGTGCTGGTTGGCCGACACCCAGCAGTCCGGAATCGGTGG 298
QY      324 GCATCCAGCATACGGCCCAATGTGCACAACATCAGCCCTGGGCGACAGCAGAGAGGA 383
Db      297 GCATCCAGCATACGGCCCAATGTGCACAACATCAGCCCTGGGCGACAGCAGAGAGGA 228
QY      384 GAGACAGAGAAAAGAAAACACAGCATGAGACACAGTAATGATTAATTAATTAATTA 443
Db      237 GAGACAGAGAAAAGAAAACCCAGCATGAGAACCCGTAATGTAATTAATTAATTAATTA 178
QY      444 TTTAGCCCTCTGCTGCTGCTTACTGCGCAGAGAAATGATCAATTTTCACTGTTGA 503
Db      177 TTTAGCCCTCTGCTGCTGCTTACTGCGCAGAGAAATGATCAATTTTCACTGTTGA 118
QY      504 CTTGACAGCTTTCTTTTGGCCACAAGAGAGAAATTTAACACTGTTCAAAACCCGGGGGA 563
Db      117 CTTGACAGCTTTCTTTTGGCCACAAGAGAGAAATTTAACACTGTTCAAAACCCGGGGGA 58
QY      564 GTTGGCTGTGTTAAGAAAGACCATTAATGCTTTAG 600
Db      57 GTTGGCTGTGTTAAGAAAGACCATTAATGCTTTAG 21

RESULT 21
A613995/c 396 bp mRNA linear EST 06-OCT-1997
DEFINITION no86c08.s1 NCI-CCAP_AAI Homo sapiens cDNA clone IMAGE:113710 3'
            similar to SW:NTNL_RAT P20789 NEUROTENSIN RECEPTOR ; mRNA sequence.
ACCESSION A613995
VERSION   A613995.1 GI:2466129
KEYWORDS EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 396)
           NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
           Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
           Emmert-Buck, M.D., Ph.D.
           cDNA Library Preparation: Stratagene, Inc., David B. Kitzman,
           Ph.D.
           cDNA Library Arraying: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CCAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www.bio.llnl.gov/bbrp/image/image.html
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 395.
           Location/Qualifiers
FEATURES
   source          1..396
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone_image="113710"
                   /clone_lib="NCI-CCAP_AAI"
                   /tissue_type="adrenal adenoma"
                   /lab_host="SOLR (kanamycin resistant)"
                   /note="Organ: adrenal gland; Vector: Bluescript SK-;
                   Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
                   Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5'
                   adaptor sequence: 5' GAATTCGACAGAG 3' 3' adaptor
                   sequence: 1.6 kb"
BASE COUNT      56 a 135 c 103 g 102 t
ORIGIN

```





cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbp/image/image.html](http://www.bio.llnl.gov/dbp/image/image.html)  
 Insert Length: 826 Std Error: 0.00  
 Seg primer: -40up from Gibco  
 High quality sequence stop: 395  
 POLYA-No.

## FEATURES

## source

Location/Qualifiers  
 1..396  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:217941"  
 /clone\_lib="NCI-CGAP\_Ut2"  
 /tissue\_type="moderately-differentiated endometrial  
 adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: Salt;  
 Site\_2: Not; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.85 kb. Life Technologies catalog #:  
 1139-012"

BASE COUNT 62 a 124 c 96 g 114 t  
 ORIGIN

Query Match 62.4%; Score 390; DB 9; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 390; Conservative 0;

58 GCGGGCGCTGTCGTCGTGAGTGCATGTACGCCAGCGCTTCGTGTTGGCGTG 117  
 117 GCGGGCGCTGTCGTCGTGAGTGCATGTACGCCAGCGCTTCGTGTTGGCGTG 117  
 396 GCGGGCGCTGTCGTCGTGAGTGCATGTACGCCAGCGCTTCGTGTTGGCGTG 337  
 118 CTGCACGACAGCGCGCAGACAGCCTGCAGCAACACCCCGGAATCTGCTCCAGGA 177  
 336 CTGCACGACAGCGCGCAGACAGCCTGCAGCAACACCCCGGAATCTGCTCCAGGA 277  
 178 CACCGTGTACAGAGCGGGGTGATGACCGAGCTGAGTGAAGAAAGCTCTCGAAGAGG 237  
 276 CACCGTGTACAGAGCGGGGTGATGACCGAGCTGAGTGAAGAAAGCTCTCGAAGAGG 217  
 238 GAGGAGATCATGTATGACCCCGGAAGTAGACCTGCTCCAGCTGCTGGGTTGGCCGC 237  
 216 GAGGAGATCATGTATGACCCCGGAAGTAGACCTGCTCCAGCTGCTGGGTTGGCCGC 157  
 298 AGCCATGATCCTCGAATCGTGTGGGCAATCCAGCATAGCGCCAAATGTCAACAATCAG 357  
 156 AGCCATGATCCTCGAATCGTGTGGGCAATCCAGCATAGCGCCAAATGTCAACAATCAG 97  
 358 CCCTGGGACAGACAGAGAGGAGAGACAGAGAAAAGAAACACACATGAGAAC 417  
 96 CCCTGGGACAGACAGAGAGGAGAGACAGAGAAAAGAAACACACATGAGAAC 37  
 418 CAGTAATGAATAAACCAATAAATATTTA 447  
 36 CAGTAATGAATAAACCAATAAATATTTA 7

RESULT 24  
 BE350014/c 534 bp mRNA linear EST 18-JUL-2000  
 LOCUS  
 DEFINITION  
 ht07g12.x1 NCI-CGAP\_Kid13 Homo sapiens cDNA clone IMAGE:3146086 3'  
 similar to SW:GP39\_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39. ; mRNA sequence.

ACCESSION BE350014  
 VERSION BE350014  
 KEYWORDS GI:9261867  
 SOURCE human  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 534)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE  
 JOURNAL  
 COMMENT  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail@nln.gov](mailto:cgaps-remail@nln.gov)  
 Tissue procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life  
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
 Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
 Seg primer: -40up from Gibco  
 High quality sequence stop: 408.

## FEATURES

## source

Location/Qualifiers  
 1..534  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3146086"  
 /clone\_lib="NCI-CGAP\_Kid13"  
 /tissue\_type="2 pooled Wilms' tumors, one primary and one  
 metastatic to brain"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site\_1: Salt;  
 Site\_2: Not; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies."

BASE COUNT 98 a 172 c 143 g 121 t  
 ORIGIN

Query Match 62.4%; Score 390; DB 10; Length 534;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTTCTCCTTGACAGAGACTGGCGCGGACCGGAAGAGCAAGCGCGTGCACAAACG 60  
 390 AGTTCTCCTTGACAGAGACTGGCGCGGACCGGAAGAGCAAGCGCGTGCACAAACG 331  
 61 GCGGCTGTGTCGTGTCGTGAGTGCATGTACGCCAGCGCTTCGTGTTGGCGTGCTG 120  
 330 GCGGCTGTGTCGTGTCGTGAGTGCATGTACGCCAGCGCTTCGTGTTGGCGTGCTG 271  
 121 CAGCGACAGCGCGCAGACAGCAGCTGACGAACACCCCGGAATCTGCTCCAGAGCAC 180  
 270 CAGCGACAGCGCGCAGACAGCAGCTGACGAACACCCCGGAATCTGCTCCAGAGCAC 211  
 181 CGTGTACAGAGCGGGGTGATGACCGAGCTGAGTGAAGAAAGCTCTCCGAGAAGGGAG 240  
 210 CGTGTACAGAGCGGGGTGATGACCGAGCTGAGTGAAGAAAGCTCTCCGAGAAGGGAG 151  
 241 GAGGATCATGTATGACCCCGGAAGTAGACCTGCTCCAGCTGCTGGGTTGGCCGAGC 300  
 150 GAGGATCATGTATGACCCCGGAAGTAGACCTGCTCCAGCTGCTGGGTTGGCCGAGC 91  
 301 CATGATCCTCCGAATCTGTTGGGCATCCAGCAATAGCCCAATGTCAACAATCAGCCC 360  
 90 CATGATCCTCCGAATCTGTTGGGCATCCAGCAATAGCCCAATGTCAACAATCAGCCC 31  
 361 TGGGACAGACAGAGAGAGAGAGAGAG 390  
 30 TGGGACAGACAGAGAGAGAGAGAGAGAG 1

RESULT 25  
 A1765236/c 456 bp mRNA linear EST 21-DEC-1999  
 LOCUS  
 DEFINITION  
 w172h08.x1 NCI-CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398911 3'  
 similar to SW:GP39\_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39. ; mRNA sequence.

ACCESSION A1765236  
 VERSION A1765236  
 KEYWORDS GI:5231745  
 SOURCE human

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 456)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/brp/image/image.html](http://www.bio.lnl.gov/brp/image/image.html)  
 Insert length: 961 Std Error: 0.00  
 Seq primer: -400P from Glibco  
 High quality sequence stop: 453.  
 Location/Qualifiers  
 1..456  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:2398911"  
 /clone\_lib="NCI-CGAP\_Kid12"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI;  
 plasmid DNA from the normalized library NCI-CGAP\_Kid5 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (cloneids 1323912-1325831, 1471368-1472903 and  
 1492104-1493253). Subtraction by Bento Soares and M.  
 Fatima Bonaldo."

BASE COUNT 93 a 122 c 99 g 142 t  
 ORIGIN  
 Query Match 60.8%; Score 380; DB 9; Length 456;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 157 CCGCCGAACTGCTGCGAGACACCGGTACAGAGCGGTTGATGACGAGCTGAGGA 216  
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 DB 456 CCGCCGAACTGCTGCGAGACACCGGTACAGAGCGGTTGATGACGAGCTGAGGA 397  
 QY 217 GAAAAACGTCGCGAGAGAGGAGAGATCATGCCCGGAAGTAGAGACTGCTCA 276  
 ||||||||  
 DB 396 GAAAAACGTCGCGAGAGAGGAGAGATCATGCCCGGAAGTAGAGACTGCTCA 337  
 QY 277 GTGCTGTTGGGTTGGCCGACGATGATCTCCGAATCTGGTTGGCATCCACATAC 336  
 ||||||||  
 DB 336 GTGCTGTTGGGTTGGCCGACGATGATCTCCGAATCTGGTTGGCATCCACATAC 277  
 QY 337 GGGCAATGTACAAACATGACCCCTGGGACAGACAGAGAGGAGAGAGAGAA 396  
 ||||||||  
 DB 276 GGGCAATGTACAAACATGACCCCTGGGACAGACAGAGAGGAGAGAGAGAA 217  
 QY 397 GAAAAACGATGAGACAGACAGTAATGAATAAATTAATTTTAAAGCCCTCTG 456  
 ||||||||  
 DB 216 GAAAAACGATGAGACAGACAGTAATGAATAAATTAATTTTAAAGCCCTCTG 157  
 QY 457 TTCTGTCTTACTGCGGAGGAAATGTAACCAATTTTCAAGTTGACCTTGACACTTCT 516  
 ||||||||  
 DB 156 TTCTGTCTTACTGCGGAGGAAATGTAACCAATTTTCAAGTTGACCTTGACACTTCT 97  
 QY 517 TTGGCCAGAGAGAGAGATTTAACAATGTTTCAAAACCGGGGAGTGTGGCTGTGTA 576  
 ||||||||  
 DB 96 TTGGCCAGAGAGAGAGATTTAACAATGTTTCAAAACCGGGGAGTGTGGCTGTGTA 37

QY 577 AAGAAAGACCA 587  
 ||||||||  
 DB 36 AAGAAAGACCA 26

RESULT 26  
 BF054837  
 LOCUS 381 bp mRNA linear EST 16-OCT-2000  
 DEFINITION 7171b01.X1 NCI CGAP Brn20 Homo sapiens cDNA clone IMAGE:3340177 5',  
 similar to SM:GPR39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
 GPR39, mRNA sequence.  
 BF054837  
 BF054837.1 GI:10808733  
 EST.  
 KEYWORDS  
 VERSION  
 ACCESSION  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 381)  
 AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 UNPUBLISHED (1998)  
 COMMENT Other ESTs: 7171b01.x1  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
 Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim  
 Jacobson, Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL, send email to:  
[infelimage.lnl.gov](mailto:infelimage.lnl.gov)  
 Putative full length read  
 The vector to vector length is 382  
 Seq primer: -40RP from Glibco.  
 Location/Qualifiers  
 1..381  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3340177"  
 /clone\_lib="NCI-CGAP\_Brn20"  
 /tissue\_type="Oligodendroglioma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: PAMPI; mRNA made from  
 oligodendroglioma tissue, cDNA made by oligo-dT priming.  
 Directionally cloned. Size-selected on agarose gel,  
 average insert size 500 bp. Primary library,  
 non-amplified."

BASE COUNT 123 a 81 c 94 g 83 t  
 ORIGIN  
 Query Match 59.0%; Score 369; DB 12; Length 381;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 GGAGAGATCATGTACGCCCGGAAGTAGAGACCTGTCACAGTCTGTTGGTTGGCCG 296  
 ||||||||  
 DB 1 GGAGAGATCATGTACGCCCGGAAGTAGAGACCTGTCACAGTCTGTTGGTTGGCCG 60  
 QY 297 CAGCCATGATCCCTCCGAATCTGTTGGGATCCAGCATAGGCGCAATGTCAACAATCA 356  
 ||||||||  
 DB 61 CAGCCATGATCCCTCCGAATCTGTTGGGATCCAGCATAGGCGCAATGTCAACAATCA 120  
 QY 357 GCGCTGGCGACAGCAGCAGGAGGAGAGACAGAGAAAGAAAACACAGCATGAGAC 416  
 ||||||||  
 DB 121 GCGCTGGCGACAGCAGCAGGAGGAGAGACAGAGAAAGAAAACACAGCATGAGAC 180  
 QY 417 ACAGTAATGAATAAACATTAATTTAGGCCCTCTGTTCTGTGCTTACTGGCCAGG 476

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|||||
Db 181 ACAGTAATGATAAACAATAAATATTAGCCCTCGTCTGTGCTTACTGGCCAGC 240
Oy 477 AATGATACCAATTTTTCAGTGTGGACTTGCACAGCTTTTGGCCACAGACAGAGA 536
Db 241 AATGATACCAATTTTTCAGTGTGGACTTGCACAGCTTTTGGCCACAGACAGAGA 300
Oy 537 AATTAACTGTTTAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCT 596
Db 301 AATTAACTGTTTAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCT 360
Oy 597 TTAGACAGT 605
Db 361 TTAGACAGT 369

RESULT 27
BF054680 371 bp mRNA linear EST 16-OCT-2000
LOCUS 7169f08.y1 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:333975 5'
DEFINITION similar to SW:GPR39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.;, mRNA sequence.
ACCESSION BF054680
VERSION BF054680.1 GI:10808576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 371)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Other ESTs: 7169f08.x1
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.
CDNA Library Preparation: David B. Kriman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov
Seq primer: -40R from Gibco
High quality sequence stop: 361.
Location/Qualifiers
FEATURES
Source
1..371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="333975"
/clone_lib="NCI_CGAP_Brn20"
/tissue_type="Oligodendrogloma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: brain; Vector: PAMPI; mRNA made from
oligodendrogloma tissue; cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 114 a 81 c 93 g 83 t
ORIGIN
Query Match 58.9%; Score 368; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 238 GAGGAGATCATGTACGCCGGAAGTAGACCTGTCGATGCTGTGGTTGGCCGC 297
Db 1 GAGGAGATCATGTACGCCGGAAGTAGACCTGTCGATGCTGTGGTTGGCCGC 60

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Oy 298 AGCATGATCTCTCCGATGCTGGTGGCATCCAGCATAGCCCAATGTCAACAATCAG 357
Db 61 AGCATGATCTCTCCGATGCTGGTGGCATCCAGCATAGCCCAATGTCAACAATCAG 120
Oy 358 CCGTGGGACAGACGACGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 121 CCGTGGGACAGACGACGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Oy 418 CAGTAATGATAAACAATAAATATTAGCCCTCGTCTGTGCTTACTGGCCAGCA 477
Db 181 CAGTAATGATAAACAATAAATATTAGCCCTCGTCTGTGCTTACTGGCCAGCA 240
Oy 478 AATGATACCAATTTTTCAGTGTGGACTTGCACAGCTTTTGGCCACAGACAGAGA 537
Db 241 AATGATACCAATTTTTCAGTGTGGACTTGCACAGCTTTTGGCCACAGACAGAGA 300
Oy 538 TTTAACACTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTT 597
Db 301 TTTAACACTGTTTCAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTT 360
Oy 598 TTAGACAGT 605
Db 361 TTAGACAGT 368

RESULT 28
A1742092/c 578 bp mRNA linear EST 19-DEC-1999
LOCUS wg38h03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:2367413 3' similar to SW:GPR39_HUMAN O43194 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR39.;, mRNA sequence.
ACCESSION A1742092
VERSION A1742092.1 GI:5110380
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 578)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 806 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 460.
Location/Qualifiers
FEATURES
Source
1..578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2367413"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7AD-Pac (Pharmacia) with
a modified polylinker. Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326653 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

```

BASE COUNT 102 a 176 c 142 g 158 t  
ORIGIN

Query Match 58.4%; Score 365; DB 9; Length 578;  
Best Local Similarity 99.8%; Pred. No. 0;

Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGGACAGAGACTGGCCGGGAGCGCAAGACAGGAGCGCTGCACAAAGG 60  
|||||

DB 455 AGTTCTCTTGGACAGAGACTGGCCGGGAGCGCAAGACAGGAGCGCTGCACAAAGG 396  
|||||

QY 61 GGCCCTGTGGTGGTGGAGTGGCGCATGTACGCGCAGCGCTTCTGTGGTTGGCGTCTG 120  
|||||

DB 395 GGCCCTGTGGTGGTGGAGTGGCGCATGTACGCGCAGCGCTTCTGTGGTTGGCGTCTG 336  
|||||

QY 121 CAGGACAGCGGCGGACAGCAGCAGCTGCAGCAACCGCGCAAACTGCTGGAGAGACAC 180  
|||||

DB 335 CAGGACAGCGGCGGACAGCAGCAGCTGCAGCAACCGCGCAAACTGCTGGAGAGACAC 276  
|||||

QY 181 CGTGTACAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 240  
|||||

DB 275 CGTGTACAGAGCGGGTTGATGACCGAGCTGAGTAGAAAAAGTCTCCGAGAGGGAG 216  
|||||

QY 241 GAGGATCATGTACCGCCGGAAGTAGAGCTGTCAGTCTGCTTGGTTGGCCGACG 300  
|||||

DB 215 GAGGATCATGTACCGCCGGAAGTAGAGCTGTCAGTCTGCTTGGTTGGCCGACG 156  
|||||

QY 301 CATGATCTCCGAACTGCTTGGGATCCAGATACGGGCAATGTACAAACATCAGCCG 360  
|||||

DB 155 CATGATCTCCGAACTGCTTGGGATCCAGATACGGGCAATGTACAAACATCAGCCG 96  
|||||

QY 361 TGGGACAGACAGAGAGGAGAGACAGAAAAAAGACAGCATGAGAAC 416  
|||||

DB 95 TGGGACAGACAGAGAGGAGAGACAGAAAAAAGACAGCATGAGAAC 40  
|||||

RESULT 29  
AM087372/c 432 bp mRNA Linear EST 15-OCT-1999  
LOCUS  
DEFINITION  
xbl9602.x1 NCI-CGAP\_Kid13 Homo sapiens CDNA clone IMAGE:2576786.3,  
similar to SW:GP39, HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GPR39, mRNA sequence.

ACCESSION  
AM087372  
VERSION  
AM087372.1 GI:6043177  
KEYWORDS  
EST.

SOURCE  
ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 432)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bdrp/image/image.html](http://www.bio.llnl.gov/bdrp/image/image.html)

FEATURES  
source  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40up from gibco  
High quality sequence stop: 306.  
Location/Qualifiers  
1..432

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2576786"

/clone\_lib="NCI-CGAP Kid13"  
/tissue\_type="2 pooled Wilms' tumors, one primary and one  
metastatic to brain"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: pCMV-Sport6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies."

BASE COUNT 92 a 116 c 89 g 134 t 1 others  
ORIGIN

Query Match 55.5%; Score 347; DB 10; Length 432;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AAGTAGAGCCCTCCGACAGTCTGCTTGGTTGGCCGCGCAGCATATCTCGAATCTGG 319  
|||||

DB 353 AAGTAGAGCCCTCCGACAGTCTGCTTGGTTGGCCGCGCAGCATATCTCGAATCTGG 294  
|||||

QY 320 TTGGGCAATCCAGATACAGGCGCAATGTCAACAATCAGCCCTGGGACAGACAGAGA 379  
|||||

DB 293 TTGGGCAATCCAGATACAGGCGCAATGTCAACAATCAGCCCTGGGACAGACAGAGA 234  
|||||

QY 380 GGGAGAGACAGAGAAAAAAGAACACAGCATGAGAACACAGTAATGAATAAACCATTA 439  
|||||

DB 233 GGGAGAGACAGAGAAAAAAGAACACAGCATGAGAACACAGTAATGAATAAACCATTA 174  
|||||

QY 440 AATATTAGGCCCTCTGCTTGGCTTACCTGGCCAGAGAAATGTTACCAATTTTACGT 499  
|||||

DB 173 AATATTAGGCCCTCTGCTTGGCTTACCTGGCCAGAGAAATGTTACCAATTTTACGT 114  
|||||

QY 500 TGGACTTGACAGCTTCTTTGGCCACAGCAGAGAGATTTAACACTTTTCAACCCG 559  
|||||

DB 113 TGGACTTGACAGCTTCTTTGGCCACAGCAGAGAGATTTAACACTTTTCAACCCG 54  
|||||

QY 560 GGGAGTTGGCTGTGTAAAGAACCAATTAATGCTTTAGACAGTG 606  
|||||

DB 53 GGGAGTTGGCTGTGTAAAGAACCAATTAATGCTTTAGACAGTG 7  
|||||

RESULT 30  
BF126050 759 bp mRNA Linear EST 24-OCT-2000  
LOCUS  
DEFINITION  
601762888F1 NIH\_MGC\_20 Homo sapiens CDNA clone IMAGE:4026092.5,  
mRNA sequence.

ACCESSION  
BF126050  
VERSION  
BF126050.1 GI:10965090  
KEYWORDS  
EST.

SOURCE  
ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 759)  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: ATCC/DCID/DMF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: L1CM855 row: 0 column: 21

FEATURES  
source  
High quality sequence stop: 723.  
Location/Qualifiers  
1..759

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4026092"  
/clone\_lib="NIH\_MGC\_20"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6)". Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 191 a 192 c 221 g 155 t

ORIGIN

Query Match 54.2%; Score 339; DB 12; Length 759;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGAGACTGGCGCGGACCGGAAGACACGGCGCTGCACAAAGC 60  
|||||  
Db 161 AGTTCTCTTGCAGAGAGACTGGCGCGGACCGGAAGACACGGCGCTGCACAAAGC 220  
|||||  
QY 61 GGGCGTGTGGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 120  
|||||  
Db 221 GGGCGTGTGGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 280  
|||||  
QY 121 CAGCGACAGGCGGACAGACAGCAGTGCAGAAACCCGCGAACTGCTGCAGAGACAC 180  
|||||  
Db 281 CAGCGACAGGCGGACAGACAGCAGTGCAGAAACCCGCGAACTGCTGCAGAGACAC 340  
|||||  
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCGAGAGGAG 240  
|||||  
Db 341 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCGAGAGGAG 400  
|||||  
QY 241 GAGGATCATGTACGCCCGGAGAGTACCTGCTGAGTGGTGGTGGTGGTGGTGGTGG 300  
|||||  
Db 401 GAGGATCATGTACGCCCGGAGAGTACCTGCTGAGTGGTGGTGGTGGTGGTGGTGG 460  
|||||  
QY 301 CATGATCTCCGAATCTGTTGGGATCCAGATACGCGC 339  
|||||  
Db 461 CATGATCTCCGAATCTGTTGGGATCCAGATACGCGC 499  
|||||

RESULT 31  
BF125134 843 bp mRNA linear EST 24-OCT-2000  
LOCUS 601762356F1 NIH\_MGC\_20 Homo sapiens CDNA clone IMAGE:4025340 5',  
DEFINITION mRNA sequence.  
BF125134  
ACCESSION BF125134.1 GI:10964174  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 843)  
NIH-MGC <http://mhc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC/DCID/DTF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LCM853 row: P column: 13  
High quality sequence stop: 711.  
Location/Qualifiers  
1. 843

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4025340"  
/clone\_1ib="NIH\_MGC\_20"  
/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6)". Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 225 a 192 c 255 g 171 t

ORIGIN

Query Match 54.2%; Score 339; DB 12; Length 843;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTCTCTTGCAGAGAGACTGGCGCGGACCGGAAGACACGGCGCTGCACAAAGC 60  
|||||  
Db 161 AGTTCTCTTGCAGAGAGACTGGCGCGGACCGGAAGACACGGCGCTGCACAAAGC 220  
|||||  
QY 61 GGGCGTGTGGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 120  
|||||  
Db 221 GGGCGTGTGGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 280  
|||||  
QY 121 CAGCGACAGGCGGACAGACAGCAGTGCAGAAACCCGCGAACTGCTGCAGAGACAC 180  
|||||  
Db 281 CAGCGACAGGCGGACAGACAGCAGTGCAGAAACCCGCGAACTGCTGCAGAGACAC 340  
|||||  
QY 181 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCGAGAGGAG 240  
|||||  
Db 341 CGTGTACAGAGAGCGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCGAGAGGAG 400  
|||||  
QY 241 GAGGATCATGTACGCCCGGAGAGTACCTGCTGAGTGGTGGTGGTGGTGGTGGTGG 300  
|||||  
Db 401 GAGGATCATGTACGCCCGGAGAGTACCTGCTGAGTGGTGGTGGTGGTGGTGGTGG 460  
|||||  
QY 301 CATGATCTCCGAATCTGTTGGGATCCAGATACGCGC 339  
|||||  
Db 461 CATGATCTCCGAATCTGTTGGGATCCAGATACGCGC 499  
|||||

RESULT 32  
A1272281 387 bp mRNA linear EST 18-NOV-1998  
LOCUS ap23c03.x1 Schiller oligodendrogloma Homo sapiens CDNA clone  
DEFINITION IMAGE:1956196 3' similar to SW-NT1 RAT P20789 NEUROTENSIN RECEPTOR  
TYPE 1; contains TAR1.t3 TAR1 repetitive element; mRNA sequence.  
A1272281  
ACCESSION A1272281.1 GI:3894552  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 387)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,  
Kritman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,  
J., Moore, B., Schellenberg, K., Stepec, M., Tan, F., Theising, B.,  
White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@wustl.edu](mailto:est@wustl.edu)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](http://info@image.llnl.gov)) for further information.  
Possible reversed clone: similarity on wrong strand  
Seq primer: -400p from 61bco  
High quality sequence stop: 386.

TITLE  
JOURNAL  
COMMENT



	JOURNAL COMMENT	<p>cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.</p> <p>DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://www.bio.lnl.gov/bdrip/image/image.html">www.bio.lnl.gov/bdrip/image/image.html</a> Insert length: 1073 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 372. Location/Qualifiers</p>					
	FEATURES	Source					
	ORGANISM	Homo sapiens					
	REFERENCE AUTHORS TITLE	<p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.</p> <p>NCI/NINDS-GCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a>. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (GCAP/BTGAEP), Tumor Gene Index Unpublished (1998)</p> <p>Contact: Robert Strausberg, Ph.D. Email: gcgaps-remail.nhl.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.</p>					
	BASE COUNT	95 a 127 c 112 g 146 t					
	ORIGIN						
Query Match	Best Local Similarity	50.4%	Score 315;	DB 9;	Length 480;		
Matches 465;	Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;		
Oy	133 GCAGACAGACACTCTCAGAACACC	CGGCGGAATGCTCGAGGACACCGTGACAGGAG	192				
Db	480 GCAGACAGACACTCTCAGAACACC	CGGCGGAATGCTCGAGGACACCGTGACAGGAG	421				
Oy	193 CGGGTTGATGACCGAGCTGAGGTAGA	AAAAAAGCTTCGCCGAAGGGGAGGAGGATCATGTA	252				
Db	420 CGGGTTGATGACCGAGCTGAGGTAGA	AAAAAAGCTTCGCCGAAGGGGAGGAGGATCATGTA	361				
Oy	253 CGCCCGGAAGTGGAGCTCTGCACTG	CGTGCCTGGGTTTTGGCCGAGGCATGATCCTCG	312				
Db	360 CGCCCGGAAGTGGAGCTCTGCACTG	CGTGCCTGGGTTTTGGCCGAGGCATGATCCTCG	301				
Oy	313 AATCTGTTGGGCATCCAGCATACG	GCCCAATGTCACAACATCACGCCCTGGGCAACAGC	372				
Db	300 AATCTGTTGGGCATCCAGCATACG	GCCCAATGTCACAACATCACGCCCTGGGCAACAGC	241				
Oy	373 AGCAGAGGAGAGACAGAGAAAAGAA	AACACACAGATGAGAAACACAGTAAATGATAA	432				
Db	240 AGCAGAGGAGAGAGAGAAAAGAA	AACACACAGATGAGAAACACAGTAAATGATAA	181				
Oy	433 ACCATAAAATATTATTTAGCCCCCT	GTGTTCTGTCTGTACTGGCCAGGAAATGTACCAATTTT	492				
Db	180 ACCATAAAATATTATTTAGCCCCCT	GTGTTCTGTCTGTACTGGCCAGGAAATGTACCAATTTT	121				
Oy	493 TCAGTGTGGACTTGACAGCTTCTTT	TGGCCACAGCAAGAGAAATTTAACA	552				
Db	121 TCAGTGTGGACTTGACAGCTTCTTT	TGGCCACAGCAAGAGAAATTTAACA	552				

DB	120	TCAGGTGTGAAGCTTACAGACTCTCTTTTGGCACAACAGACAGAGAAATTTACACTGTTTCA	61
QY	553	AAACCCGGGGAGTTCGCTGTCTTTAAAGAAAGCACTTTAAAGCTTAG	600
DB	60	AAACCCGGGGAGTTCGCTGTCTTTAAAGAAAGCACTTTAAAGCTTAG	13
RESULT 35			
LOCUS	AA665640/c		
DEFINITION	AA665640	337 bp	mRNA
ACCESSION	AA665640		linear
VERSION	AA665640.1		EST 14-NOV-1997
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 337) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepec, M., Tan, F., Thelking, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.		
TITLE	WashU-NCI human EST project		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 325.		
FEATURES	Location/Qualifiers		
SOURCE	1..337		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1126871"		
	/clone.lib="Gessler Wilms tumor"		
	/sex="pooled (6)"		
	/lab.host="DH10B"		
	/note="Vector: pSPORT1, Site_1: SalI; Site_2: NotI; RNA was prepared from a pool of 6 anonymous Wilms' tumor RNAs prepared by acid-phenol, followed by one round of oligo dt selection. cdna library preparation was with the BRL/life Tech. Superscript Plasmid system. An oligo-dt NotI primer for first strand synthesis generated ggcgcgcgcctn at the 3' end of the clones. A 5' SalI adaptor was used with sequence 5'-gtcaccacgcgtcg-3'. Resulting cDNAs were size selected (average size 2 kb), NotI digested, and ligated into NotI/SalI-cut pSPORT1. Library was constructed by Dr. Manfred Gessler."		
BASE COUNT	78 a	81 c	74 g 104 t
ORIGIN			
Query Match	50.2%	Score 314;	DB 9; Length 337;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 314;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
DB	293	GGCGAGCCATATCTCTCGATCTGTGGTGGCATTCACATACGGCCCAATGTCAACCA	352
DB	314	GGCGAGCCATATCTCTCGATCTGTGGTGGCATTCACATACGGCCATGTCAACCA	255
QY	353	ATTCAGCCCTGGGCAACACAGACAGAGAGGAGAGACAGAGAAAGAAACACAGCATGA	412
DB	254	ATTCAGCCCTGGGCAACACAGACAGAGAGGAGAGACAGAGAAAGAAACACAGCATGA	195
QY	413	GAACACAGTAATGAATTAACCATTAATTTAGCCCCCTGTGTTGCTTACTGGC	472
DB	194	GAACACAGTAATGAATTAACCATTAATTTAGCCCCCTGTGTTGCTTACTGGC	135



QY	473	CAGGAAATGGTACCAATTTTTCAGTGTGGAGCTTGACACCTCTTTTGGCACAACAGACA	532
Db	134	CAGGAAATGGTACCAATTTTTCAGTGTGGAGCTTGACACCTCTTTTGGCACAACAGACA	75
QY	533	GAGAAATTTAACACTGTCTTCCAAACCCGGGGAGCTTGCTGTGTTAAAGAAACCAATTAA	592
Db	74	GAGAAATTTAACACTGTCTTCCAAACCCGGGGAGCTTGCTGTGTTAAAGAAACCAATTAA	15
QY	593	TGCTTTAGCACTG 606	
Db	14	TGCTTTAGCACTG 1	
RESULT 36			
AA970361/c			
LOCUS	AA970361	354 bp	mRNA
DEFINITION	op22906.s1 Soares_NFL_T_GBC_S1 Homo sapiens	linear	EST 20-MAY-1998
ACCESSION	IMAGE:1580506 3', mRNA sequence.		
VERSION	AA970361		
KEYWORDS	AA970361.1 GI:3145874		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Seq primer: -40m13 fwd, RT from Amersham.		
FEATURES			
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:1580506"		
	/clone_lib="Soares_NFL_T_GBC_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with		
	a modified polylinker; Site.1: Not I; Site.2: Eco RI;		
	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NHDL19W, testis NHT, and B-cell		
	NCLICAP-GCBI) were mixed, and ss circles were made in		
	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The driver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I. M. A. G. E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo.		
BASE COUNT	80 a	78 g	108 t
ORIGIN	88 c		
Query Match	50.2%;	Score 314;	DB 9; Length 354;
Best Local Similarity	100.0%;	Pred. NO. 0;	
Matches 314;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	293	GCCGAGCCATGATCTCTCGAATCTGTGGGCAATCCAGATACGCCCATGTCTACACA	352
Db	315	GCCGAGCCATGATCTCTCGAATCTGTGGGCAATCCAGATACGCCCATGTCTACACA	256
QY	353	ATCAGCCTTGGGCGACACGACGAGGAGGAGACAGAGAAAAAACAACAGCATGA	412
Db	255	ATCAGCCTTGGGCGACACGACGAGGAGGAGGAGACAGAGAAAAAACAACAGCATGA	196
QY	413	GACACACTAATATGATTAACACATTAATTTTATTTTGGCCCTCTGTCTGTGCTTACTGGC	472
Db	195	GACACACTAATATGATTAACACATTAATTTTATTTTGGCCCTCTGTCTGTGCTTACTGGC	136

QY	473	CAGGAAATGATACCAATTTTCAGCTGTGGACCTTGACAGCTTTCTTTGCCACAGCAAGA	532
Db	135	CAGGAAATGATACCAATTTTCAGCTGTGGACCTTGACAGCTTTCTTTGCCACAGCAAGA	76
QY	533	GAGAAATTAACACGTCTTCAACCCGGGGGAGTTGGCTGTGTTAAAGAAACCACTTAA	592
Db	75	GAGAAATTAACACGTCTTCAACCCGGGGGAGTTGGCTGTGTTAAAGAAACCACTTAA	16
QY	593	TGCTTTAGACAGTG	606
Db	15	TGCTTTAGACAGTG	2
RESULT 37			
LOCUS	AA075710/c	373 bp	mRNA
DEFINITION	zmb9d04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545095 3' similar to contains Alu repetitive element; mRNA sequence.		
ACCESSION	AA075710		
VERSION	AA075710.1	GI:1615580	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 373)		
AUTHORS	Hillier, L., Lennon, G., Becker, M., Donald, M.F., Chiapelli, B., Chisose, S., Dietrich, N., Dubugue, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierrey-Meg, J., Trevisakis, E., Underwood, K., Wohlmann, P., Watson, R., Wilson, R. and Matre, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)		
TITLE	97044478		
JOURNAL	Contact: Wilson RK		
MEDLINE	Washington University School of Medicine		
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.		
	This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.		
	Insert Length: 427 Std Error: 0.00		
	Seq Primer: -40M13 fwd. from Amerisham		
	High quality sequence stop: 240.		
	Location/Qualifiers		
FEATURES	1. 373		
source	/organism="Homo sapiens"		
	/db_xref="GDB:3923283"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:545095"		
	/clone_lib="Stratagene ovarian cancer (#937219)"		
	/sex="female"		
	/dev_stage="adult, 64 years"		
	/lab_host="SOLR (kanamycin resistant)"		
	/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Papillary serous carcinoma, isolated from ascites, 64 year old caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."		
BASE COUNT	83 a	96 c	80 g 114 t
ORIGIN			
Query Match	50.2%	Score 314;	DB 9; Length 373;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

293 GCCGACCATGATCCTCCGAATCTGGTTGGGATCCAGCATACGGCCATGTCAACAACA 352

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT 38	AA084249/c	LOCUS	412 bp	mrna	linear	EST 31-JUL-1997
DEFINITION	AA084249	zn17f09.s1	Stratagene neuroepithelium NT2RMT	937234	Homo sapiens	
CDNA clone IMAGE:547721 3',			mrna sequence.			

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT 38	AA084249/c	LOCUS	412 bp	mrna	linear	EST 31-JUL-1997
DEFINITION	AA084249	zn17f09.s1	Stratagene neuroepithelium NT2RMT	937234	Homo sapiens	
CDNA clone IMAGE:547721 3',			mrna sequence.			

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

RESULT	38
AA084249/c	
LOCUS	
DEFINITION	412 bp mRNA linear EST 31-JUL-1997
AA084249	
zn17f09.s1	Stratagene neuroepithelium NT2RMT 937234 Homo sapiens
CDNA clone IMAGE:547721 3', mRNA sequence.	

library synthesis. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTTCTAGATCGGAGCGGCCGCTT)15-3'. Not I blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

BASE COUNT 100 a 76 c 89 g 47 t  
ORIGIN

Query Match 49.9%; Score 312; DB 12; Length 312;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GCACAGCACCCTGACAGACACCCGCGAAGCTGCTGAGAGACACCGTGTACAGAGCGG 195  
DB 1 GCACAGCACCCTGACAGACACCCGCGAAGCTGCTGAGAGACACCGTGTACAGAGCGG 60  
QY 196 GTTGATGACGAGCTGAGAGAGAAACGCTCCGAGAGAGGAGAGATCATGTACGC 255  
DB 61 GTTGATGACGAGCTGAGAGAGAAACGCTCCGAGAGAGGAGAGATCATGTACGC 120  
QY 256 CCGAAGTAGAGCCTGCTCCAGTCTGCTTGGGCGGACGACCATGTATCTCCGAT 315  
DB 121 CCGAAGTAGAGCCTGCTCCAGTCTGCTTGGGCGGACGACCATGTATCTCCGAT 180  
QY 316 CTGGTGGGCGATCCAGCATACGGCAATGTACACAAATCAGCCCTGGGCGACAGCAGC 375  
DB 181 CTGGTGGGCGATCCAGCATACGGCAATGTACACAAATCAGCCCTGGGCGACAGCAGC 240  
QY 376 AGGAGGAGAGACAGAGAAAGAAACACAGCATGAGAACACAGTAATTAATAAACCC 435  
DB 241 AGGAGGAGAGACAGAGAAAGAAAGAAACACAGCATGAGAACACAGTAATTAATAAACCC 300  
QY 436 ATTAATATTTTA 447  
DB 301 ATTAATATTTTA 312

RESULT 40  
AA173739 349 bp mRNA linear EST 09-MAR-1998  
LOCUS AA173739/c  
DEFINITION zp04h05.r1 Stratiogene ovarian cancer (#937219) Homo sapiens cDNA  
clone IMAGE:595449 5', mRNA sequence.

ACCESSION AA173739  
VERSION AA173739.1 GI:1753890  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 349)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kritman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Merra, M., Martin,  
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE WashU-NCI human EST Project  
JOURNAL Unpublished (1997)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Insert Length: 792 Std. Error: 0.00  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 236.

FEATURES  
Source

Location/Qualifiers  
1..349  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:595449"  
/clone\_lib="Stratiogene ovarian cancer (#937219)"  
/sex="female"  
/dev\_stage="adult, 64 years"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI  
; Cloned unidirectionally. Primer: Oligo dT. Papillary  
serous carcinoma, isolated from ascites, 64 year old  
caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector;  
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor  
sequence: 5' CTCGAGCTTTTGTATTTT 3' "

BASE COUNT 79 a 84 c 78 g 108 t  
ORIGIN

Query Match 49.1%; Score 307; DB 9; Length 349;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCATGATCTCCGGAATCTGTGGGATCCAGATCCGCCATTCATCAATCAGCC 359  
DB 310 CCATGATCTCCGGAATCTGTGGGATCCAGATCCGCCATTCATCAATCAGCC 251  
QY 360 CTGGGAGACAGAGAGAGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419  
DB 250 CTGGGAGACAG 191  
QY 420 GTAATGAATTAACCATTAATATTTTACGCCCTCTGTCTTCTTCTTCTTCTTCTT 479  
DB 190 GTAATGAATTAACCATTAATATTTTACGCCCTCTGTCTTCTTCTTCTTCTTCTT 131  
QY 480 TGGTACCAATTTTTCAGTGTGACTTGAACAGTCTCTTCTTCCACAGAGAGAGATTT 539  
DB 130 TGGTACCAATTTTTCAGTGTGACTTGAACAGTCTCTTCTTCCACAGAGAGAGATTT 71  
QY 540 TAACACTGTTTCAACCCGCGGAGTGGCTGTGTTAAAGAGACCATTAATGCTTTTA 599  
DB 70 TAACACTGTTTCAACCCGCGGAGTGGCTGTGTTAAAGAGACCATTAATGCTTTTA 11  
QY 600 GACAGTG 606  
DB 10 GACAGTG 4

RESULT 41  
BG057775 408 bp mRNA linear EST 25-JAN-2001  
LOCUS BG057775/c  
DEFINITION 7f75g10.x1 lupski dorsal root ganglion Homo sapiens cDNA clone  
IMAGE:3302971.3 similar to SM-GP39\_HUMAN O4194 PUTATIVE G  
PROTEIN-COUPLED RECEPTOR GPR39. ;, mRNA sequence.

ACCESSION BG057775  
VERSION BG057775.1 GI:13523767  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 408)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

TITLE Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Dr. James Lupski  
cDNA library Preparation: Lupski Laboratory  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:

info@image.llnl.gov  
Seq primer: -40UP from gibco  
High quality sequence stop: 376.  
Location/Qualifiers

## FEATURES

source

1. .408  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3302971"  
/clone\_lib="lupski\_dorsal\_root\_ganglion"  
/sex="male"  
/tissue\_type="dorsal root ganglia"  
/dev\_stage="adult, 36 yr"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6 (Life Technologies); Site\_1:  
NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
directionally cloned using the following adaptors:  
5'-TCGACCCAGCGGTCG-3' and  
5'-GACTGATCTTAGATCGGAGCGGCCGCT(15)-3'. Size selected >  
1 kb for average insert length 1.7 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

BASE COUNT 111 a 87 c 79 g 128 t 3 others

## ORIGIN

Query Match 49.1%; Score 307; DB 12; Length 408;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CCATGATCCTCCGATCTGTTGGGATCCAGCATACGGCCAAATGTCACAACATCAGCC 359

Db 397 CCATGATCCTCCGATCTGTTGGGATCCAGCATACGGCCAAATGTCACAACATCAGCC 338

QY 360 CTGGGACAGACGAG 419

Db 337 CTGGGACAGACGAG 278

QY 420 GTAATGATTAACCAATTAATATTAGCCCTGTTCTGTCTGTTCTGTTCTGTTCTGTTCT 479

Db 277 GTAATGATTAACCAATTAATATTAGCCCTGTTCTGTCTGTTCTGTTCTGTTCTGTTCTGTTCT 218

QY 480 TGGTACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTTCCACAAGCAGAGAGATT 539

Db 217 TGGTACCAATTTTTCAGTGTGACCTTGACAGCTTCTTTTCCACAAGCAGAGAGATT 158

QY 540 TAAACAGTTTCAAAACCCGGGGAGTTGGCTGTAAAGAAAGACATTAATGCTTTA 599

Db 157 TAAACAGTTTCAAAACCCGGGGAGTTGGCTGTAAAGAAAGACATTAATGCTTTA 98

QY 600 GACAGTG 606

Db 97 GACAGTG 91

RESULT 42  
AI566797/c 420 bp mRNA linear EST 12-MAY-1999

LOCUS t123908.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2168510 3'

DEFINITION similar to SW:NTRI\_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ; mRNA

sequence.

ACCESSION AI566797

VERSION AI566797.1 GI:4525249

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

TITLE NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTCAP), Tumor Gene Index

## JOURNAL

Unpublished (1998)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 1148 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 354

POLY-A-NO.

Location/Qualifiers

1. .420

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2168510"

/clone\_lib="NCI\_CGAP\_Brn25"

/tissue\_type="anaplastic oligodendroglioma"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGGCCGCAATGTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 89 a 114 c 88 g 128 t 1 others

ORIGIN

Query Match 47.7%; Score 298; DB 9; Length 420;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 348; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 258 GGAAGTAGACCTGCTCAGTGTGCTTGGTTGGCCGAGCCATGATCTCCGAATCT 317

Db 349 GGAAGTAGACCTGCTCAGTGTGCTTGGTTGGCCGAGCCATGATCTCCGAATCT 290

QY 318 GGTGGGATCCAGCATACGGCCAAATGTCACAACATCAGCCCTGGGACAGACAGCAG 377

Db 289 GGTGGGATCCAGCATACGGCCAAATGTCACAACATCAGCCCTGGGACAGACAGCAG 230

QY 378 GAGGAGAGACAG 437

Db 229 GAGGAGAGACAG 170

QY 438 AAAATATTAGCCCTGCTGTCTGTCTTACTGGCCAGGAATGGTACCAATTTTTCAGT 497

Db 169 AAAATATTAGCCCTGCTGTCTGTCTTACTGGCCAGGAATGGTACCAATTTTTCAGT 110

QY 498 GTTGGACTTGACAGCTTTTTCGACAGCAGCAGAGAGAAATTTAACAATCTTTTCAACC 557

Db 109 GTTGGACTTGACAGCTTTTTCGACAGCAGCAGAGAGAAATTTAACAATCTTTTCAACC 50

QY 558 GGGGAGTTGGCTGTAAAGAAAGACATTAATGCTTTAGACAGTG 606

Db 49 GGGGAGTTGGCTGTAAAGAAAGACATTAATGCTTTAGACAGTG 1

## RESULT 43

AI363261/c

LOCUS AI363261

DEFINITION 475 bp mRNA linear EST 16-FEB-1999

sequence.

ACCESSION AI363261

VERSION AI363261.1 GI:4114882



Db 602 CGTGTACAGAGCGGGTGTATGACGAGCTGAGTAGAATAAAGCTCCGAGAGGGAG 661  
QY 241 GAGGATCATGTACGCCCGAAGTAGACTCTCCAGTGTG 282  
Db 662 GAGGATCATGTACGCCCGAAGTAGACTCTCCAGTGTG 703

## RESULT 45

AM128849/c 402 bp mRNA linear EST 25-OCT-1999  
LOCUS xdd6f12.x1 NCI-CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2596847 3'  
DEFINITION similar to SW:GP39\_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GP39. ; contains Alu repetitive element; contains element MER4 MER37  
repetitive element ; mRNA sequence.

ACCESSION AM128849  
VERSION AM128849.1 GI:6116769  
KEYWORDS EST.

## SOURCE

human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 402)

## AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLNT at:[www-bio.lnl.gov/dbfp/image/image.html](http://www-bio.lnl.gov/dbfp/image/image.html)Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 303.

## FEATURES

Location/Qualifiers

1..402

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2596847"

/clone\_lib="NCI-CGAP\_Ov23"

/tissue\_type="tumor, 5 pooled (see description)"

/lab\_host="DH10B"

/note="Organ: ovary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dr.Average insert size 1.35 kb. Tumor types include: mixed  
mullerian tumor, papillary serous, clear cell, spindle

cell. All are primary tumors, metastasis positive. Life

Technologies catalog #: 11534-013"

## BASE COUNT

86 a 97 c 80 g 139 t

## ORIGIN

Query Match 43.5%; Score 272; DB 10; Length 402;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 284 TTGGGTTTGGCCGACGATGATCTCCGAATCTGTTGGCATCCAGCATACGCCCAAT 343  
|||||  
Db 344 TTGGGTTTGGCCGACGATGATCTCCGAATCTGTTGGCATCCAGCATACGCCCAAT 285  
|||||

QY 344 GTACACAATCATGCCCTGGGCGACAGCGAGGAGGAGAGACAGAGAAAAAAC 403  
|||||  
Db 284 GTACACAATCATGCCCTGGGCGACAGCGAGGAGGAGAGACAGAGAAAAAAC 225  
|||||

QY 404 ACAGCATGAGACACAGTAATGATTAATTAATTTAGCCCTCTGTCTGTG 463  
|||||  
Db 224 ACAGCATGAGACACAGTAATGATTAATTAATTTAGCCCTCTGTCTGTG 165  
|||||

QY 464 CTTACTGGCCAGGAATGTTACCAATTTTCACTGTGGACTTGACAGCTTCTTTGCCA 523  
|||||  
Db 164 CTTACTGGCCAGGAATGTTACCAATTTTCACTGTGGACTTGACAGCTTCTTTGCCA 105  
|||||  
QY 524 CAAGCAAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAG 583  
|||||  
Db 104 CAAGCAAGAGAGATTTTAACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAG 45  
|||||  
QY 584 ACCATTAAATGCTTTAGACAGTG 606  
|||||  
Db 44 ACCATTAAATGCTTTAGACAGTG 22  
|||||

Search completed: November 7, 2002, 23:07:37

Job time : 846.445 secs



Oy	181	CCTGACAGGAGCCGGTTGATGACCAGCGGTGAGGTAGAAAAAGCTTCGCAAGAAGGGAG	240
Dd	181	CCTGACAGGAGCCGGTTGATGACCAGCGGTGAGGTAGAAAAAGCTTCGCAAGAAGGGAG	240
Oy	241	GAGGATCATGTAGCCGCCGAAGTAGAACCTCCTTCCACTGCTGGTTGGGTTGGCCGAGC	300
Dd	241	GAGGATCATGTAGCCGCCGAAGTAGAACCTCCTTCCACTGCTGGTTGGGTTGGCCGAGC	300
Oy	301	CATGATCCTCCGAACTCTGTTGGGCATTCACGATACGGCCAATGTACAACAATCACGCC	360
Dd	301	CATGATCCTCCGAACTCTGTTGGGCATTCACGATACGGCCAATGTACAACAATCACGCC	360
Oy	361	TGGCGACAGACGACGAGAGGAGGAGACAGACAGAAAAGAAAACACACATGAGAACACAG	420
Dd	361	TGGCGACAGACGACGAGAGGAGGAGACAGACAGAAAAGAAAACACACATGAGAACACAG	420
Oy	421	TAAATGAATTAACCATTAATAATTATTAAGCCCCTCTGTCTGTGCTTACTGGCCAGGAAT	480
Dd	421	TAAATGAATTAACCATTAATAATTATTAAGCCCCTCTGTCTGTGCTTACTGGCCAGGAAT	480
Oy	481	GSTACCAATTTTTCAAGTGTGGATTTACAGACTCTTTGCCAAGCAAGAGAGAATTT	540
Dd	481	GSTACCAATTTTTCAAGTGTGGATTTACAGACTCTTTTTTCCCCCAGCAAGAGAGAATTT	540
Oy	541	AACACTGTTTCAAACCCGGGGGCACTTGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
Dd	541	AACACTGTTTCAAACCCGGGGGCACTTGCTGTGTTAAAGAAAGCACTTAAATGCTTTAG	600
Oy	601	ACAGGNAAAAAAAAAAAAAA 625	
Dd	601	ACAGGNAAAAAAAAAAAAAA 625	

## RESULT 2

```

US-09-867-701-10876
: Sequence: 10876, Application us/09867701
: Patent No. US20020132237A1
: GENERAL INFORMATION:
: APPLICANT: Agilate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlocker, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ. ID NOS.: 10912
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10876
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
: US-09-867-701-10876

```

Query Match	99.88;	Score 624;	DB 10;	length 625;
Best Local Similarity	100.04;	Pred. NO. 3.3e-159;		
Matches 625;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	AGTTCTCCTTCACAAAGGACCTGGCCGGAGACGCACAAAGCAACGGGGCGTGCACAAAGCG	60
Db	1	AGTTCTCCTTCACAAAGGACCTGGCCGGAGACGCACAAAGCAACGGGGCGTGCACAAAGCG	60
QY	61	GGCGCTGTCGCTGGTAGAGTGCAGTCATGACGGCGGAGCGCTCTCGTGGTGGGCGTGTG	120
Db	1	AGTTCTCCTTCACAAAGGACCTGGCCGGAGACGCACAAAGCAACGGGGCGTGCACAAAGCG	60
QY	61	GGCGCTGTCGCTGGTAGAGTGCAGTCATGACGGCGGAGCGCTCTCTCGTGGTGGGCGTGTG	120
Db	61	GGCGCTGTCGCTGGTAGAGTGCAGTCATGACGGCGGAGCGCTCTCTCGTGGTGGGCGTGTG	120
QY	121	CAGCGACAGGCGGAGCAGCACACACACTGCACAGAACACCCGGCGAAACGTCGCGAGGACAC	180
Db	121	CAGCGACAGGCGGAGCAGCACACACACTGCACAGAACACCCGGCGAAACGTCGCGAGGACAC	180

OY	181	CGTGCACGAGGCGGGTGTGATGACCGAGCTAGGTAGAAAAAGCTTCGAGAAAGGGAG	240
Db	181	CGTGCACGAGGCGGGTGTGATGACCGAGCTAGGTAGAAAAAGCTTCGAGAAAGGGAG	240
OY	241	GAGGATCATGTGACGCCCGGAAGTAGACCTGTCAGCTGCTGTGGGTTTGCCCGAGC	300
Db	241	GAGGATCATGTGACGCCCGGAAGTAGACCTGTCAGCTGCTGTGGGTTTGCCCGAGC	300
OY	301	CATGATCCTCCGAATCTGTTGGGGCATTCAGCATACGGCCAAATGTCAACAATCAAGCC	360
Db	301	CATGATCCTCCGAATCTGTTGGGGCATTCAGCATACGGCCCAATGTCAACAATCAAGCC	360
OY	361	TGGCGACAGACAGACAGGAGGGAGAGACAGAGAAAGAAAAAACACACATGAGAACACAG	420
Db	361	TGGCGACAGACAGACAGGAGGGAGAGACAGAGAAAGAAAAAACACACATGAGAACACAG	420
OY	421	TAAATGAATAAACCATTAATATTTAAGCCCTCTGTTCTGTGCTTACGTGCCAGGAAT	480
Db	421	TAAATGAATAAACCATTAATATTTAAGCCCTCTGTTCTGTGCTTACTGCCAGGAAT	480
OY	481	GGTACCAATTTTTCAGTGTTGGATTGACAGCTCTTTTGCCACACAGCAGAGAGAAATT	540
Db	481	GGTACCAATTTTTCAGTGTTGGATTGACAGCTCTTTTGCCACACAGCAGAGAGAAATT	540
OY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACCAATTAAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACCAATTAAATGCTTTAG	600
OY	601	ACAGGTNAAAAAAAAAAAAAA 625	
Db	601	ACAGGTNAAAAAAAAAAAAAA 625	

### RESULT 3

```

US-09-825-294-214
: Sequence 214, Application US/09825294
: Patent No. US20020004491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 214
: LENGTH: 1897
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(1897)
: OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

```

Query Match	99.8%	Score 624;	DB 10;	Length 1897;
Best Local Similarity	99.8%	Pred. No. 5.9e-159;		
Matches 624; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	AGTTCTCCTTGCAGAGAGACTGCGCCGGGACCGGAAGACAACGGGCGCTGCACAAACG	60
Db	1271	AGTTCTCCTTGCAGAGAGACTGCGCCGGGACCGGAAGACAACGGGCGCTGCACAAACG	1330
QY	61	GGCCGCTTCGCTGTGGAGAGTGGCAATCTACCGCAGAGCGCTTCTGTGGTGGCTGCTG	120
Db	1331	GGCCGCTTCGCTGTGGAGAGTGGCAATCTACCGCAGAGCGCTTCTGTGGTGGCTGCTG	1390
QY	121	CACGCAGCGGCGAGACAGCAACCTGCAACAACACCCCGCAAACTGCTGGCAGGACAC	180



Db	1391	CGCGACAGAGCGCGGACAGCACAGCACTGCAGAAACACCGCCGAAACTGCTGCAGAGCAC	1450
QY	181	CGTGTACAGGAGCGGGTTATGACCGAGCTGAGGTAGAAAAACGTCCTCGAGAGGGGAG	240
Db	1451	CGTGTACAGGAGCGGGTTATGATGCCAGGCTGAGGTAGAAAAACGTCCTCGAGAGGGGAG	1510
QY	241	GAGGATCATGTACGGCCGGAGAGGAGACCTCGTCCAGTGGTGGCTTGGGGTTCGGCCGAGC	300
Db	1511	GAGGATCATGTACGGCCGGAGAGGAGACCTCGTCCAGTGGTGGCTTGGGGTTCGGCCGAGC	1570
QY	301	CATGATCTCTCCGAACTCTGGTTGGGCACTACGAGCATACGCGCAATGTCAACAATACAGCC	360
Db	1571	CATGATCTCTCCGAACTCTGGTTGGGCACTACGAGCATACGCGCAATGTCAACAATACAGCC	1630
QY	361	TGGCGACAGACAGCAGGAGGGAGAGACAGAGAAAAAACAACACAGCATGAGAACACAG	420
Db	1631	TGGCGACAGACAGCAGGAGGGAGAGACAGAGAAAAAACAACAGCATGAGAACACAG	1690
QY	421	TAAATGAATAAAAACATTAATATTTAAGCCCTCTGTCTTACTGTGCGCCAGGAAT	480
Db	1691	TAAATGAATAAAAACCATTAATATTTAAGCCCTCTGTCTTACTGTGCGCCAGGAAT	1750
QY	481	GGTACCAATTTTTCAGTGTGTGCACTGACAGCTCTTTGCCACAAGCAGAGGAATTT	540
Db	1751	GGTACCAATTTTTCAGTGTGTGCACTGACAGCTCTTTGCCACAAGCAGAGGAATTT	1810
QY	541	AACACTGTTCAAACCCGGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTAG	600
Db	1811	AACACTGTTCAAACCCGGGGGAGTGGCTGTGTAAAGAAAGACCATTAATGCTTTAG	1870
QY	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	1871	ACAGTGNAAAAAAAAAAAAAAAAAAAA 1895	

```

RESULT 4
US-09-825-294-205
Sequence 205, Application US/09825294
Patent No. US2002000491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Flind, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 205
LENGTH: 1619
TYPE: DNA
ORGANISM: Homo sapiens
US-09-825-294-205

```

Query Match	98.1%	Score 613;	DB 10;	Length 1619;
Best Local Similarity	99.7%	Pred. NO. 5e-156;		
Matches 624; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1;

QY	1	AGTTCTCCCTTGCAGAGAGACTTGGCGCCGGGACCGCAAGAGACAAGGCGCTGTGCACAAAGCG	60
Db	992	AGTTCTCCCTTGCAGAGAGACTTGGCGCCGGGACCGCAAGAGACAAGGCGCTGTGCACAAAGCG	1051
QY	61	GGCGCTGTGGTGGTGAGACTGCCATGTACGGCCAGGCGCTTCTCGTGGTGTGGCGTCTGTG	120
Db	1052	GGCGCTGTGGTGGTGAGACTGCCATGTACGGCCAGGCGCTTCTCGTGGTGTGGCGTCTGTG	1111
QY	121	CAGGCACAGGCGCGCAGCACAGCAC--TGCACGAACACCGCGCGAACTGCTGCGAGACA	179
Db	1112	CAGGCACAGGCGCGCAGCACAGCACCTTGCACGAACACCGCGCGAACTGCTGCGAGACA	1171

QY	180	CCGTGACAGAGAGCGGGTTGATACCGAGCTGAGGATGAGAAAAACGTCCTCCGAGAAAGGGA	239
Db	1172	CCGTGTACAGGAGCGGGTTGATGATACCGAGCTGAGTGAAGAAAACTCTCCGAGAAAGGGA	1231
QY	240	GGAGGATCATGTATACGGCCCGGAAGTAGGACCTCGCTCCAGTGTGCTGGTGTGGCCGAC	299
Db	1232	GGAGGATCATGTATACGGCCCGGAAGTAGGACCTCGCTCCAGTGTGCTGGTGTGGCCGAC	1291
QY	300	CCATGATCTCTCCGAATCTGGTTGGGCATTCAGCATACGGCCAATGTACAACAATTCAGCC	359
Db	1292	CCATGATCTCTCCGAATCTGGTTGGGCATTCAGCATACGGCCAATGTACAACAATTCAGCC	1351
QY	360	CTGGGCAGACAGCAGCAGCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATAGAACACA	419
Db	1352	CTGGGCAGACAGCAGCAGCAGAGGAGAGACAGAGAAAAAGAAAAACACAGCATAGAACACA	1411
QY	420	GTAATGATTAATAAACCATTAATAATATTAGACCCCTCTGTCTGTGCTTACTGAGCCAGGAA	479
Db	1412	GTAATGATTAATAAACCATTAATAATAATTAGACCCCTCTGTCTGTGCTTACTGAGCCAGGAA	1471
QY	480	TGTAACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCCACAAGACAAGAGAGATT	539
Db	1472	TGTAACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGCCACAAGACAAGAGAGATT	1531
QY	540	TAAACATGTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATATGCTTTA	599
Db	1532	TAAACATGTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATATGCTTTA	1591
QY	600	GACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Db	1592	GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617	

```

RESULT 5
US-09-825-294-211
: Sequence 211, Application US/09825294
: Patent No. US20020004491A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C5
: CURRENT APPLICATION NUMBER: US/09/825,294
: CURRENT FILING DATE: 2001-04-03
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 211
: LENGTH: 1619
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-825-294-211

```

Query Match	98.1%;	Score 613;	DB 10;	Length 1619;
Best Local Similarity	99.7%;	Pred. No. 5e-156;		
Matches 624;	Conservative	0;	Mismatches 1;	Indels 1;
			Gaps	1;

QY	1	ATTTCGCCCTGGAGAGAGACTGGGCGCCGGGACGGGAAGAGACAGGGGGCGTGCATAAAAGC	60
Db	992	ATTTCCTCCTGGAGAGAGACTGGGCGCCGGGACGGGAAGAGACAGGGGGCGTGCATAAAAGC	1051
QY	61	GGCGCGTGCCTGGTGGTAGTGGCGCATGTACGCCAGGCGCTTCCTCGTGTGGCGTGTG	120
Db	1052	GGCGCGTGCCTGGTGGTAGTGGCGCATGTACGCCAGGCGCTTCCTCGTGTGGCGTGTG	1111
QY	121	CAGCGACAGGGCGGCGACACAGCACCC-TGCAGAAACACCCCGCAAAACTGCTGCAGAGACA	179
Db	1112	CAGCGACAGGGCGGCGACACAGCACCTTGGACAGAAACCCCGCAAAACTGCTGCAGAGACA	1171
QY	180	CCGTGTACAGGACCGGGGTGATTGATCCGAGCTGAGTGTGAAAAACGTCTCCGAGAGGGGGA	239

```
|||||
Db 1172 CGGTGACGAGGCGGGTGGATGACCGAGCTGAGGTAGAAAACGTCCTCGAAGAGGGGA 1231
Qy 240 GAGAGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTCGTGCTGGTTGGCCGAG 299
Db 1233 GGAGGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTCGTGCTGGTTGGCCGAG 1291
Qy 300 CGATGATCCCTCGGAATCTGTTGGGATCCAGCATAGCGCCAAATGTCACAAACATAGCC 359
Db 1292 CCATGATCCCTCGGAATCTGTTGGGATCCAGCATAGCGCCAAATGTCACAAACATAGCC 1351
Qy 360 CTGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 1352 CTGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
Qy 420 GTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 479
Db 1412 GTAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1471
Qy 480 TGTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGATTT 539
Db 1472 TGTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGATTT 1531
Qy 540 TTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTTTAAAGAAAGACATTAATGCTTTA 599
Db 1532 TTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTTTAAAGAAAGACATTAATGCTTTA 1591
Qy 600 GACAGTGNAAAAAAGAAAAAAGAAAAA 625
Db 1592 GACAGTGNAAAAAAGAAAAAAGAAAAA 1617
```

## RESULT 6

```
US-09-867-701-2375
; Sequence 2375, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 2001-05-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2375
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n - A,T,C or G
US-09-867-701-2375
```

Query Match 69.3%; Score 433.2; DB 10; Length 558;

Best Local Similarity 95.6%; Pred. No. 1e-107; Indels 11; Gaps 9;

Matches 539; Conservative 0; Mismatches 14;

```
Qy 1 AGTTCTCTTGCAGAGACTGGCGCGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 1 ACTTCTCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Qy 61 GCGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 120
Db 61 GCGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 118
Qy 121 CAGGACAGAGGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 119 CAGGACAGAGGCGGCA--ACAGACAGCTGACGAGAACCCCGCGAAGAACTGCTGAGAGACAC 176
```

```
Qy 181 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAACGTCCTCGAAGAGGGAG 240
Db 177 CGGTACAGAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAACGTCCTCGAAGAGGGAG 236
Qy 241 GAGAGATCATGTACG--CCCGAAGTAGAGACCTGCTCCAGTCGTGCTGGTTGGCCGAG 299
Db 237 GAGAGATCATGTACGCCCGGAAGTAGAGACCTGCTCCAGTCGTGCTGGTTGGCCGAG 296
Qy 300 CCATGA--TCCCTCGGAATCTGTTGGGATCCAGCATAGCGCCCAATGTCACAAACATAGCC 358
Db 297 CATGATTCCTCCGAATCTGTTGGGATCCAGCATAGCGCCCAATGTCACAAACATAGCC 356
Qy 359 CCGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 357 CCGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Qy 418 CAGTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 477
Db 417 CAGTAATGTAAT--AAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 474
Qy 478 AATGTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGAGAA 537
Db 475 AATGTACCAATTTTTCAGTTGAGCTTGACAGCTTCTTTTGCACAGAGAGAGAGAGAA 532
Qy 538 TTTAACACTGTTTCAAAACCCGGGG 561
Db 533 NTTAACAATTTGTTTCAANCCGGGG 556
```

## RESULT 7

```
US-09-867-701-4240/c
; Sequence 4240, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 2001-05-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240
```

Query Match 63.3%; Score 395.4; DB 10; Length 409;

Best Local Similarity 99.5%; Pred. No. 1.4e-97; Indels 1; Gaps 1;

Matches 407; Conservative 0; Mismatches 1;

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Qy 198 TGATGACGAGCTGAGGTAGAAAAACGTCCTCGAAGAGGGAGAGAGATCATGTACGCC 257
Db 409 TGATGACGAGCTGAGGTAGAAAAACGTCCTCGAAGAGGGAGAGAGATCATGTACGCC 350
Qy 258 GGAAGTAGAGACCTCGTCAGAGTGTGCTGGTTGGCCGAGAGATCATGTACGCCATCT 317
Db 349 GGAAGTAGAGACCTCGTCAGAGTGTGCTGGTTGGCCGAGAGATCATGTACGCCATCT 291
Qy 318 GGTGGGATCCAGCATGAGTACGGCCAAATGTACAAACATGAGCCCTGGGACAGACGAGAG 377
Db 290 GGTGGGATCCAGCATGAGTACGGCCAAATGTACAAACATGAGCCCTGGGACAGACGAGAG 231
Qy 378 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
Db 230 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 171
Qy 438 AAAATATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
Db 170 AAAATATTTAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
```

QY 498 GTTGACCTTGACAGCTTCTTTGGCCACAGCAAGAGAAATTTAACTGTTTCAAAACC 557  
 |||  
 Db 110 GTTGACCTTGACAGCTTCTTTGGCCACAGCAAGAGAAATTTAACTGTTTCAAAACC 51  
 |||  
 QY 558 GGGGAGCTTGGCTGTGTGTTAAAGAAAGCACTTAATGCTTTAGACAGTG 606  
 |||  
 Db 50 GGGGAGCTTGGCTGTGTGTTAAAGAAAGCACTTAATGCTTTAGACAGTG 2

# RESULT 8 US-09-825-294-208/C

; Sequence 208, Application US/09825294  
 ; Patent No. US200200491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Fling, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C5  
 ; CURRENT APPLICATION NUMBER: US/09/825,294  
 ; CURRENT FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 215  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 208  
 ; LENGTH: 1362  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-825-294-208

Query Match 57.9%; Score 361.6; DB 10; Length 1362;  
 Best Local Similarity 98.9%; Pred. No. 3,5e-88;  
 Matches 364; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTGGCAGAGAGCTGGCGCCGGACGCGAAGACAGCGCGCTGCACAAAGCG 60  
 |||  
 Db 1215 AGTTCTCCTTGGCAGAGAGCTGGCGCCGGACGCGAAGACAGCGCGCTGCACAAAGCG 1156  
 |||  
 QY 61 GGGCGTGTGGCTGTGTGAGAGTGGCGATGTAGCGCGAGCGGCTTCGTGGTGGGCTGTG 120  
 |||  
 Db 1155 GGGCGTGTGGCTGTGTGAGAGTGGCGATGTAGCGCGAGCGGCTTCGTGGTGGGCTGTG 1096  
 |||  
 QY 121 CAGCGACAGCGCGCAGCAGCAGCACTGACAGAACCCCGCGAAGCTGCTCGAGAGAC 180  
 |||  
 Db 1095 CAGCGACAGCGCGCAGCAGCAGCACTGACAGAACCCCGCGAAGCTGCTCGAGAGAC 1036  
 |||  
 QY 181 CGGTACAGAGCGGGGTGTATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAGGGGAG 240  
 |||  
 Db 1035 CGGTACAGAGCGGGGTGTATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAGGGGAG 976  
 |||  
 QY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGCTCAGTCTGGTGGTGGCGCGAGC 300  
 |||  
 Db 975 GAGGATCATGTACGCCCGGAAGTAGACCTGCTCAGTCTGGTGGTGGCGCGAGC 916  
 |||  
 QY 301 CATGATCTTCCGAATCTGTTGGGCATTCAGCATACGCCCAATGTCAACAATCAGCCC 360  
 |||  
 Db 915 CATGATCTTCCGAATCTGTTGGGCATTCAGCATACGCCCAATGTCAACAATCAGCCT 856  
 |||  
 QY 361 TGGGCAAGA 368  
 |||  
 Db 855 CAGGAAGA 848

# RESULT 9 US-09-867-701-1516/C

; Sequence 1516, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1516  
 ; LENGTH: 373  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-867-701-1516

Query Match 57.8%; Score 361; DB 10; Length 373;  
 Best Local Similarity 99.7%; Pred. No. 2,6e-88;  
 Matches 372; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 234 AGGGAGAGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGTTGGTGG 293  
 |||  
 Db 373 AGGGAGAGATCATGTACGCCCGGAAGTAGACCTGTCAGTCTGTTGGTGGTGG 315  
 |||  
 QY 294 CCGCAGCATGATCTTCCGAATCTGTTGGGCATTCAGCATACGCCCAATGTCAACAA 353  
 |||  
 Db 314 CCGCAGCATGATCTTCCGAATCTGTTGGGCATTCAGCATACGCCCAATGTCAACAA 255  
 |||  
 QY 354 TCAGCCCTGGGACACAGCAGAGAGAGAGAGACAGAGAAAGAAACACACATGAG 413  
 |||  
 Db 254 TCAGCCCTGGGACACAGCAGAGAGAGAGAGACAGAGAAAGAAACACACATGAG 195  
 |||  
 QY 414 AACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 473  
 |||  
 Db 194 AACACAGTAATGATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 135  
 |||  
 QY 474 AGGAATGTGTACCAATTTTCACTGTTGACCTGACAGCTTCTTTTCCACACAAAGAG 533  
 |||  
 Db 134 AGGAATGTGTACCAATTTTCACTGTTGACCTGACAGCTTCTTTTCCACACAAAGAG 75  
 |||  
 QY 534 AGAATTTAACACTGTTTCAACCCGGGAGAGTGGCTGTGTTAAAGAAACATTAAT 593  
 |||  
 Db 74 AGAATTTAACACTGTTTCAACCCGGGAGAGTGGCTGTGTTAAAGAAACATTAAT 15  
 |||  
 QY 594 GCTTTAGACAGTG 606  
 |||  
 Db 14 GCTTTAGACAGTG 2

# RESULT 10 US-09-867-701-1532

; Sequence 1532, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1532  
 ; LENGTH: 390  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(390)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-867-701-1532

Query Match 56.5%; Score 353; DB 10; Length 390;  
 Best Local Similarity 98.5%; Pred. No. 3,8e-86;

Matches 386; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

```

Oy 218 AAAAAGCTCCGAGAGAGGAGAGATCATGTACGCCCGAAGTAGACCTCGCCAG 277
    |||||||
Db 1 AAAAAGCTCCGAGAGAGGAGAGATCATGTACGCCCGAAGTAGACCTCGCCAG 60
    |||||||
Oy 278 TGTGCTGGTGGTGGCCCGACCATGATCTCCGAATCTGGTGGGATCCAGCTTAG 337
    |||||||
Db 61 TGTGCTGGTGGTGGCCCGACCATGATCTCCGAATCTGGTGGGATCCAGCTTAG 119
    |||||||
Oy 338 GCCAATGTACAAATCATGACCCCTGGGAGACAGACGAGAGAGAGAGAGAAAG 397
    |||||||
Db 120 GCCAATGTACAAATCATGACCCCTGGGAGACAGACGAGAGAGAGAGAGAAAG 178
    |||||||
Oy 398 AAAAAGACGATGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 457
    |||||||
Db 179 AAAAAGACGATGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 238
    |||||||
Oy 458 TGTGCTGGTGGGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 516
    |||||||
Db 239 TGTGCTGGTGGGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 298
    |||||||
Oy 517 TTTGCCACAGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 576
    |||||||
Db 299 TTTGCCACAGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 358
    |||||||
Oy 577 AAAAAAGACCATTAATGCTTTAGACAGTGA 608
    |||||||
Db 359 AAAAAAGACCATTAATGCTTTAGACAGTGA 390
    |||||||

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RESULT 11  
US-09-867-701-2409/C

```

; Sequence 2409; Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2409
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-2409

```

Query Match 49.7%; Score 310.8; DB 10; Length 349;  
Best Local Similarity 96.8%; Pred. No. 8.9e-75;  
Matches 328; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

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Oy 274 CCAGTGTCTGGGTTGGCCGCG--AGCCATGATCTCCGAATCTGGTGGGATCCA 330
    |||||||
Db 339 CCAGTGTCTGGGTTGGCCGCGCGCCATGATCTCCGAATCTGGTGGGATCCA 280
    |||||||
Oy 331 GCATAGGCCAATGTACAAATCATGACCCCTGGGAGACAGACGAGAGAGAGAGAG 390
    |||||||
Db 279 GCATAGGCCAATGTACAAATCATGACCCCTGGGAGACAGACGAGAGAGAGAGAG 220
    |||||||
Oy 391 AGAAAAAGAAACACAGCATGAGACACAGTAAATGAATTAATTAATTAATTAATTA 450
    |||||||
Db 219 AGAAAAAGAAACACAGCATGAGACACAGTAAATGAATTAATTAATTAATTAATTA 160
    |||||||
Oy 451 CCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 510
    |||||||
Db 159 CCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 100
    |||||||
Oy 511 GCTTCTTTTGGCACAAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCT 570
    |||||||

```

Db 99 GCTTCTTTTGGCACAAGAGAGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCT 40

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Oy 571 GTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 609
    |||||||
Db 39 GTGTTAAGAAAGACCATTAATGCTTTAGACAGTGA 1
    |||||||

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RESULT 12

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US-09-867-701-7826
; Sequence 7826; Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7826
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7826

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Query Match 33.2%; Score 207.8; DB 10; Length 381;  
Best Local Similarity 98.3%; Pred. No. 6e-47;  
Matches 231; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Oy 1 AGTTCCTCTTGGAGAGAGTGGGCGCGGAGACGGGAGAGACAGGCGCTGCACAAAGC 60
    |||||||
Db 149 AGTTCCTCTTGGAGAGAGTGGGCGCGGAGACGGGAGAGACAGGCGCTGCACAAAGC 208
    |||||||
Oy 61 GGGCTGTGGTGGTGGAGTGCATGTACGCGCAGCGCTTCTGTTGGCTGCTG 120
    |||||||
Db 209 GGGCTGTGGTGGTGGAGTGCATGTACGCGCAGCGCTTCTGTTGGCTGCTG 267
    |||||||
Oy 121 CAGCAGAGGGCGGACAGACAGCCTGCACAGAAACCCCGCAACTGCTGCGAGACAC 180
    |||||||
Db 268 CAGCAGAGGGCGGACAGACAGCCTGCACAGAAACCCCGCAACTGCTGCGAGACAC 327
    |||||||
Oy 181 CCGTACAGAGCGGGTTGATGACGAGCTGAGTGAATAAGCTCCGAGAG 235
    |||||||
Db 328 CCGTACAGAGCGGGTTGATGACGAGCTGAGTGAATAAGCTCCGAGAG 381
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RESULT 13

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US-09-867-701-8894/C
; Sequence 8894; Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8894
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8894

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Query Match 27.4%; Score 171.2; DB 10; Length 201;  
Best Local Similarity 98.3%; Pred. No. 3.3e-37;



512

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:53:42 ; Search time 23.4202 Seconds  
(without alignments)  
8184.096 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agttctccttcgagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCPUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	56.4	9.0	1872	1 US-08-153-848-39	Sequence 39, Appl
C 2	56.4	9.0	1872	3 US-08-289-843A-39	Sequence 39, Appl
C 3	56.4	9.0	1872	4 US-09-088-337B-39	Sequence 39, Appl
C 4	56.4	9.0	1872	5 PCT-0S93-11153-39	Sequence 39, Appl
C 5	50	8.0	6379	1 US-08-499-215-1	Sequence 1, Appl
C 6	49.4	7.9	7218	1 US-08-232-463-14	Sequence 14, Appl
C 7	46.6	7.5	1176	4 US-09-200-090-3	Sequence 3, Appl
C 8	46	7.4	289	4 US-09-007-005-17	Sequence 17, Appl
C 9	46	7.4	289	4 US-09-244-796-17	Sequence 17, Appl
C 10	45.6	7.3	1342	3 US-08-832-399-1	Sequence 1, Appl
C 11	45.6	7.3	1342	4 US-09-372-498-1	Sequence 1, Appl
C 12	45.6	7.3	1575	3 US-08-858-876A-1	Sequence 1, Appl
C 13	45.6	7.3	1575	4 US-09-472-880-1	Sequence 1, Appl
C 14	44	7.0	1233	4 US-09-200-090-1	Sequence 1, Appl
C 15	43	6.9	1335	4 US-09-668-680-12	Sequence 12, Appl
C 16	42.2	6.8	1137	3 US-09-082-088-1	Sequence 1, Appl
C 17	42.2	6.8	1137	4 US-09-546-117-1	Sequence 1, Appl
C 18	40.8	6.5	1951	3 US-08-922-865-1	Sequence 1, Appl
C 19	40.8	6.5	1951	4 US-09-510-949-1	Sequence 1, Appl
C 20	40.2	6.4	30001	1 US-08-125-468-1	Sequence 1, Appl
C 21	40.2	6.4	30001	2 US-08-474-933-1	Sequence 1, Appl
C 22	39.4	6.3	1280	4 US-09-199-737-1	Sequence 1, Appl
C 23	39.4	6.3	1280	4 US-08-900-230-1	Sequence 1, Appl
C 24	39.4	6.3	1280	4 US-09-058-333A-1	Sequence 1, Appl
C 25	39	6.2	1063	4 US-09-077-675A-1	Sequence 1, Appl
C 26	39	6.2	1947	1 US-07-951-715A-3	Sequence 3, Appl
C 27	39	6.2	1947	2 US-08-459-448A-3	Sequence 3, Appl

C 28	39	6.2	1947	3 US-08-459-595A-3	Sequence 3, Appl
C 29	39	6.2	1947	3 US-08-459-504B-3	Sequence 3, Appl
C 30	39	6.2	1947	3 US-08-459-444-3	Sequence 3, Appl
C 31	39	6.2	1947	4 US-09-547-422-3	Sequence 2, Appl
C 32	39	6.2	3468	1 US-07-951-715A-2	Sequence 4, Appl
C 33	39	6.2	3468	1 US-07-951-715A-4	Sequence 4, Appl
C 34	39	6.2	3468	1 US-07-951-715A-8	Sequence 4, Appl
C 35	39	6.2	3468	1 US-08-459-448A-2	Sequence 8, Appl
C 36	39	6.2	3468	2 US-08-459-448A-2	Sequence 4, Appl
C 37	39	6.2	3468	2 US-08-459-448A-4	Sequence 4, Appl
C 38	39	6.2	3468	2 US-08-459-448A-8	Sequence 8, Appl
C 39	39	6.2	3468	3 US-08-459-595A-2	Sequence 2, Appl
C 40	39	6.2	3468	3 US-08-459-595A-4	Sequence 4, Appl
C 41	39	6.2	3468	3 US-08-459-595A-8	Sequence 8, Appl
C 42	39	6.2	3468	3 US-08-459-504B-2	Sequence 2, Appl
C 43	39	6.2	3468	3 US-08-459-504B-4	Sequence 4, Appl
C 44	39	6.2	3468	3 US-08-459-504B-8	Sequence 8, Appl
C 45	39	6.2	3468	3 US-08-459-504B-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-153-848-39/C  
Sequence 39, Application US/08153848  
Patent No. 5759804  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schwellkart, Vicki L.  
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Ricknell  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,848  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5759804and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1872 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 202..1341  
US-08-153-848-39







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; NAME/KEY: CDS
; LOCATION: 2300..3802
; OTHER INFORMATION: /product="amoc"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3805..4830
; OTHER INFORMATION: /product="amod"
US-08-499-215-1

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Query Match 8.0%; Score 50; DB 1; Length 6379;

Best Local Similarity 50.0%; Pred. No. 0.0054;  
Matches 125; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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QY 58 GCGGCGCTGTGGTGTGAGTGCAGTATGAGCGCGCTTCTGCTGTGCGTG 117
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1473 GCGGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1414
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 118 GTGACGACGAGCGCGGACGACGACGCTGACGACGACGACGACGACGACG 177
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1413 GTCTGTGACGACGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1354
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 178 CACCGTGTACGAGCGGCTGTATGACCGAGCTGAGTGAAGTGAAGTGAAGT 237
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1353 GACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1294
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 238 GAGGAGATCATGTATGACGCGCGGAGTAGAGAGCTGCTGCTGCTGCTGCTG 297
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1293 CGAGGCGGCTGAGACCTGCGAGGATCTTCTGCGACGACGATGCGCTGATG 1234
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 298 AGCCATGATC 307
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1233 CCCATGCTC 1224

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RESULT 6  
US-08-232-463-14/C  
; Sequence 14, Application US/08232463  
; Patent No. 5670367

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; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHUEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOULPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29, 768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)836-4109
; TELEX: 899149

```

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
US-08-232-463-14

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Query Match 7.9%; Score 49.4; DB 1; Length 7218;

Best Local Similarity 2.8%; Pred. No. 0.0083;  
Matches 11; Conservative 21; Mismatches 157; Indels 0; Gaps 0;

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QY 73 GGTGAGTGGGATGTACGCGGCGCTTCTGCTGTGGGCTGTGAGCGACGAGCG 132
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1434 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1375
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 133 GCGACGACGACCTGCGACGACGACCGCGGAACTGCTGAGAGACGCTGACAGAG 192
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1374 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1315
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 193 CGGCTGTATGACCGAGCTGAGTGAAGAACTCTCCGAGAGGAGGAGATCATGTA 252
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1314 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1255
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 253 CGCGCGGAGTAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1254 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1195
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 313 AATCTGTGGGATGCTGACGACATGCGCAATGTCACAGACATGCGCTGCGAGCAG 372
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1194 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1135
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 373 AGCAGAGGAGGAGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 432
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1134 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1075
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 433 ACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 461
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1074 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1046
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RESULT 7

US-09-200-090-3/C  
; Sequence 3, Application US/09200090  
; Patent No. 6420137

```

; GENERAL INFORMATION:
; APPLICANT: Strand, Joann
; APPLICANT: Hadcock, John R.
; TITLE OF INVENTION: No. 6420137el cDNA Encoding The Long and Short
; TITLE OF INVENTION: Forms of The Human Neurolensin Subtype 2 Receptor
; FILE REFERENCE: 0630/0E792
; CURRENT APPLICATION NUMBER: US/09/200, 090
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: human
US-09-200-090-3

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Query Match 7.5%; Score 46.6; DB 4; Length 1176;

Best Local Similarity 49.0%; Pred. No. 0.002; Mismatches 129; Indels 0; Gaps 0;

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QY 111 TGCGGTGCTGACGACGACGACGACGACGACGACGACGACGACGACGACG 170
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DB 1090 TGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 171 GCGAGACACCGTGTACAGAGCGGCTGTATGACGAGCTGAGGTGAAGAAACGTC 230
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

Db 1030 AGACACGCGCTGTGTAGAGAGAGAGCTACAGCTGAGCTGACGTAGAAAAGTGTGG 971  
Qy 231 AGAAGGAGAGAGATCATGTACGCCGGAAGTAGACCTGTCAGCTGCTGGTT 290  
Db 970 TCACCATGTAGAGTGTAGTAATGTACAGTGGTCCAGCCGTCATAGGTA 911  
Qy 291 TGGCCCGACCATGATCTCCGAAATGTTGGCATCCAGCATACGGCAATGTACAA 350  
Db 910 CGTAGCATGATGAGCTCGGCGCATGTACGGCAGCAGACATGACATACATAGACCA 851  
Qy 351 CAATCAGCCTCG 363  
Db 850 CGATGCTCCAG 838

## RESULT 8

US-09-007-005-17  
Sequence 17, Application US/09007005B  
Patent No. 6238558  
GENERAL INFORMATION:  
APPLICANT: Szostak, Jack W.  
APPLICANT: Roberts, Richard W.  
APPLICANT: Liu, Rihc  
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN  
FILE REFERENCE: 00786/350003  
CURRENT APPLICATION NUMBER: US/09/007,005B  
CURRENT FILING DATE: 1998-01-14  
EARLIER APPLICATION NUMBER: 60/035,963  
EARLIER FILING DATE: 1997-01-27  
EARLIER APPLICATION NUMBER: 60/064,491  
EARLIER FILING DATE: 1997-11-06  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 289  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Translation template  
NAME/KEY: misc\_feature  
LOCATION: (1)...(289)  
OTHER INFORMATION: n = A,T,C or G  
US-09-007-005-17

Query Match 7.4%; Score 46; DB 4; Length 289;

Best Local Similarity 9.3%; Pred. No. 0.0015;  
Matches 23; Conservative 103; Mismatches 120; Indels 0; Gaps 0;

Qy 161 CGAACTGCTGCGAGACACCGGTACAGAGCGGTTGATGACCGAGCTAGTAGAAA 220  
Db 36 CRARARURARCARARURRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 95  
Qy 221 AACGTCCTCCGAGAGAGAGAGATCATGTACGCCGGAAGTAGACCTGTCAGTCG 280  
Db 96 NRSNR 155  
Qy 281 TGGTGGGTTGGCCGAGCATGATCTCCGAATCTGTGGGATCCAGATACGGCC 340  
Db 156 NRSNR 215  
Qy 341 AATGTCAACAATCAGCCCTGGCGAGACAGAGAGAGAGAGAGAGAGAGAGAAA 400  
Db 216 NRSRCRARGRCRURGRURARARCRURRURGRRCRCRURAAAAA 275  
Qy 401 AACACA 406  
Db 276 AAAAAA 281

RESULT 9  
US-09-244-796-17

Sequence 17, Application US/09244796  
Patent No. 6281344  
GENERAL INFORMATION:  
APPLICANT: Szostak, Jack W.  
APPLICANT: Roberts, Richard W.  
APPLICANT: Liu, Rihc  
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN  
FILE REFERENCE: 00786/350007  
CURRENT APPLICATION NUMBER: US/09/244,796  
CURRENT FILING DATE: 1999-02-05  
EARLIER APPLICATION NUMBER: 60/035,963  
EARLIER FILING DATE: 1997-01-27  
EARLIER APPLICATION NUMBER: 60/064,491  
EARLIER FILING DATE: 1997-11-06  
EARLIER APPLICATION NUMBER: 09/007,005  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 289  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Translation template  
NAME/KEY: misc\_feature  
LOCATION: (1)...(289)  
OTHER INFORMATION: n = A,T,C or G  
US-09-244-796-17

Query Match 7.4%; Score 46; DB 4; Length 289;

Best Local Similarity 9.3%; Pred. No. 0.0015;  
Matches 23; Conservative 103; Mismatches 120; Indels 0; Gaps 0;

Qy 161 CGAACTGCTGCGAGACACCGGTACAGAGCGGTTGATGACCGAGCTAGTAGAAA 220  
Db 36 CRARARURARCARARURRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 95  
Qy 221 AACGTCCTCCGAGAGAGAGAGATCATGTACGCCGGAAGTAGACCTGTCAGTCG 280  
Db 96 NRSNR 155  
Qy 281 TGGTGGGTTGGCCGAGCATGATCTCCGAATCTGTGGGATCCAGATACGGCC 340  
Db 156 NRSNR 215  
Qy 341 AATGTCAACAATCAGCCCTGGCGAGACAGAGAGAGAGAGAGAGAGAGAGAAA 400  
Db 216 NRSRCRARGRCRURGRURARARCRURRURGRRCRCRURAAAAA 275  
Qy 401 AACACA 406  
Db 276 AAAAAA 281

## RESULT 10

US-08-832-399-1/C

Sequence 1, Application US/08832399

Patent No. 6008050  
GENERAL INFORMATION:  
APPLICANT: Bergsma, Dierk  
APPLICANT: Shabon, Uman  
TITLE OF INVENTION: NOVEL HUMAN NEUTROTENSIN RECEPTOR TYPE 2  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: PA  
ZIP: 19406

COMPUTER READABLE FORM:







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:07 ; Search time 1598.8 Seconds

(without alignments)  
11441.218 Million cell updates/sec

Title: US-09-970-966-210

Sequence: 1 agtctcctgagagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Genembi:\*  
1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pal:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlg\_mus:\*  
34: em\_hlg\_pla:\*  
35: em\_hlg\_rod:\*  
36: em\_hlg\_mam:\*  
37: em\_hlg\_vrt:\*  
38: em\_sy:\*  
39: em\_higo\_hum:\*  
40: em\_higo\_mus:\*  
41: em\_higo\_other:\*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.4	99.6	826	9 BC011449	BC011449 Homo sapi
2	607	97.1	129676	9 AC079773	AC079773 Homo sapi
3	604.4	96.7	1832	9 AK094501	AK094501 Homo sapi
4	598.4	95.7	1890	6 AX136281	AX136281 Sequence
5	479.4	76.7	587	6 AX136698	AX136698 Sequence
6	412.4	66.0	444	6 AX150120	AX150120 Sequence
7	393	62.9	1524	6 AX358762	AX358762 Sequence
8	393	62.9	1524	6 AX362255	AX362255 Sequence
9	361.6	57.9	1362	6 AX319942	AX319942 Sequence
10	361.6	57.9	1362	6 AF034633	AF034633 Homo sapi
11	361.6	57.9	1362	6 AX319944	AX319944 Sequence
12	302	48.3	209885	2 AC124493	AC124493 Mus muscu
13	300.8	48.1	92874	2 AC112072	AC112072 Rattus no
14	230.6	36.9	1797	10 AB041649	AB041649 Mus muscu
15	140	22.4	190503	2 AC128363	AC128363 Rattus no
16	59.8	9.6	3917	10 AB017027	AB017027 Mus muscu
17	58.2	9.3	1254	6 E11480	E11480 cDNA encodi
18	58.2	9.3	1257	6 AX280911	AX280911 Sequence
19	58.2	9.3	4131	9 HSNENRA	X70070 H. sapiens m
20	56.4	9.0	1140	6 E37240	E37240 Novel physl
21	56.4	9.0	1140	6 E63120	E63120 Peptide der
22	56.4	9.0	1148	9 AF100206	AF100206 Macaca mu
23	56.4	9.0	1583	9 HSD03642	U03642 Human G pro
24	56.4	9.0	1754	9 BC032688	BC032688 Homo sapi
25	56.4	9.0	1801	9 HSHG110RP	X89271 H. sapiens m
26	56.4	9.0	1872	6 AR107256	AR107256 Sequence
27	56.4	9.0	1872	6 AR194356	AR194356 Sequence
28	56.4	9.0	169216	2 AC090238	AC090238 Homo sapi
29	56.4	9.0	171744	9 AP001786	AP001786 Homo sapi
30	54.8	8.8	3248	9 AK097232	AK097232 Homo sapi
31	50	8.0	6379	1 RERAMO	D37875 Nocardia co
32	50	8.0	6379	6 E08269	E08269 gDNA of alk
33	50	8.0	6379	6 E10607	E10607 Alkenonoo
34	50	8.0	6379	6 E10980	E10980 Gene of alk
35	50	8.0	6379	6 I36963	I36963 Sequence 1
36	49.4	7.9	7218	6 I66494	I66494 Sequence 14
37	48.4	7.7	208050	1 AL646083	AL646083 Ralstonia
38	47.4	7.6	25362	1 SCF56	AL133424 Streptomy
39	47.4	7.6	99437	2 AC103419	AC103419 Rattus no
40	47.4	7.6	167929	2 AC128436	AC128436 Rattus no
41	47.2	7.6	1583	9 BC022501	BC022501 Homo sapi
42	47	7.5	35100	1 SC3A7	AL031155 Streptomy
43	47	7.5	115666	2 AC105744	AC105744 Oryza sat
44	46.2	7.4	125020	9 AF429315	AF429315 Homo sapi
45	46	7.4	289	6 AR162089	AR162089 Sequence

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL
BC011449	BC011449	Homo sapiens, clone IMAGE:4026092, mRNA.	BC011449	BC011449.1	GI:15277472	Homo sapiens.	Homo sapiens	1	(bases 1 to 826)	
BC011449	BC011449	Homo sapiens, clone IMAGE:4026092, mRNA.	BC011449	BC011449.1	GI:15277472	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Strausberg, R.	Submitted	(25-JUL-2001)	National Institutes of Health, Mammalian

WV

REMARK	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590, USA
COMMENT	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCRD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbiology.org>  
contact: amadan@systemsbiology.org  
Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia  
Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
Series: IRAL Plate: 25 Row: n Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES	Location/Qualifiers
source	1. . 826

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4026092"
/tissue_type="Skin, melanotic melanoma."
/clone_1bp="N1H_MGC_20"
/lab_host="DH10B-R"
/notes="Vector: pOTB7"

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BASE COUNT	237 a	197 c	228 g	164 t
ORIGIN				

Query Match	99.6%	Score 622.4	DB 9	Length 826
Best Local Similarity	99.7%	Pred. No. 1.3e-132		
Matches 623	Conservative 0	Mismatches 2	Indels 0	Gaps 0

QY	1	AGTTCTCCTTCCACAGAGACTGTGCCCGGGAAAGCCAAAGCAAGGGGGCTGTGCACAAAGCG	60
Db	190	AGTTCTCCTTCCACAGAGACTGTGCCCGGGAAAGCCAAAGCAAGGGGGCTGTGCACAAAGCG	24.9
QY	61	GGCCCTGTCCGTTGGTAGTGTGCGATGTACGCGCAGGCGCTTCTCGTGGTTGGCCTCTG	120
Db	250	GGCCCTGTCCGTTGGTAGTGTGCGATGTACGCGCAGGCGCTTCTCGTGGTTGGCCTCTG	30.9
QY	121	CAGGACAGAGGGGGACGACACACTCTGCAGAAACACCCGGCGAAACTGTGTCCAGAGACAC	180
Db	310	CAGGACAGAGGGGGACGACACACTCTGCAGAAACACCCGGCGAAACTGTGTCCAGAGACAC	36.8
QY	181	CGTGTACAGAGACGGGGTTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCCAGAAAGGGAG	240
Db	370	CGTGTACAGAGACGGGGTTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCCAGAAAGGGAG	42.9
QY	241	GAGATCATGTAGACGCCGGGAAAGTGTGAGACCTGTCTCACTCGTGTGGGTTTGGCCGAGC	300
Db	430	GAGATCATGTAGACGCCGGGAAAGTGTGAGACCTGTCTCACTCGTGTGGGTTTGGCCGAGC	48.9
QY	301	CATGATCCTCCGAATCTGTGTGGGCATCCACAGCATACGCCCATGTCAACAATTCAGCCC	360
Db	490	CATGATCCTCCGAATCTGTGTGGGCATCCACAGCATACGCCCATGTCAACAATTCAGCCC	54.9
QY	361	TGGGCACACACGACACAGAGGGAGACACAGAAAAAACAACACACATGACAGACACAG	420
Db	550	TGGGCACACACGACACAGAGGGAGACACAGAAAAAACAACACACATGACAGACACAG	60.9
QY	421	TAAATGAATAAACCATTAATATTTAGCCCTCTGTCTGTGCTTACTGTGCCAGAAAT	480
Db	610	TAAATGAATAAACCATTAATATTTAGCCCTCTGTCTGTGCTTACTGTGCCAGAAAT	66.9
QY	481	GGTACCAATTTTTCAGTGTGGACCTGTACAGCTTCTTTTCCACACAGCAAGAGAGATTT	540
Db	670	GGTACCAATTTTTCAGTGTGGACCTGTACAGCTTCTTTTCCACACAGCAAGAGAGATTT	72.9

Oy	541 AACACTGTTTAAACCCGGGGAGCTTGTCGTGTTAAGAAGAACATTAATGCTTAG	600
Db	730 AACACTGTTTAAACCCGGGGAGCTTGTCGTGTTAAGAAGACCATTAATGCTTAG	789
Oy	601 ACAGTGNAAAAAAAAAAAAAAA	625
Db	790 ACAGTGTAAAAA	814

RESULT 2	AC079773/c	AC079773	129676 bp	DNA	linear	PRI 09-JAN-2002
LOCUS						
DEFINITION		Homo sapiens	BAC clone Rpl1-258B17	from 2,	complete sequence.	
ACCESSION		AC079773				
VERSION		AC079773.8	GI:15145561			
KEYWORDS		HTG.				
SOURCE		Homo sapiens.				
ORGANISM		Homo sapiens				

REFERENCE	1 (bases 1 to 129676)
AUTHORS	Sulston, J.E. and Waterston, R.
TITLE	Toward a complete human genome sequence
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE	99063792
PMID	9847074
REFERENCE	2 (bases 1 to 129676)

TITLE	Direct Submission
JOURNAL	Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 129676)
AUTHORS	Waterston, R. H.
TITLE	Direct Submission
JOURNAL	Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	5 (bases 1 to 129676)
AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	On Aug 9, 2001 this sequence version replaced gi:1446838.

Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [saplens@wustl.edu](mailto:saplens@wustl.edu)  
----- Summary Statistics -----  
Center project name: H\_NH0258B17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis



MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

## SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frenken, E., Tatenno, M., Catanesse, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

RP11-258B17 contains a single plasmid region from 1230 to 1239.

## FEATURES

## source

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  /db_xref="taxon:9606"
  /chromosome="2"
  /map="2"
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  /clone_1fb="RPCT-11"
  /clone_1fb="MER2-type"
  /rpt_family="MER2-type"
  /note="match to EST BF804362 (NID:g12133351)"
  941..1253
  /rpt_family="AT-rich"
  1388..1412
  /rpt_family="AT-rich"
  1387..3331
  /rpt_family="L1"
  2346..2370
  /rpt_family="L1"
  9444..9466
  /rpt_family="TTTGG)n"
  11961..11969
  /rpt_family="AT-rich"
  /note="match to EST A1054234 (NID:g3322021) q177b02.x1"
  12697..12739
  /rpt_family="TTG)n"
  14016..14171
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  20170..20305
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20618..20756
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21300..21325
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23084..23228
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25485..25805
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26466..26655
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## Query Match

Best Local Similarity 99.8%; Score 607; DB 9; Length 129676;  
Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTTCTCCTTGACAGAGACTGGCCGCGGACGAGCAAGACGACGCGCTTCACAAACG 60  
|||||  
Db 119919 AGTTCTCCTTGACAGAGACTGGCCGCGGACGAGCAAGACGACGCGCTTCACAAACG 119860

QY 61 GGGCTGTGCTGTGAGTGGCATGTACGGCAGCGCCCTTCTCGTGTGGCGTGTG 120  
 |||||  
 Db 119859 GGGGCTGTGCTGTGAGTGGCATGTACGGCAGCGCCCTTCTCGTGTGGCGTGTG 119800  
 QY 121 CAGCCAGACGGCGGACACAGCAGCAGTGCAGAAACCCCGGCAACTGCTGCGAGACAC 180  
 |||||  
 Db 119799 CAGCCAGACGGCGGACACAGCAGCAGTGCAGAAACCCCGGCAACTGCTGCGAGACAC 119740  
 QY 181 CGGTGTACAGAGGGGTGTATGACGAGTGGTGAAGAAACGCTCCGAGAGGGGAG 240  
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 Db 119739 CGGTGTACAGAGGGGTGTATGACGAGTGGTGAAGAAACGCTCCGAGAGGGGAG 119680  
 QY 241 GAGGATCATGTACGCGCCGGAAGTAGACCTGCTCAGTGTGCTGGTTGGCCGAGC 300  
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 Db 119679 GAGGATCATGTACGCGCCGGAAGTAGACCTGCTCAGTGTGCTGGTTGGCCGAGC 119620  
 QY 301 CATGATCTCTCCGATGTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCCC 360  
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 Db 119619 CATGATCTCTCCGATGTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCCC 119560  
 QY 361 TGGGCGACACGACGAGGAGGAGACAGAGAAAGAAACACAGCATGAGAACACAG 420  
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 Db 119559 TGGGCGACACGACGAGGAGGAGACAGAGAAAGAAACACAGCATGAGAACACAG 119500  
 QY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGTGCTTACTGGCCAGGAAT 480  
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 Db 119499 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGTGCTTACTGGCCAGGAAT 119440  
 QY 481 GGTACCAATTTTTCAGTGTGACACTGTGACAGCTCTTTTGGCCAGACAGAGAGAAATTT 540  
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 Db 119439 GGTACCAATTTTTCAGTGTGACACTGTGACAGCTCTTTTGGCCAGACAGAGAGAAATTT 119380  
 QY 541 AACACTGTTTCAAAACCGGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 600  
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 Db 119379 AACACTGTTTCAAAACCGGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 119320  
 QY 601 ACAGTGTNA 608  
 |||||  
 Db 119319 ACAGTGTNA 119312  
 RESULT 3  
 AK094501 1832 bp mRNA linear pri 15-JUL-2002  
 LOCUS Homo sapiens cDNA FLJ37182 fls, clone BRALZ2001350, weakly similar  
 DEFINITION to Homo sapiens Gz-selective GTPase-activating protein (GGS20)  
 mRNA.  
 ACCESSION AK094501  
 VERSION AK094501.1 GI:21753575  
 KEYWORDS oligo cloning; fls (full insert sequence).  
 SOURCE Homo sapiens alzheimer cortex cDNA to mRNA, clone\_11b:BRALZ2  
 clone:BRALZ2001350.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1  
 AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,  
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,  
 Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,  
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,  
 Wagaitsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,  
 Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K.  
 and Isogai, T.  
 TITLE NED0 human cDNA sequencing project  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1832)  
 AUTHORS Isogai, T. and Yamamoto, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 COMMENT (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NED0 human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'-6' end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and  
 RAB; annotation: HRI and RAB.  
 Location/Qualifiers  
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 BASE COUNT 411 a 501 c 513 g 407 t  
 ORIGIN  
 Query Match 96.7%; Score 604.4; DB 9; Length 1832;  
 Best Local Similarity 99.8%; Pred. No. 1.9e-128;  
 Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGTTCTCCTTGCAGAGAGTGGCGCGGAGCGGAGAGCAAGGCGGTGCACAAAGC 60  
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 Db 1226 AGTTCTCCTTGCAGAGAGTGGCGCGGAGCGGAGAGCAAGGCGGTGCACAAAGC 1285  
 QY 61 GGGCTGTGCTGTGAGTGGCATGTACGGCAGCGCCCTTCTCGTGTGGCGTGTG 120  
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 Db 1286 GGGCTGTGCTGTGAGTGGCATGTACGGCAGCGCCCTTCTCGTGTGGCGTGTG 1245  
 QY 121 CAGCCAGACGGCGGACACAGCAGCAGTGCAGAAACCCCGGCAACTGCTGCGAGACAC 180  
 |||||  
 Db 1346 CAGCCAGACGGCGGACACAGCAGCAGTGCAGAAACCCCGGCAACTGCTGCGAGACAC 1405  
 QY 181 CGGTGTACAGAGGGGTGTATGACGAGTGGTGAAGAAACGCTCCGAGAGGGGAG 240  
 |||||  
 Db 1406 CGGTGTACAGAGGGGTGTATGACGAGTGGTGAAGAAACGCTCCGAGAGGGGAG 1465  
 QY 241 GAGGATCATGTACGCGCCGGAAGTAGACCTGCTCAGTGTGCTGGTTGGCCGAGC 300  
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 Db 1466 GAGGATCATGTACGCGCCGGAAGTAGACCTGCTCAGTGTGCTGGTTGGCCGAGC 1525  
 QY 301 CATGATCTCTCCGATGTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCCC 360  
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 Db 1526 CATGATCTCTCCGATGTGTTGGGATCCAGCATACGCCCAATGTCAACAATCAGCCC 1585  
 QY 361 TGGGCGACACGACGAGGAGGAGACAGAGAAAGAAACACAGCATGAGAACACAG 420  
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 Db 1586 TGGGCGACACGACGAGGAGGAGACAGAGAAAGAAACACAGCATGAGAACACAG 1645  
 QY 421 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGTGCTTACTGGCCAGGAAT 480  
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 Db 1646 TAAATGAATAAACCATAAATATTTAGCCCTCTGCTGTGCTTACTGGCCAGGAAT 1705  
 QY 481 GGTACCAATTTTTCAGTGTGACACTGTGACAGCTCTTTTGGCCAGACAGAGAAATTT 540  
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 Db 1706 GGTACCAATTTTTCAGTGTGACACTGTGACAGCTCTTTTGGCCAGACAGAGAAATTT 1765  
 QY 541 AACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 600  
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 Db 1766 AACACTGTTTCAAAACCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCTTTAG 1825  
 QY 601 ACAGTGT 606  
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 Db 1826 ACAGTGT 1831

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RESULT 4
LOCUS AX136281 1890 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 203 from Patent EP1067182.
ACCESSION AX136281
VERSION AX136281.1 GI:14272687
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1890)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: Ep 1067182-A 203 10-JAN-2001;
Helix Research Institute (JP)
FEATURES
source location/Qualifiers
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PLHPE"
BASE COUNT 419 a 528 c 533 g 410 t
ORIGIN

Query Match
Best Local Similarity 95.7%; Score 598.4; DB 6; Length 1890;
Matches 599; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCTTGCAGAGAGACTGGCCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCT 66
DB 1290 CCTTGCAGAGAGACTGGCCGCGGAGCGAAGAGCAAGCGGCGCTGCACAAAGCGGCGCT 1349
QY 67 GTGCGGTGTGAGATGCCGATGTACGCCAGCGGCGCTTCTGCTGTTGGCGTCTGCAGCGA 126
DB 1350 GTGCGGTGTGAGATGCCGATGTACGCCAGCGGCGCTTCTGCTGTTGGCGTCTGCAGCGA 1409
QY 127 CAGGCGGAGACAGACGCTGCAAGCAACCCCGGAAACTGCTGCGAGAGGAGAGAT 186
DB 1410 CAGGCGGAGACAGACGCTGCAAGCAACCCCGGAAACTGCTGCGAGAGGAGAGAT 1469
QY 187 CAGGAGCGGGTGTATGATCCGAGCTGAGTGAAGAAACGTCTCCGAGAAAGGAGAGAT 246
DB 1470 CAGGAGCGGGTGTATGATCCGAGCTGAGTGAAGAAACGTCTCCGAGAAAGGAGAGAT 1529
QY 247 CATGTACGCCCGGAGATAGCACTCTGTCAGTGTCTTGGGTTGGCCGAGGCATGAT 306
DB 1530 CATGTACGCCCGGAGATAGCACTCTGTCAGTGTCTTGGGTTGGCCGAGGCATGAT 1589
QY 307 CCTCCCAATCTGGTTGGGATCTCCAGATAGGCGCAATGTACACATCAACCTCTGGGCA 366
DB 1590 CCTCCCAATCTGGTTGGGATCTCCAGATAGGCGCAATGTACACATCAACCTCTGGGCA 1649
QY 367 GACACAGAGAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAAACAGCAATATG 426
DB 1650 GACACAGAGAGAGGAGAGACAGAGAAAGAAACACAGCATGAGAAACAGCAATATG 1709
QY 427 AATTAACCATTAATAATATTAGCCCTCTGTTCTGTCTTACTAGGCCAGAAATGTATCC 486
DB 1710 AATTAACCATTAATAATATTAGCCCTCTGTTCTGTCTTACTAGGCCAGAAATGTATCC 1769
QY 487 AATTTTTCAGTGTGAGCTTGTGACAGCTCTTTTGGCCAGCAAGAGAAATTAACACT 546
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DB 1770 AATTTTTCAGTGTGAGCTTGTGACAGCTTCTTTGGCCACAGCAAGAGAAATTAACACT 1829
QY 547 GTTTCAACCCCGGGGAGTTGGCTGTGTAAAGAAACCAATTAATCTTTAGACAGTG 606
DB 1830 GTTTCAACCCCGGGGAGTTGGCTGTGTAAAGAAACCAATTAATCTTTAGACAGTG 1889

RESULT 5
LOCUS AX136698/c 587 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 620 from Patent EP1067182.
ACCESSION AX136698
VERSION AX136698.1 GI:14273102
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 587)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: Ep 1067182-A 620 10-JAN-2001;
Helix Research Institute (JP)
FEATURES
source location/Qualifiers
1..587
/organism="Homo sapiens"
/db_xref="taxon:9606"
117 a 162 c 140 g 162 t 6 others
BASE COUNT 117 a 162 c 140 g 162 t 6 others
ORIGIN

Query Match
Best Local Similarity 76.7%; Score 479.4; DB 6; Length 587;
Matches 498; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 90 CCGGACGGCGCTTCTGCTGTTGGCGCTGTCAGCGACAGCGGCGCAGACACACCTGCA 149
DB 516 CCGNACAGCGGCTTCTGCTGTTGGCGCTGTCAGCGACAGCGGCGCAGACACCTGCA 459
QY 150 CGAACACCCCGCCAACTGCTGCGAGGACACCGTGTACAGAGCGGGTGTATGACCGAGC 209
DB 458 CGAACACCCCGCCAACTGCTGCGAGGACACCGTGTACAGAGCGGGTGTATGACCGAGC 399
QY 210 TGAGTAGAAGAAACGTCCTCCGAGAGGAGGAGATCATGTACGCCGGAAGTAGAGACC 269
DB 398 TGAGTAGAAGAAACGTCCTCCGAGAGGAGGAGATCATGTACGCCGGAAGTAGAGACC 339
QY 270 TCGTCCAGTCGTGCTTGGGTTGGCCGACACCATATGATCTCCGAATCTGTTGGCATCC 329
DB 338 TCGTCCAGTCGTGCTTGGGTTGGCCGACACCATATGATCTCCGAATCTGTTGGCATCC 279
QY 330 ACGATTCGGCCATGTACACACATACAGCCCTGGGACAGACAGCAGAGAGAGAGACA 389
DB 278 ACGATTCGGCCATGTACACACATACAGCCCTGGGACAGACAGCAGAGAGAGAGACA 219
QY 390 GAGAAAGAGAAACACAGCATGGAACACAGTAATGAATTAATTAATTTTATGAC 449
DB 218 GAGAAAGAGAAACACAGCATGGAACACAGTAATGAATTAATTAATTTTATGAC 159
QY 450 CCCTCTGTTCTGTCTTACTGCGCAGAAATGTATCAATTTTCACTGTTGACCTTGAC 509
DB 158 CCCTCTGTTCTGTCTTACTGCGCAGAAATGTATCAATTTTCACTGTTGACCTTGAC 99
QY 510 AACTCTTTTGGCACAAGAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGGC 569
DB 98 AACTCTTTTGGCACAAGAGAGAAATTTAACTGTTTCAACCCGGGGAGTTGGC 39
QY 570 TGTGTTAAGAAAGACCATTAATGCTTTAGACAGTG 606
DB 38 TGTGTTAAGAAAGACCATTAATGCTTTAGACAGTG 2

RESULT 6
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AX150120/c  
 LOCUS AX150120 444 bp DNA linear PAT 08-JUN-2001  
 DEFINITION Sequence 95 from Patent WO0136685.  
 ACCESSION AX150120  
 VERSION AX150120.1 GI:14348148  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Kiroes, R.A., Moskal, J.R. and Yamamoto, H.  
 TITLE Differential gene expression in cancer  
 JOURNAL Patent: WO 0136685-A 95 25-MAY-2001;  
 NIXIS Neurotherapies, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 BASE COUNT 95 a 113 c 94 g 142 t  
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 Query Match 66.0%; Score 412.4; DB 6; Length 444;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-84;  
 Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 204 CCGACCTGAGTGAAGAAACGCTCCGAGAGGAGGAGGAGTCAATGTACGCCGGAAGT 263  
 DB 431 CCGACCTGAGTGAAGAAACGCTCCGAGAGGAGGAGGAGTCAATGTACGCCGGAAGT 372  
 QY 264 AGGACCTGCTCCAGTCGCTGGGTTGGCCGAGCCATGATCTCCGAACTCGTTGG 323  
 DB 371 AGGACCTGCTCCAGTCGCTGGGTTGGCCGAGCCATGATCTCCGAACTCGTTGG 312  
 QY 324 GCATCCAGCATCGGCCAATGTACAAATCAGCCCTGGGAGACAGACAGAGAGGA 383  
 DB 311 GCATCCAGCATCGGCCAATGTACAAATCAGCCCTGGGAGACAGACAGAGAGGA 252  
 QY 384 GAGACAG 443  
 DB 251 GAGACAG 192  
 QY 444 TTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 503  
 DB 191 TTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 132  
 QY 504 CTTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 563  
 DB 131 CTTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 72  
 QY 564 GTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 618  
 DB 71 GTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 17  
 RESULT 7  
 AX358762 1524 bp DNA linear PAT 13-FEB-2002  
 LOCUS AX358762  
 DEFINITION Sequence 15 from Patent WO0193983.  
 ACCESSION AX358762  
 VERSION AX358762.1 GI:18675282  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Baker, R.P., Desnoyers, L., Gerltzen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0193983-A 15 13-DEC-2001;

Genentech Inc. (US)  
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 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 321 a 433 c 435 g 335 t  
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 Query Match 62.9%; Score 393; DB 6; Length 1524;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-80;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTTCTCTTCGAG 60  
 DB 1132 AGTTCTCTTCGAG 1191  
 QY 61 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 DB 1192 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251  
 QY 121 CAGCGACAGCGCGGAG 180  
 DB 1252 CAGCGACAGCGCGGAG 1311  
 QY 181 CGTGTACAG 240  
 DB 1312 CGTGTACAG 1371  
 QY 241 GAGATCATGTACGCGCGGAG 300  
 DB 1372 GAGATCATGTACGCGCGGAG 1431  
 QY 301 CATGATCTCTCCGAAATCTGCTGGGATCCAGATACGCGCAATGTACAAATCAGCCC 360  
 DB 1432 CATGATCTCTCCGAAATCTGCTGGGATCCAGATACGCGCAATGTACAAATCAGCCC 1491  
 QY 361 TGGGACAGACAG 333  
 DB 1492 TGGGACAGACAG 1524  
 RESULT 8  
 AX362255 1524 bp DNA linear PAT 15-FEB-2002  
 LOCUS AX362255  
 DEFINITION Sequence 15 from Patent WO0208288.  
 ACCESSION AX362255  
 VERSION AX362255.1 GI:18694585  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Baker, R.P., Desnoyers, L., Gerltzen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0208288-A 15 31-JAN-2002;  
 Genentech, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 BASE COUNT 321 a 433 c 435 g 335 t  
 ORIGIN  
 Query Match 62.9%; Score 393; DB 6; Length 1524;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-80;  
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTTCTCTTCGAG 60  
 DB 1132 AGTTCTCTTCGAG 1191



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LSYINPLDLTVSSOOFERYVFOVLCRSLDHANEKRLRVHAHSTDSARVOPRPL  
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HEVY

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ORIGIN				

Query Match	57.9%;	Score 361.6;	DB 9;	Length 1362;
Best Local Similarity	98.9%;	Pred. No. 1.1e-72;		
Matches 364; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

OY	1	AGTTCTCCTTGAGAGGAACTGGCCGGGAGCCGAAGAGCAACGGGCGCTGTGCACAAAGCG	60
Db	1215	AGTTCTCCTTGAGAGGAACTGGCCGGGAGCCGAAGAGCAACGGGCGCTGTGCACAAAGCG	1156
OY	61	GGCGCTGTGCGTGTGAGAGTGGCCATGTACGGCAGGCGCTTCTGTGTGTTGGCGTGTG	120
Db	1155	GGCGCTGTGCGTGTGAGAGTGGCCATGTACGGCAGGCGCTTCTGTGTGTTGGCGTGTG	1096
OY	121	CAGGCACAGGGGGGAGCAGCAGCAGCCTGCACGAACACCCGGCGGAATCTGCTGCGAGGACAC	180
Db	1095	CAGGCACAGGGGGGAGCAGCAGCAGCCTGCACGAACACCCGGCGGAATCTGCTGCGAGGACAC	1036
OY	181	CGTGTACAGAGAGGGGGTTGATGACCGGAGCTGAGGTATGAAAAACGTCCTCCGAAGAAGGGAG	240
Db	1035	CGTGTACAGAGAGGGGGTTGATGACCGGAGCTGAGGTATGAAAAACGTCCTCCGAAGAAGGGAG	976
OY	241	GAGGATCATGTATACGCCCGGAAGTAGGACCTCTCCAGTCGTGCTTGAGGTTTGCGCGAC	300
Db	975	GAGGATCATGTATACGCCCGGAAGTAGGACCTCTCCAGTCGTGCTTGAGGTTTGCGCGAC	916
OY	301	CATGATCCTCCGAATCTGGTTGGCATCCAGCATACGGCCAAATGTACAAACATCAGCCC	360
Db	915	CATGATCCTCCGAATCTGGTTGGCATCCAGCATACGGCCAAATGTACAAACATCAGCCT	856
OY	361	TGGCGAGA 368	
Db	855	CAGGAGA 848	

RESULT	11				
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LOCUS	AX319944	2528 bp	DNA		
DEFINITION	Sequence	3 from Patent WO0181634.			
ACCESSION	AX319944				
VERSION	AX319944.1	GI:17901491			
KEYWORDS					
SOURCE	human.				
					PAT 14-DEC-2001
				linear	

**REFERENCE**  
**AUTHORS** 1 Galvin, K. A. and Rudolph-Owen, L. A.  
**TITLE** Methods and compositions for the diagnosis and treatment of  
**JOURNAL** Cardiovascular and tumorigenic disease using 4941  
**PATENT** Patent: WO 0181634-A 3 01 NOV-2001;  
**FEATURES** Millennium Pharmaceuticals, Inc. (US)  
Location/Qualifiers

BASE COUNT	516 a	766 c	677 g	567 t	2 others
ORIGIN					

Query Match	57.9%;	Score 361.6;	DB 6;	Length
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Query Match	57.9%;	Score 361.6;	DB 6;	Length 2528;
Best Local Similarity	98.9%;	Pred. No. 1.2e-72;		
Matches 364;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	AGTCTCCTTGGCAGAGGAC	TGGCGCCGGGAGCCGAAAGAC	CAACGGGCGCTGCA	CAAAAGCG	60
Db	1256	AGTTCTCCTTGGCAGAGGAC	TGGCGCCGGGAGCCGAAAGAC	CAACGGGCGCTGCA	CAAAAGCG	1197
QY	61	GGCCTGTTCGTGTGTGAGAGT	GGCATGTACGGCAGAGGGCTTCTCGTGGTGGCCTGCTG			120
Db	1196	GSCCGTTCGTGTGTGTGAGAGT	GGCATGTACGGCAGAGGGCTTCTCGTGGTGGCCTGCTG			1137
QY	121	CAGCGACAGGGCGGCAGCACAGC	CACTGCACGAAACCCGCGAAACTGCTGCGAGACAC			180
Db	1136	CAGCGACAGGGCGGCAGCACAGC	CACTGCACGAAACCCGCGAAACTGCTGCGAGAGAC			1077
QY	181	CGTGTACAGAGAGGGGGTGTGAT	GCACCGAGCTGAGGTATGAAAAACGTCCTCGAGAAAGGGAG			240
Db	1076	CGTGTACAGAGAGGGGGTGTGAT	GCACCGAGCTGAGGTATGAAAAACGTCCTCGAGAAAGGGAG			1017
QY	241	GAGGATTCATGTACGCCCGGAAGT	AGTAGACCTCGTCACATGCTGGGTTTGGCCGAC			300
Db	1016	GAGGATTCATGTACGCCCGGAAGT	AGTAGACCTCGTCACATGCTGGGTTTGGCCGAC			957
QY	301	CATGATTCCTCCGAATCTGGTGTGGG	CATCCAGCATACGGCCAAATGTACAAACATCAGCCC			360
Db	956	CATGATTCCTCCGAATCTGGTGTGGG	CATCCAGCATACGGCCAAATGTACAAACATCAGCCT			897
QY	361	TGGCGACA	368			
Db	896	CAGGAGA	889			

RESULT	12
AC124493/c	
LOCUS	
DEFINITION	AC124493 209885 bp DNA linear HTG_05-JUL-2002
VERSION	Mus musculus chromosome UUK clone RP23-662P13, WORKING DRAFT
KEYWORDS	SEQUENCE, 5 unordered pieces.
SOURCE	AC124493.2 GI:21699722
	HTG; HTGS_PHRASE1; HTGS_DRAFT; HTGS_FUZZTOP.
	house mouse.

REFERENCE AUTHORS TITLE JOURNAL	(bases 1 to 209885) McPherson,J.D. and Waterston,R.H. The sequence of Mus musculus clone unpublished 2 (bases 1 to 209885)
REFERENCE AUTHORS TITLE JOURNAL	McPherson,J.D. and Waterston,R.H. Direct Submission Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 209885)
REFERENCE AUTHORS TITLE JOURNAL	McPherson,J.D. and Waterston,R.H. Direct Submission Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT	On Jul 5, 2002 this sequence version replaced gl:21426614.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)

RESULT 13	AC112072	92874 bp	DNA	linear	HTG 17-JUL-2002
LOCUS	AC112072	92874 bp	DNA	linear	HTG 17-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-286021, ***	Sequencing in progress			
ACCESSION	AC112072	50 unordered pieces			
VERSION	AC112072.3	GI:21744373			
KEYWORDS	HTG: HTGS_PHASE1.				
SOURCE	Notway rat.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 92874)				
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C., Alsbrooks,S.L., Amaraltinge,H.C., Are,J.R., Ayale,M., Banks,T., Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,M., Brown,M., Bryant,N.P., Butch,K., Burch,P., Burrell,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,R.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gottell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B., Homs,J.F., Howard,S., Huber,J., Huliy,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,U., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Louisgeed,H., Lozadó,R.J., Lu,X., Lucier,A., Luchler,R., Luna,R., Ma,J., Maheswari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., Mcloed,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S., Ogund,M., Okunou,G., Oragunye,N., Oyedero,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Qulles,M., Ren,Y., Rives,M., Rojas,A., Rojlookan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N., Slison,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,				

Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wang, Q.,  
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,  
Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,  
Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 92874)  
Worley, K. C.  
Direct Submission  
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 92874)  
Worley, K. C.  
Direct Submission  
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 13, 2002 this sequence version replaced gi:20303189.  
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Center: Baylor College of Medicine  
Genome Center  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
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Project Information  
Center project name: GRJD  
Center clone name: CH230-286021  
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Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 32512 bases at least Q40  
Consensus quality: 34515 bases at least Q30  
Consensus quality: 35930 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draat\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draat_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 50 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1057: contig of 1057 bp in length  
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\* 2411 2510: gap of unknown length  
\* 2511 3571: contig of 1061 bp in length  
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\* 3672 5259: contig of 1588 bp in length  
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\* 6437 6536: gap of unknown length  
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\* 7806 8911: contig of 1106 bp in length  
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\* 10471 11914: contig of 1444 bp in length  
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\* 20648 20747: gap of unknown length  
\* 20748 22171: contig of 1424 bp in length  
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\* 59616 61878: contig of 2263 bp in length  
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\* 67531 68852: contig of 1322 bp in length  
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\* 77023 79345: contig of 2323 bp in length  
\* 79346 79445: gap of unknown length  
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\* 82317 82416: gap of unknown length  
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\* 84867 84966: gap of unknown length  
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Best Local Similarity	74.8%; Pred. No. 1.6e-58;
Matches 445; Conservative	0; Mismatches 138; Indels 12; Gaps 5
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DB	75434 GCGGGAGGCTGTGGAAGATGACGGGCTTCGGGCTGTAGCGGCTGCTGTTTGTGTAGAC 75493
OY	81 GCGCATGTATGCGCGCAGCGCTTCTGCTGGTGTGGCGTGTGCAGACGACGGGACAGACA 140
DB	75494 TGAAGTAGGACAGCTGTCTTCTCTCGTTTGGCATGTCTGCAGAGTCTACCCGGCAGACA 75553
OY	141 GCACCTGCACGAACACCCCGCAAACTGCTGCGAGACACCGTATACAGAGCGGGTTGA 200
DB	75554 GAACCTGCCAGAAAACCTTCGCGAACTGCTGAGAAGACACGTTGTAGAGAGAGGGTTGA 75613
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DB	75614 CCACGAGCTGAGTGTAGAAAAGGTGTGCGAAGAGGGGAGAGATCATGTATGCCCTGA 75673
OY	261 AGTAGGACCTGCTCAGATGTCTTGGTGTGGCGCAGACCATGATCCTCCGATCTGCT 320
DB	75674 AGTAGGACTTGTGTCCAGTATGTTTGGTGTTCCTGCTGCGCCATGATCCTCGATTTGAT 75733
OY	321 TGGGATCCAGCATACGGCCATGTCAACAATCAGCCCTGCGGACAGCAGCAGAGAG 380
DB	75734 TTGGATCCACACACGGCCAGTGTCCACAGATGATGCTCTGGGACGGGAGAGAGAG 75793
OY	381 GGAGAGACAGAAAAAGAAAAACACAGCATGTGAACACGTAATGATATAAA--CCT 437
DB	75794 AAAAAAGGGA-CGGGAGAAAAACGATGTAGAACAAAAATAAATAAACAACCAT 75852
OY	438 AAAATATTAGCCCTCTCTCTG--TGCTACTGGGACAGAAATGGTATCAATTTTCAG 496
DB	75853 AAAATATTAGCCCTTGTGTTCTGTCTTACTGCTGGGAAACGTTACCAATCTTTCAG 75912
OY	497 TGTGGACTTGACAGCTTC--TTTTGCCACAAGCAGAGAGATTTAACAGTGTTCAA 553
DB	75913 TCTGTGCTTACGGGCTTCTTTTTCGCCACGGGCAAGAATTAATGCTGCTTCAA 75972
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DB	75973 GCTCAGGGGACTTGGCTATGTT---AAAAAGCGTAAATGCTTCGACAGTGA 76023
RESULT 14	
LOCUS	AB041649 1797 bp mRNA linear ROD 30-JUN-2000
DEFINITION	Mus musculus brain cDNA, clone MNCB-0671.
ACCESSION	AB041649
VERSION	AB041649.1 GI:7670499
KEYWORDS	fls (full insert sequence).
SOURCE	Mus musculus (strain:C57BL) adult female cDNA to mRNA, clone:lib:Sugano mouse brain mncb clone:MNCB-0671. Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (sites)
AUTHORS	Osada, N., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Sugano, S. and Hashimoto, K.
TITLE	Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 1797)
AUTHORS	Hashimoto, K., Osada, N., Kusuda, J. and Sugano, S.

TITLE		Direct Submission	
JOURNAL		Submitted (13-APR-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181) URL: http://www.nih.go.jp/yoken/genebank/ Lib Name: Sugano mouse brain mncb Lab host: TOP10 Vector: pME185-FL3	
COMMENT		1st strand cDNA was primed with an oligo(dT) primer [ATGTCGCCCTTTTCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME185-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing ( 5' end primer [CTTTCGCTCTTAAGAGCTGCG], 3' end primer [CGACCTGCAGCTCGAGACACA] ). A part of this sequence is reported in AU035640.	
FEATURES		Location/Qualifiers	
Source		1..1797	
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CDS		BASE COUNT 391 a 487 c 511 g 408 t ORIGIN	
Query Match		36.9%; Score 230.6; DB 10; Length 1797; Best Local Similarity 75.5%; Pred. No. 1,4e-42;	
Matches 312; Conservative		0; Mismatches 99; Indels 2; Gaps 2;	
QY	21	GCGCGCGGGAGCCGGAAGACCAACGGGCGCGCTGCACAAACGGCGCGCTGTCGGGTGGAGT	80
DB	1378	GCCGGGAGGCTTGAAGAGTGAAGGGGCGTCGGCGCTGACCTGCTGCTCTTGGTGGAGA	1437
QY	81	GCGCATGTACCGCGCAGGCGCTTCTCTGCTGGTGGCGTGTCTGCAGCAGACGGCGGACACA	140
DB	1438	TGAAGCGGGACAGCGCTGGGGTTCCTTGGTGGCATGCTGCAGAGTCAGGCGGACAGAGA	1497
QY	141	GCACCTGCAGCAACACCCGCGCAACCTGCTGGAGAGACACCGTATACAGAGACGGGTTGA	200
DB	1498	GCACCTGCAGACACCTTCCGAACTGTGTGAAGACTCGTTGTAGAGGAGAGGGTTGA	1557
QY	201	TGACCGAGCTGAGTGAAGAAAACGTCTCCGAAGAGGGAGAGAGATGTATGTACGCCCGGA	260
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QY	381	GGAGAGACAGAGAAAAGAAAACACAGCATGAGGAACACAGTAATGAAATAAAA	433
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RESULT 15  
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DEFINITION  
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Rattus norvegicus clone CH230-22808, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 69 unordered pieces.  
AC128363  
AC128363.1 GI:21909012  
HTG: HTGS\_PHASE1.  
SOURCE  
ORGANISM  
Rattus norvegicus  
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Munz, D.M., Adams, C., Adlo-Oduola, B., All-oshman, F.R., Allen, C.,  
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Weinstock, G. and Gibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 190503)  
Worley, K.C.  
Direct Submission  
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
COMMENT  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center project name: GZCA  
Center clone name: CH230-22808  
Summary Statistics

Sequencing vector: Plasmid.  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap version 0.990329  
Consensus quality: 13119 bases at least Q40  
Consensus quality: 13608 bases at least Q30  
Consensus quality: 14183 bases at least Q20  
NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 69 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.  
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1001: contig of 1001 bp in length  
1101: gap of unknown length  
1102: contig of 1178 bp in length  
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44717: contig of 2346 bp in length  
44817: gap of unknown length  
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* 47412 48687: contig of 1276 bp in length
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Db 169598 CACACAGCCAGTATCACCAATCAGAC 169625
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Search completed: November 7, 2002, 13:31:03  
Job time : 1917.05 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:50:02 : Search time 123.06 Seconds  
(without alignments)  
11437.514 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agtctccttcagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY\_NTC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq\_101002:\*

- 1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
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- 19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
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- 21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	624	99.8	625	24	ABT03280	Human ovarian carc
2	624	99.8	625	24	ABLA0348	Ovarian carcinoma
3	624	99.8	625	24	ABLA0348	Ovarian carcinoma
4	624	99.8	1897	24	ABT03284	Human ovarian carc
5	624	99.8	1897	24	ABLA0352	Ovarian carcinoma
6	613	98.1	1619	24	ABT03277	Human ovarian carc
7	613	98.1	1619	24	ABT03281	Human ovarian carc
8	613	98.1	1619	24	ABLA0345	Ovarian carcinoma
9	613	98.1	1619	24	ABLA0349	Ovarian carcinoma

10	606.6	97.1	1608	24	ABO54231	Human ovarian anti
11	606.6	97.1	1953	21	AAE22400	Human secreted pro
12	606.6	97.1	1956	22	AAE64188	Human secreted pro
13	598.4	95.7	1890	22	AAE93845	Human cDNA encodin
14	479.4	76.7	587	22	AAE94186	Primer specific fo
15	433.2	69.3	558	24	ABE79397	Human ovarian carc
16	412.4	66.0	444	22	AAH50766	Human tumour assoc
17	395.4	63.3	409	24	ABE81262	Human encoding huma
18	393	62.9	1524	24	ABK33543	CDNA encoding huma
19	361.6	57.9	1362	24	ABT03279	Human ovarian carc
20	361.6	57.9	1362	24	ABLA0347	Ovarian carcinoma
21	361.6	57.9	2528	22	AAE18690	Human G protein co
22	361	57.8	373	24	ABE78538	Human ovarian carc
23	353	56.5	390	24	ABE78554	Human ovarian carc
24	310.8	49.7	349	24	ABE79431	Human ovarian carc
25	207.8	33.2	381	24	ABE84848	Human ovarian carc
26	174.4	27.9	468	22	AAE54063	Murine transport a
27	171.2	27.4	201	24	ABE85916	Human ovarian carc
28	58.2	9.3	1254	17	AAE33127	Human neurotensin
29	58.2	9.3	1257	23	ABE98007	Non-endogenous hum
30	58.2	9.3	4149	23	AAE76503	DNA encoding novel
31	58	9.3	3609	22	AAE94581	Human full-length
32	56.4	9.0	1140	20	AAE83839	G-protein-coupled
33	56.4	9.0	1140	21	AAE15693	G-protein coupled
34	56.4	9.0	1140	22	ABA02182	Human APJ G protei
35	56.4	9.0	1143	21	AAE30623	Human G protein-co
36	56.4	9.0	1143	21	AAE30726	DNA encoding human
37	56.4	9.0	1370	22	AAE94107	Human full-length
38	56.4	9.0	1464	21	AAE10298	DNA encoding human
39	56.4	9.0	1583	24	ABE84189	Human cDNA differe
40	56.4	9.0	1872	15	AAO66176	Seven transmembran
41	56.4	9.0	1872	19	AAE18354	Human R20 seven tr
42	56.4	9.0	1872	21	AAE91723	Human 7TM receptor
43	56.4	9.0	1872	24	ABE54252	Human 7 transmembr
44	56.4	9.0	10210	24	AAE18100	Human angiotensin
45	56	9.0	3249	23	AAE76504	DNA encoding novel

## ALIGNMENTS

RESULT 1	ABT03280	standard: cDNA: 625 BP.
ID	ABT03280	
XX	ABT03280:	
AC	05-SEP-2002 (first entry)	
XX		
DT	Human ovarian carcinoma associated coding sequence SEQ ID NO: 210.	
XX		
DE	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;	
XX		
KW	cytostatic; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200239885-A2.	
XX		
PD	23-MAY-2002.	
XX		
XX	13-NOV-2001: 2001MO-US45395.	
PF		
XX	14-NOV-2000: 2000US-0713550.	
PR	03-APR-2001: 2001US-0825294.	
XX		
PR	02-OCT-2001: 2001US-0970566.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Xu J, Stolk JN, Algate PA, Fling SP, Molesh DA;	
XX		
DR	WPI, 2002-500186/53.	
XX		
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for	

PT detecting the presence of ovarian cancer in a patient, and in  
 PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PS Claim 2, page 194, 197pp: English.

CC The present invention provides human ovarian cancer associated proteins  
 CC and coding sequences. The sequences can be used in the diagnosis and  
 CC treatment of ovarian cancers. The present sequence is a coding sequence  
 CC of the invention.

XX Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match 99.8%; Score 624; DB 24; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-154;  
 Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AGTTCCTCTTGCAAGAGACTGGCGCGGAGCGGGAAGAGCAAGCGGCGCTGCACAAAGCG 60
   |||||||
DB 1 AGTTCCTCTTGCAAGAGACTGGCGCGGAGCGGGAAGAGCAAGCGGCGCTGCACAAAGCG 60
OY 61 GGGCGTGTGGGTGGAGTGGCGATGTACGGCGGAGCGGCTTCTCGGTGGTGGCGTCTG 120
   |||||||
DB 61 GGGCGTGTGGGTGGAGTGGCGATGTACGGCGGAGCGGCTTCTCGGTGGTGGCGTCTG 120
OY 121 CACGACAGCGCGGACAGACAGCTGACAGAAACACCGCGAAACTGCTGCGAGACAC 180
   |||||||
DB 121 CACGACAGCGCGGACAGACAGCTGACAGAAACACCGCGAAACTGCTGCGAGACAC 180
OY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAACGCTCCGAGAGAGGAG 240
   |||||||
DB 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAACGCTCCGAGAGAGGAG 240
OY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGCGGAGC 300
   |||||||
DB 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGCGGAGC 300
OY 301 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGAGCGGCAATGTACAAATCAAGCC 360
   |||||||
DB 301 CATGATCTCTCCGAATCTGGTGGGATCCAGCATACGAGCGGCAATGTACAAATCAAGCC 360
OY 361 TGGGACAGACAGCGAGGAGGAGAGACAGAGAAAACACACAGATGAGACAG 420
   |||||||
DB 361 TGGGACAGACAGCGAGGAGGAGAGACAGAGAAAACACACAGATGAGACAG 420
OY 421 TAATGAATTAACCAATTAATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
   |||||||
DB 421 TAATGAATTAACCAATTAATTTAGCCCTCTGTTCTGCTTACTGGCCAGGAAT 480
OY 481 GGATCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCACAAGCAGAGAAATTT 540
   |||||||
DB 481 GGATCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCACAAGCAGAGAAATTT 540
OY 541 AACACGTTTCAAAACCGGGGAGTGGCTGTCTAAAGAAAACCATTAATGCTTTAG 600
   |||||||
DB 541 AACACGTTTCAAAACCGGGGAGTGGCTGTCTAAAGAAAACCATTAATGCTTTAG 600
OY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
   |||||||
DB 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625

```

RESULT 2  
 ABL40348  
 ID ABL40348 standard; cDNA; 625 BP.

XX ABL40348;

XX 28-JUN-2002 (first entry)

DE Ovarian carcinoma O1034C EST clone nucleotide sequence.

KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

KW expressed sequence tag; EST; ss.

XX Homo sapiens.

XX US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

XX 01-MAY-2000; 2000US-0561778.

XX 15-AUG-2000; 2000US-0640173.

XX 07-SEP-2000; 2000US-0656668.

XX 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOL/) STOLK J A.

XX (ALIN/) ALGATE P A.

XX (FLIN/) FLING S P.

XX Xu J, Stolk JA, Algate PA, Fling SP.

XX WPI: 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

XX prevention and/or treatment of cancer, especially ovarian cancer

XX Claim 1a: Page 125, 131pp: English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides  
 CC that may be utilised in cancer therapy, for example in a vaccine or  
 CC gene therapy. Polypeptides and polynucleotides of the invention are  
 CC useful for detecting a cancer in a patient, for stimulating and/or  
 CC expanding T-cells specific for a tumour protein, and for inhibiting the  
 CC development of a cancer in a patient. They are also useful for  
 CC stimulating an immune response in a patient, and for treating a cancer in  
 CC a patient and for determining the presence of a cancer in a patient.  
 CC The isolated polynucleotides of the invention are useful for their  
 CC ability to selectively form duplex molecules with complementary stretches  
 CC of the entire desired gene or gene fragments, and for designing and  
 CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the ovarian carcinoma O1034C EST clone nucleotide  
 CC sequence.

XX Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;

Query Match 99.8%; Score 624; DB 24; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-154;  
 Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AGTTCCTCTTGCAAGAGACTGGCGCGGAGCGGGAAGAGCAAGCGGCGCTGCACAAAGCG 60
   |||||||
DB 1 AGTTCCTCTTGCAAGAGACTGGCGCGGAGCGGGAAGAGCAAGCGGCGCTGCACAAAGCG 60
OY 61 GGGCGTGTGGGTGGAGTGGCGATGTACGGCGGAGCGGCTTCTCGGTGGTGGCGTCTG 120
   |||||||
DB 61 GGGCGTGTGGGTGGAGTGGCGATGTACGGCGGAGCGGCTTCTCGGTGGTGGCGTCTG 120
OY 121 CACGACAGCGCGGACAGACAGCTGACAGAAACACCGCGAAACTGCTGCGAGACAC 180
   |||||||
DB 121 CACGACAGCGCGGACAGACAGCTGACAGAAACACCGCGCGAAACTGCTGCGAGACAC 180
OY 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAACGCTCCGAGAGAGGAG 240
   |||||||
DB 181 CGTGTACAGAGCGGGTGTATGACCGAGCTGAGGTAGAAAACGCTCCGAGAGAGGAG 240
OY 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGCGGAGC 300
   |||||||
DB 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCAGTGGTGGTGGTGGTGGCGGAGC 300

```

QY	301	CATGATATCCCTCCCAATGTGGTTGGGCAATCCAGCATACGCGCAATGTGACAAATCAGCCC	360
Db	301	CATGATATCCCTCCCAATGTGGTTGGGCAATCCAGCATACGCGCAATGTGACAAATCAGCCC	360
QY	361	TGGGCAAGACACGACGACGAGGAGAGACAGAGAAAAACACAGCATGAGAACACAG	420
Db	361	TGGGCAAGACACGACGAGGAGAGAGACAGAGAAAAACACAGCATGAGAACACAG	420
QY	421	TAAATGAATAAACCATTAATATTATGCCCCCTGTCTGTCTGCTTACTGGCCAGAGAAAT	480
Db	421	TAAATGAATAAACCATTAATATTATGCCCCCTGTCTGTCTGCTTACTGGCCAGAGAAAT	480
QY	481	GGTACCAATTTTTCAGTGTGTGACCTTGACAGCTTCTTTGGCACAAGACAGAGAAATTT	540
Db	481	GGTACCAATTTTTCAGTGTGTGACCTTGACAGCTTCTTTGGCACAAGACAGAGAAATTT	540
QY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTGTTAAAGAAAGACCATTAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTGTTAAAGAAAGACCATTAATGCTTTAG	600
QY	601	ACAGTGNNAAAAAAGAAAAA 625	
Db	601	ACAGTGNNAAAAAAGAAAAA 625	
RESULT 3			
ABL87898			
ID	ABL87898	standard; DNA; 625 BP.	
AC	ABL87898;		
XX			
DT	17-MAY-2002	(first entry)	
DE	Human ovarian cancer related DNA clone SEQ ID NO:10876.		
XX			
OS	Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200192581-A2.		
XX			
PD	06-DEC-2001.		
XX			
PF	29-MAY-2001; 2001WO-US17756.		
PR	26-MAY-2000; 2000US-207484P.		
XX			
PA	(CORI-) CORIXA CORP.		
PI	Algate PA, Harlocker SL, Jones R;		
DR	WPI; 2002-122075/16.		
XX			
PS	Claim 1; SEQ ID 10876; 489pp; English.		
XX			
CC	The present invention describes a composition (I) comprising: carriers		
CC	and immunostimulants; and a polypeptide (II) of a ovarian tumour		
CC	polypeptide encoded by a polynucleotide (III) having a cDNA sequence		
CC	(SI) from the 10912 nucleotide sequences as given in ABL77023 to		
CC	AB187934, (III) encoding (II) having a sequence (S2), a T cell		
CC	population of (II), or antigen presenting cells that express (II).		
CC	(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to		
CC	(SI) can be used for detecting ovarian cancer in a patient's biological		
CC	sample preferably serum or ovarian tissue. The method comprises		
CC	contacting a biological sample from a patient with (IV), detecting the		
CC	amount of polynucleotide hybridising to (IV) and comparing the amount to		
CC	a predetermined cutoff value and thereby detecting ovarian cancer in the		

CC	patient where the amount of polynucleotide hybridizing to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising CC (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polyptides CC and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques.
XX	Sequence 625 BP; 182 A; 144 C; 182 G; 116 T; 1 other;
SQ	
Query Match	99.8%; Score 624; DB 24; Length 625; Best Local Similarity 100.0%; Pred. No. 4.6e-154; Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AGTTCTCCTTCGAGAGACTGGCGCCGGGAGCGCAAGAACAACGGCCGTGCACAAACG 60 Db 1 AGTTCCTCTTGACAGAGACTGGCGCGGGAGCGCAAGAACAACGGCCGTGCACAAACG 60
OY	61 GGCGCTGTGCGTGTGAAGTGGCATGTACGGCAGCGGCTTCTGTGTGGTGGCTGTG 120 Db 61 GGCGGTGTGCGGTGGGTGGATGGCATGTACGGCAGCGGCTTCTGTGTGGTGGCTGTG 120
OY	121 CAGGACAGGGGGGACAGACACCTGTGACAGAACACCCGGCGAATCTGTGGAGAGAC 180 Db 121 CAGGACAGGGGGGACAGACACCTGTGACAGAACACCCGGCGAATCTGTGGAGAGAC 180
OY	181 CGTGTACAGAGACGGGTTGATGACCAGCTGAGTAGAAAAACGTCTCGAAGAGGGAG 240 Db 181 CGTGTACAGAGAGCGGTTGATGACCAGCTGAGTAGAAAAACGTCTCGAAGAGGGAG 240
OY	241 GAGGATCATGTACGCCGGGAAGTAGACCTGTCTCAGTGTGCTTGGTTGGCCGAC 300 Db 241 GAGGATCATGTACGCCGGGAAGTAGACCTGTCTCAGTGTGCTTGGTTGGCCGAC 300
OY	301 CATGATCCTCGGAATCTGGTTGGGCATCGACATACGGCGCAATGTACAAACATCAGCCC 360 Db 301 CATGATCCTCGGAATCTGGTTGGGCATCGACATACGGCGCAATGTACAAACATCAGCCC 360
OY	361 TGCGCAGACAGCAGCAGAGGAGAGACAGAAAAAAGAAAACACAGCATGAGAACAG 420 Db 361 TGCGCAGACAGCAGCAGAGGAGAGAGACAGAAAAAAGAAAACACAGCATGAGAACAG 420
OY	421 TAAATGAATAAAAACCATTAATATTATTAGCCCCCTGTGTCTGTACTGTGCGCAGGAAT 480 Db 421 TAAATGAATAAAAACCATTAATATTATTAGCCCCCTGTGTCTGTACTGTGCGCAGGAAT 480
OY	481 GSTACCAATTTTTCAGTGTGTGACACTTCTTTTGGCACAAAGCAAAGAAATTT 540 Db 481 GSTACCAATTTTTCAGTGTGTGACACTTCTTTTGGCACAAAGCAAAGAAATTT 540
OY	541 AACACTGTTTTCAAAACCCGGGGAGTTGGCTGTATAAAGAAAGACATTAAATGCTTAG 600 Db 541 AACACTGTTTTCAAAACCCGGGGAGTTGGCTGTATAAAGAAAGACATTAAATGCTTAG 600
OY	601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625 Db 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
RESULT 4	
ABT03284	
ID	ABR03284 standard; cDNA; 1897 BP.
XX	ABT03284;
XX	05-SEP-2002 (first entry)
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 214.
XX	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW	cytostatic; gene; ss.

XX	Homo sapiens.
OS	
XX	WO200239885-A2.
PN	
XX	23-MAY-2002.
PD	
XX	13-NOV-2001; 2001WO-US45395.
PE	
XX	14-NOV-2000; 2000US-0713550.
PR	03-APR-2001; 2001US-0825294.
PR	02-OCT-2001; 2001US-0970966.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX	
DR	WPI; 2002-500186/53.
XX	
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for
PT	detecting the presence of ovarian cancer in a patient, and in
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
PT	
XX	
PS	Claim 2; Page 196; 197pp; English.
XX	
CC	The present invention provides human ovarian cancer associated proteins
CC	and coding sequences. The sequences can be used in the diagnosis and
CC	treatment of ovarian cancers. The present sequence is a coding sequence
CC	of the invention.
XX	
50	Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;

	Query Match	99.8%	Score 624:	DB 24:	Length 1897:
	Best Local Similarity	99.8%	Pred. No. 7,4e-154:		
	Matches 624:	Conservative 0:	Mismatches 1:	Indels 0:	Gaps 0
QY	1	AGTTCTCCTTGCAGAGACTGGCGCCGCGAGACGAAAGACAACGGCGCTGTGCACAAAGCG	60		
Db	1271	AGTTCTCCTTGCAGAGACTGGCGCCGCGAGACGGAAGACCAACGGGCCCTGTGCACAAAGCG	1330		
QY	61	GGCGCTGTTCGGTGATGGAGTGGCATGTACGGCGACAGCGCCTTCTGTGTTGGCGTGTG	120		
Db	1331	GGCGCTGTTCGGTGATGGAGTGGCATGTACGGCGAGCGCCTTCTGTGTTGGCGTGTG	1390		
QY	121	CAGCACAGCGCGCGACAGCAGCACCCTGCACGAACCCCGGCAAACTGCTGGAGAGACAC	180		
Db	1391	CAGCACAGCGCGCGACAGCAGCACCCTGCACGAACCCCGGCAAACTGCTGGAGAGACAC	1450		
QY	181	CGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCCGAGAAGGGGAG	240		
Db	1451	CGTGTACAGAGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCCTCCGAGAAGGGGAG	1510		
QY	241	GAGGATCATGTACGCCCGCGAAGTAGAGACTCGTCCAAGTCGTCTTGGGTTTGGCCGACG	300		
Db	1511	GAGGATCATGTACGCCCGCGAAGTAGAGACTCGTCCAAGTCGTCTTGGGTTTGGCCGACG	1570		
QY	301	CATGATCCTCCGAATCTGTTGGGCAATCAGAGATACGGGCAATGTACAAACATCAGGCC	360		
Db	1571	CATGATCCTCCGAATCTGTTGGGCAATCAGAGATACGGGCAATGTACAAACATCAGGCC	1630		
QY	361	TGGGCAGACAGCAGAGAGGAGAGACAGAAAAAAGAAAACACAGCATGAGAACACAG	420		
Db	1631	TGGGCAGACAGCAGAGAGGAGAGACAGAAAAAAGAAAACACAGCATGAGAACACAG	1690		
QY	421	TAAATGAATTAATAACATTAATATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAT	480		
Db	1691	TAAATGAATTAATAACATTAATATTAGCCCTCTGTCTGTGCTTACTGGCCAGGAAT	1750		
QY	481	GGTACCAATTTTTTCAGTGTGGCACTTGACAGCTCTTTTGGCACAAGCAAGAGAGATTT	540		
Db	1751	GGTACCAATTTTTTCAGTGTGGCACTTGACAGCTCTTTTGGCACAAGCAAGAGAGATTT	1810		

QY	541	AACACGTGTTTCAAAACCCGGGGGAGTTGGCGTGTAAAGAAAGACATTAAATGCTTAG	600
Db	1811	AACACGTGTTTCAAAACCCGGGGGAGTTGGCGTGTAAAGAAAGACATTAAATGCTTAG	1870
QY	601	ACACGTGMAAAAAAAAAAAAAA	625
Db	1871	ACACGTGMAAAAAAAAAAAAAA	1895

RESULT5	
ABL40352	
ID	ABL40352 standard; cDNA; 1897 BP
XX	
AC	ABL40352;
XX	
DT	28-JUN-2002 (first entry)

DE Ovarian carcinoma O1034C/O591S consensus nucleotide sequence.

KM Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer  
 KW ss.  
 KW

05 Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	260..685

```

FT      /product= "Ovarian carcinoma protein O1034C/O591S"

```

PN US2002004491-A1.

PD 10-JAN-2002

PF 03-APR-2001; 2001US-0825294

PR 10-SEP-1999; 99US-0394374.

PR 15-AUG-2000; 2000US-0640173.

PR 14-NOV-2000; 2000US-0713550.

PA (XUJ/) XU J.

PA (ALGA/) ALGATE P A

XX XX  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4

XX  
4  
0  
0  
0  
1  
7  
1  
0  
0  
7  
2  
0  
0

DR P-PSDB; ABB09417.

PT Ovarian tumour polyp

[illegible][illegible]

CC that may be utilised in cancer therapy, for example in a vaccine or

CC useful for detecting a cancer in a patient, for stimulating and/or

development of a cancer in a patient. They are also useful for stimulating an immune response in a patient and for treating a cancer.

CC a patient and for determining the presence of a cancer in a patient, who isolated polynucleotides of the invention are useful for the

ability to selectively form duplex molecules with complementary stretches of the native gene or gene fragments and for detecting and

CC preparing ribozyme molecules for inhibiting expression of tumour polynucleotides in tumour cells. Polynucleotides and polynucleotides of the

expression of a polypeptide in appropriate host cells. The current invention are also useful in recombinant DNA molecules to direct

CC sequence represents the ovarian carcinoma O1034C/0591S consensus nucleotide sequence



XX Sequence 1897 BP; 435 A; 521 C; 532 G; 407 T; 2 other;  
SQ

Query Match	99.8%	Score 624	DB 24	Length 1897
Best Local Similarity	99.8%	Pred. No.	7.4e-154	
Matches 624	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY	1	ACTTTCCTCTGCAGAGAGACTGGGCGCGGAGACGGAAAGCAAGGGGGCTGCACAAACCG	60
Db	1271	ACTTTCCTCTGCAGAGAGACTGGGCGCGGAGACGGAAAGCAAGGGGGCTGCACAAACCG	1330
QY	61	GGCGCTGTGGGTGGTAGTGGCCATGTATACGCGAGGCGCTTCGTGGTGGCGTGTG	120
Db	1331	GGCGCTGTGGGTGGTAGTGGCCATGTATACGCGAGGCGCTTCGTGGTGGCGTGTG	1390
QY	121	CAGCGACAGCGCGCACACAGCACTGTGCAGAACACCGCGCGAAACGTCTCGAGAGAC	180
Db	1391	CAGCGACAGCGCGCACACAGCACTGTGCAGAACACCGCGCGAAACGTCTCGAGAGAC	1450
QY	181	CGTGTACAGACGCGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAAAGGGAG	240
Db	1451	CGTGTACAGACGCGGTTGATGACCGAGCTGAGGTAGAAAAAGTCTCCGAGAAAGGGAG	1510
QY	241	GAGGATCATGTACGCCCCGGAAGTAGACCTCGTCCAGCTGTGTTGGGTTGGCGGACG	300
Db	1511	GAGGATCATGTACGCCCCGGAAGTAGACCTCGTCCAGCTGTGTTGGGTTGGCGGACG	1570
QY	301	CATTGATCCCTCCGAATTGGTTGGGGCAATCCAGACATACGCGCAATGTCAACAATCAGCCC	360
Db	1571	CATTGATCCCTCCGAATTGGTTGGGGCAATCCAGACATACGCGCAATGTCAACAATCAGCCC	1630
QY	361	TGGGCAGACAGACAGCAGAGGGAGAGACAGAGAAAAAGAAAAACACACATGTAGAAACAG	420
Db	1631	TGGGCAGACAGCAGCAGGGAGGGAGAGACAGAGAAAAAGAAAAACACACATGTAGAAACAG	1690
QY	421	TAAATGAATTAATAACCATTAATAATTATAGCCCCCTGTGTCGTGCTACTGCGCAGGAAT	480
Db	1691	TAAATGAATTAATAACCATTAATAATTATAGCCCCCTGTGTCGTGCTACTGCGCAGGAAT	1750
QY	481	GGTACCATTTTTCACTGTTGGCACTTGCACAGCTTCTTTTGCACACAGCAAGAGAAATTT	540
Db	1751	GGTACCATTTTTCACTGTTGGCACTTGCACAGCTTCTTTTGCACACAGCAAGAGAAATTT	1810
QY	541	AACACTGTTTCAAAACCCGGGGAGTGGCTGTTTAAAGAAAGACCAATTAAATGCTTTAG	600
Db	1811	AACACTGTTTCAAAACCCGGGGAGTGGCTGTTTAAAGAAAGACCAATTAAATGCTTTAG	1870
QY	601	ACAGGTGNAAAAAAAAAAAAAA 625	
Db	1871	ACAGGTGNAAAAAAAAAAAAAA 1895	

	RESULT	6
ABT03277	ID	ABT03277 standard; cDNA; 1619 BP.
XX		
AC		ABT03277;
XX		
DT		05-SEP-2002 (first entry)
XX		
DE		Human ovarian carcinoma associated coding sequence SEQ ID NO: 205.
XX		
KW		Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KM		Cytostatic; gene; ss.
XX		
OS		Homo sapiens.
XX		
PN		M0200239885-A2.
XX		
PD		23-MAY-2002.
XX		
PF		13-NOV-2001; 2001MO-US45395.
XX		

PR 14-NOV-2000; 2000US-0713550.  
PR 03-APR-2001; 2001US-0825294.  
PR 02-OCT-2001; 2001US-0970966.

PA (CORI-) CORIXA CORP.

PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;  
XY

DR WPI; 2002-500186/53.  
YY

PT NOVEL ovarian cancer polypeptide and polynucleotide, useful for  
PT detecting the presence of ovarian cancer in a patient, and in  
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
PT -

PS Claim 2; Page 189-190; 197pp; English.  
xy

CC The present invention provides human ovarian cancer associated proteins  
CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.

SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match	98.1%	Score 613	DB 24	Length 1619
Best Local Similarity	99.7%	Pred. No. 5.4e-151		
Matches 624	Conservative 0	Mismatches 1	Indels 1	Gaps 1

QY	1	AGTCTCCTTTGACAGAGACATCGGCGCGGACGCGGAAGACAAACGGCGCTGGCAAAAGG	60
Db	992	AGTCTCCTTTGACAGAGACATCGGCGCGGACGCGGAAGACAAACGGCGCTGGCAAAAGG	1051
QY	61	GGCCCTGTCCGTGGTGGAGTGGCCCATGTACGCCGACGGCCTTCTCGTGGTGGCGTGTG	120
Db	1052	GGCCCTGTCCGTGGTGGAGTGGCCCATGTACGCCGACGGCCTTCTCGTGGTGGCGTGTG	1111
QY	121	CAGGACAGCGCGGACGACAGCACAC-TGCACGAACCCCGCGAAACTCTCTCGAGAGCA	179
Db	1112	CAGGACAGCGCGGACGACAGCACACTTTCGACGAACCCCGCGAAACTCTCTCGAGAGCA	1171
QY	180	CCGTGTACAGGAGCGGGTTGATGACCCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGA	239
Db	1172	CCGTGTACAGGAGCGGGTTGATGACCCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGA	1231
QY	240	GGAGGATCATGTACGCCCGGAAATAGAGACTCTGCAGTCTGCTGGTGTGGCCGAG	299
Db	1232	GGAGGATCATGTACGCCCGGAAATAGAGACTCTGCAGTCTGCTGGTGTGGCCGAG	1291
QY	300	CCATGATCTCTCCGAATCTGGTTGGGATCCAGATATCGGCCAATGTCAACAAATCAGCC	359
Db	1292	CCATGATCTCTCCGAATCTGGTTGGGATCCAGATATCGGCCAATGTCAACAAATCAGCC	1351
QY	360	CTGGGCGACAGCAGCAGCAGAGGAGGAGACAGAAAAAGAAAAACAACAGCATGAGAACACA	419
Db	1352	CTGGGCGACAGCAGCAGCAGAGGAGGAGAGACAGAAAAAGAAAAACAACAGCATGAGAACACA	1411
QY	420	GTAATTAATTAATAACATATAATATTATACCCCTCGTCTGCTTACTGGCCAGGAAA	479
Db	1412	GTAATTAATTAATAACATATAATATTATAGCCCTCTGTCTGTGTTACTGGCCAGGAAA	1471
QY	480	TGGTACCAATTTTTCAGTGTGGACTTGAACGCTTTTGGCACAGCAAGAGAGAAAT	539
Db	1472	TGGTACCAATTTTTCAGTGTGGACTTGAACGCTTTTGGCACAGCAAGAGAGAAAT	1531
QY	540	TAACACGTGTTCAAAACCCGGGAGTGTGGCTGTGTTAAAGAAAGCACTTAATGCTTTA	599
Db	1532	TAACACGTGTTCAAAACCCGGGAGTGTGGCTGTGTTAAAGAAAGCACTTAATGCTTTA	1591
QY	600	GACAGTGMAAAAAAAAAAAAAAA 675	
Db	1592	GACAGTGMAAAAAAAAAAAAAAA 1617	

RESULT 7  
ABT03281  
ID ABT03281 standard; cDNA; 1619 BP.  
XX  
AC ABT03281;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 211.  
XX  
KW Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;  
KW cytosolic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200239885-A2.  
XX  
PD 23-MAY-2002.  
XX  
PE 13-NOV-2001; 2001WO-US45395.  
XX  
PR 14-NOV-2000; 2000US-0713550.  
PR 03-APR-2001; 2001US-0825294.  
PR 02-OCT-2001; 2001US-0970966.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;  
XX  
DR WPI; 2002-500186/53.  
XX  
PT Novel ovarian cancer polypeptide and polynucleotide, useful for  
PT detecting the presence of ovarian cancer in a patient, and in  
PT pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer  
PT  
XX  
PS Claim 2; Page 195; 197pp; English.  
XX  
CC The present invention provides human ovarian cancer associated proteins  
CC and coding sequences. The sequences can be used in the diagnosis and  
CC treatment of ovarian cancers. The present sequence is a coding sequence  
CC of the invention.  
XX  
SQ Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;  
Query Match 98.1%; Score 613; DB 24; Length 1619;  
Best Local Similarity 99.7%; Pred. No. 5.4e-151;  
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 AGTTCCTTCGAGAGAGACTGGCGCGGAGCGAGCAAGAGCAAGCGGCGTGCACAAAGCG 60  
DB 992 AGTTCCTTCGAGAGAGACTGGCGCGGAGCGAGCAAGAGCAAGCGGCGTGCACAAAGCG 1051  
QY 61 GCGCGTGTGGTGTGGAGTGGCATGTACGCGCAGCGCCCTTCTGCTGTGGCTGTG 120  
DB 1052 GCGCGTGTGGTGTGGAGTGGCATGTACGCGCAGCGCCCTTCTGCTGTGGCTGTG 1111  
QY 121 CAGCGACAGCGGCGAGCAGCACC-TGCAGCAACACCGCGGAAACCTCTCGAGAGGACA 179  
DB 1112 CAGCGACAGCGGCGAGCAGCACCCTTGACAGAACCCCGGAAACCTCTCGAGAGGACA 1171  
QY 180 CCGGTACAGAGAGCGGTTGATGACCGAGCAGTGTAGTAAACGCTCTCCGAGAGGGA 239  
DB 1172 CCGGTACAGAGAGCGGTTGATGACCGAGCAGTGTAGTAAACGCTCTCCGAGAGGGA 1231  
QY 240 GGAGATCATGTACGCCCGGAGAGAGACCTGTCCAGTGTGCTTTGGCTTTGGCCGAG 299  
DB 1232 GGAGATCATGTACGCCCGGAGAGAGACCTGTCCAGTGTGCTTTGGCTTTGGCCGAG 1291  
QY 300 CCATGATCTCCGAATCTGTGGGATCCAGCATATGCGGCAATGTCAACAATCAGCC 359  
DB 1292 CCATGATCTCCGAATCTGTGGGATCCAGCATATGCGGCAATGTCAACAATCAGCC 1351

QY 360 CTGGCGAGACAGCAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419  
DB 1352 CTGGCGAGACAGCAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411  
QY 420 GTAATGAAATTAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 479  
DB 1412 GTAATGAAATTAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1471  
QY 480 TGGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCAGAGAGAGAGAGAG 539  
DB 1472 TGGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTTGGCAGAGAGAGAGAGAG 1531  
QY 540 TAACACTGTTTCAACCCCGGGAGTGGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAG 599  
DB 1532 TAACACTGTTTCAACCCCGGGAGTGGCTGTGTTAAAGAGAGAGAGAGAGAGAGAGAG 1591  
QY 600 GACAGTGNAAAAAAAAAAAAAAAAAAAA 625  
DB 1592 GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617  
RESULT 8  
ABL40345  
ID ABL40345 standard; cDNA; 1619 BP.  
XX  
AC ABL40345;  
XX  
DT 28-JUN-2002 (first entry)  
XX  
DE Ovarian carcinoma sequence isolate 57887 extended cDNA.  
XX  
KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002004491-A1.  
XX  
PD 10-JAN-2002.  
XX  
PE 03-APR-2001; 2001US-0825294.  
XX  
PR 10-SEP-1999; 99US-0394374.  
PR 01-MAY-2000; 2000US-0561778.  
PR 15-AUG-2000; 2000US-0640173.  
PR 07-SEP-2000; 2000US-0656668.  
PR 14-NOV-2000; 2000US-0713550.  
XX  
PA (XUJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
XX  
PI Xu J, Stolk JA, Algate PA, Fling SP;  
XX  
DR WPI; 2002-171027/22.  
XX  
PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,  
PT prevention and/or treatment of cancer, especially ovarian cancer  
PT  
XX  
PS Claim 1a; Page 119-120; 131pp; English.  
XX  
CC The invention relates to ovarian tumour polynucleotides and polypeptides  
CC that may be utilised in cancer therapy, for example in a vaccine or  
CC gene therapy. Polypeptides and polynucleotides of the invention are  
CC useful for detecting a cancer in a patient, for stimulating and/or  
CC expanding T-cells specific for a tumour protein, and for inhibiting the  
CC development of a cancer in a patient. They are also useful for  
CC stimulating an immune response in a patient, and for treating a cancer in  
CC a patient and for determining the presence of a cancer in a patient.  
CC The isolated polynucleotides of the invention are useful for their  
CC ability to selectively form duplex molecules with complementary stretches  
CC of the entire desired gene or gene fragments, and for designing and

CC preparing ribozyme molecules for inhibiting expression of tumour  
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the  
 CC invention are also useful in recombinant DNA molecules to direct  
 CC expression of a polypeptide in appropriate host cells. The current  
 CC sequence represents the extended cDNA sequence of ovarian carcinoma  
 CC isolate 57887 given in record ABL48956.

XX Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 98.1%; Score 613; DB 24; Length 1619;  
 Best Local Similarity 99.7%; Pred. No. 5.4e-151;

Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AGTTCTCTTGCAGAGAGACTGGCCGCGGAGCCGGAAGACAGCGCGCTGCACAAAGCG 60  
 DB 992 AGTTCTCTTGCAGAGAGACTGGCCGCGGAGCCGGAAGACAGCGCGCTGCACAAAGCG 1051  
 QY 61 GCGCGTGTGGGTGGAGTGGCATGTACGGCAGCGCTTCTGCTGTGGCTGCTG 120  
 DB 1052 GCGCGTGTGGGTGGAGTGGCATGTACGGCAGCGCTTCTGCTGTGGCTGCTG 1111  
 QY 121 CAGGACAGCGCGGAGCAGCAGCACC-TGCACAGACACCGCGGAACCTGCTGGAGAGACA 179  
 DB 1112 CAGGACAGCGCGGAGCAGCAGCACCCTTGCAGACACCGCGGAACCTGCTGGAGAGACA 1171  
 QY 180 CCGTGTACAGACCGCGGTGATGACCGAGCTGAGTAGAAAAACGTCTCCGAGAGGGGA 239  
 DB 1172 CCGTGTACAGACCGCGGTGATGACCGAGCTGAGTAGAAAAACGTCTCCGAGAGGGGA 1231  
 QY 240 GAGAGATCATGTAGCGCCGCGGAAGTAGGACCTGTCACAGTGTGGTGGTGGCCGCGAG 299  
 DB 1232 GAGAGATCATGTAGCGCCGCGGAAGTAGGACCTGTCACAGTGTGGTGGTGGCCGCGAG 1291  
 QY 300 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATACGCGCAATGTACAAACATCAGCC 359  
 DB 1292 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATACGCGCAATGTACAAACATCAGCC 1351  
 QY 360 CTGGGACAGACGAGCAGAGAGAGAGACAGACAGAAAGAAACACAGCATGAGAACACA 419  
 DB 1352 CTGGGACAGACGAGCAGAGAGAGAGACAGACAGAAAGAAACACAGCATGAGAACACA 1411  
 QY 420 GTAATGATTAACCAATTAATATTATTTAGCCCTCTGTCGTGGTGTACTGGCCAGAGAA 479  
 DB 1412 GTAATGATTAACCAATTAATATTATTTAGCCCTCTGTCGTGGTGTACTGGCCAGAGAA 1471  
 QY 480 TGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAGCAGAGAGAAAT 539  
 DB 1472 TGTACCAATTTTTCAGTGTGGACTTGACAGCTTCTTTGCCACAGCAGAGAGAAAT 1531  
 QY 540 TAAACAGTGTTCAAACCCGCGGAGGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 599  
 DB 1532 TAAACAGTGTTCAAACCCGCGGAGGTGGCTGTGTTAAAGAAAGACATTAATGCTTTA 1591  
 QY 600 GACAGTGNAAAAAAGAAAAA 625  
 DB 1592 GACAGTGNAAAAAAGAAAAA 1617

RESULT 9

ABLA0349  
 ID ABLA0349 standard; cDNA; 1619 BP.

XX ABLA0349;

DT 28-JUN-2002 (first entry)

XX Ovarian carcinoma O591s nucleotide sequence.

XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;

OS Homo sapiens.

XX

PN US2002004491-A1.

XX 10-JAN-2002.

XX 03-APR-2001; 2001US-0825294.

XX 10-SEP-1999; 99US-0394374.

PR 01-MAY-2000; 2000US-0561778.

PR 15-AUG-2000; 2000US-0640173.

PR 07-SEP-2000; 2000US-0656668.

PR 14-NOV-2000; 2000US-0713550.

XX (XUJ/) XU J.

XX (STOL/) STOLK J A.

XX (ALGA/) ALGATE P A.

XX (FLIN/) FLING S P.

XX Xu J, Stolk JA, Algate PA, Fling SP;

XX WPI; 2002-171027/22.

XX Ovarian tumour polypeptide and polynucleotide useful in diagnosis,

XX prevention and/or treatment of cancer, especially ovarian cancer.

XX Claim 1a: Page 125-126; 131pp: English.

XX The invention relates to ovarian tumour polynucleotides and polypeptides

XX that may be utilised in cancer therapy, for example in a vaccine or

XX gene therapy. Polypeptides and polynucleotides of the invention are

XX useful for detecting a cancer in a patient, for stimulating and/or

XX expanding T-cells specific for a tumour protein, and for inhibiting the

XX development of a cancer in a patient. They are also useful for

XX stimulating an immune response in a patient, and for treating a cancer in

XX a patient and for determining the presence of a cancer in a patient.

XX The isolated polynucleotides of the invention are useful for their

XX ability to selectively form duplex molecules with complementary stretches

XX of the entire desired gene or gene fragments, and for designing and

XX preparing ribozyme molecules for inhibiting expression of tumour

XX polypeptides in tumour cells. Polypeptides and polynucleotides of the

XX invention are also useful in recombinant DNA molecules to direct

XX expression of a polypeptide in appropriate host cells. The current

XX sequence represents the ovarian carcinoma O591s nucleotide sequence.

XX

Sequence 1619 BP; 399 A; 415 C; 432 G; 373 T; 0 other;

Query Match 98.1%; Score 613; DB 24; Length 1619;

Best Local Similarity 99.7%; Pred. No. 5.4e-151;

Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AGTTCTCTTGCAGAGAGACTGGCCGCGGAGCCGGAAGACAGCGCGCTGCACAAAGCG 60

DB 992 AGTTCTCTTGCAGAGAGACTGGCCGCGGAGCCGGAAGACAGCGCGCTGCACAAAGCG 1051

QY 61 GCGCGTGTGGGTGGAGTGGCATGTACGGCAGCGCTTCTGCTGTGGCTGCTG 120

DB 1052 GCGCGTGTGGGTGGAGTGGCATGTACGGCAGCGCTTCTGCTGTGGCTGCTG 1111

QY 121 CAGGACAGCGCGGAGCAGCAGCACC-TGCACAGACACCGCGGAACCTGCTGGAGAGACA 179

DB 1112 CAGGACAGCGCGGAGCAGCAGCACCCTTGCAGACACCGCGGAACCTGCTGGAGAGACA 1171

QY 180 CCGTGTACAGAGCGGTTATGACAGCTGAGGTAGAAAAAGCTCCGAGAGGGGA 239

DB 1172 CCGTGTACAGAGCGGTTATGACAGCTGAGGTAGAAAAAGCTCCGAGAGGGGA 1231

QY 240 GAGAGATCATGTAGCGCCGCGGAAGTAGGACCTGTCAGTGTGGTGGTGGCCGCGAG 299

DB 1232 GAGAGATCATGTAGCGCCGCGGAAGTAGGACCTGTCAGTGTGGTGGTGGCCGCGAG 1291

QY 300 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATACGCGCAATGTACAAACATCAGCC 359

DB 1292 CCATGATCTCTCGAATCTGTGTGGCATCCAGCATACGCGCAATGTACAAACATCAGCC 1351





PD	21-DEC-2000.
PF	01-JUN-2000; 2000MO-US14973.
PR	11-JUN-1999; 99US-0138630.
XX	(HUMA-) HUMAN GENOME SCI INC.
XX	(ROSE/) ROSEN C A.
PA	Rosen CA, Ruben SM, Komatsoulis GA;
PI	WPI; 2001-071258/08.
DR	P-PSDB: AAB75518.
XX	
PT	Nucleic acid molecules encoding human secreted proteins, used in
PT	preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT	Parkinson's diseases and cancers -
XX	
PS	Claim 1; Page 443-444; 542pp; English.
XX	
CC	Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide
CC	sequences AAF64176 - AAF64224. The specification includes amino acid
CC	sequences AAB75555 - AAB75606 which represent fragments of the human
CC	secreted proteins, and protein sequences with which they share homology.
CC	The proteins and polynucleotides, their agonists and antagonists have
CC	activities dependent on the tissues and cells in which they are
CC	expressed, examples of these activities include, immunosuppressive;
CC	antiarrhythmic; antirheumatic; antiproliferative; cyostatic; cardiant;
CC	vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
CC	vincidine; fungicide; ophthalmological; and vulnerary. The proteins,
CC	polynucleotides, agonists and antagonists can be used to treat or detect
CC	or diagnose various diseases and disorders including, autoimmune
CC	diseases e.g. rheumatoid arthritis, hyperproliferative disorders
CC	e.g. neoplasms of the breast or liver, cardiovascular disorders
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC	infections caused by bacteria, viruses and fungi and ocular disorders
CC	e.g. corneal infection. The polypeptides can also be used to aid wound
CC	healing and epithelial cell proliferation, to prevent skin ageing due to
CC	sunburn, to maintain organs before transplantation, for supporting cell
CC	culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC	polypeptides can also be used as a food additive or preservative to
CC	increase or decrease storage capabilities. Included in the invention are
CC	polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which
CC	are used in the isolation, identification and characterisation of the
CC	proteins of the invention.
XX	
SO	Sequence 1956 BP; 430 A; 543 C; 524 G; 456 T; 3 other;
Query Match	97.1%; Score 606.6; DB 22; Length 1956;
Best Local Similarity	99.7%; Pred. No. 2,8e-149;
Matches	606; Conservative 1; Mismatches 1; Indels 0; Gaps 0
DY	1 AATTCTCCTTGCAGAGAGACTGGCGCCGGAGCGGAAGACGAGCGCGCTGCACAAAGC 60
DB	684 AATTCTCCTTGCAGAGAGACTGGCGCCGGAGCGGAAGACGAGCGCGCTGCACAAAGC 625
OY	61 GCGCGTGCAGTGGAGAGTGGCATGTACGCGGACGCGCTTCTGTTGGTGGCGAGTGC 120
DB	624 GCGCGTGCAGTGGAGAGTGGCATGTACGCGGACGCGCTTCTGTTGGTGGCGAGTGC 565
OY	121 CAGCGACAGCGCGGACAGCAGCAGCTGCACGAACACCCGCCGAATCTGTCGAGAGACAC 180
DB	564 CAGCGACAGCGCGGACAGCAGCAGCTGCACGAACACCCGCCGAATCTGTCGAGAGACAC 505
OY	181 CGTGTACAGAGACCGGGTTATATACCGAGCTGAGGTGAAATAACGTCTCCGAGAGGGGAG 240
DB	504 CGTGTACAGAGACCGGGTTATATACCGAGCTGAGGTGAAATAACGTCTCCGAGAGGGGAG 445
OY	241 GAGGATCATGTACGCGCCGGAAGTAGGAACTGTCGACAGTGTGGTGGTTGGCCGCACAG 300
DB	444 GAGGATCATGTACGCGCCGGAAGTAGGAACTGTCGACAGTGTGGTGGTTGGCCGCACAG 385

Qy	301	CANGATCCGCCGAATCGTTGGGCATCCAGCATACGGCCAAATGTCACAAATCAGCCC	360
Db	384	CATGATCTCCGAATCTGGTGGCATCCAGCATACGGCCAAATGTCACAAATCAGCCC	325
Qy	361	TGGGCAGACACGAGCGAGGAGAGACAGAGAAAAGAAAACACACATGAGAACAG	420
Db	324	TGGGCAGACACGAGCGAGGAGAGAGACAGAGAAAAGAAAACACACATGAGAACAG	265
Qy	421	TAATTAATTAATAAATTAATAATTAATTAAGCCCTCTGTTCTGTGCTTACTGGCCAGAAAT	480
Db	264	TAATTAATTAATAAATTAATAATTAATTAAGCCCTCTGTTCTGTGCTTACTGGCCAGAAAT	205
Qy	481	GGTACCAATTTTTCAGTGTGGACTGTGACAGCTTCTTTGGCCACACAGAGAAATTT	540
Db	204	GGTACCAATTTTTCAGTGTGGACTGTGACAGCTTCTTTGGCCACACAGAGAAATTT	145
Qy	541	AACACGTGTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAAAAGACATTAATGCTTAA	600
Db	144	AACACGTGTTCAAAACCCGGGGAGTTGGCTGTGTAAAGAAAAGACATTAATGCTTAA	85
Qy	601	ACAGTGTNA 608	
Db	84	ACAGTGTNA 77	
RESULT 13			
ID	AAF93845	AAF93845 standard; cDNA; 1890 BP.	
XX	XX	AAF93845;	
AC	XX	23-MAY-2001 (first entry)	
DT	XX	Human cDNA encoding a membrane or secretory protein clone pSEC0181.	
XX	XX	Human; secretory protein; membrane protein; vaccine; gene therapy;	
KM	XX	rheumatoid arthritis; diabetes; ss.	
OS	XX	Homo sapiens.	
PN	XX	EPI067182-A2.	
PD	XX	10-JAN-2001.	
XX	XX	07-JUL-2000; 2000EP-0114090.	
XX	XX	08-JUL-1999; 99JP-0194179.	
PR	XX	11-JAN-2000; 2000JP-0118775.	
PR	XX	02-MAY-2000; 2000JP-0183766.	
PA	XX	(HELI-) HELIX RES INST.	
PI	XX	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;	
DR	XX	MPI: 2001-093989/11.	
DR	XX	P-PSDB; AAB88418.	
PT	XX	Nucleic acids encoding secretory proteins/membrane proteins, useful in	
PT	XX	gene therapy or as candidate target molecules in drug development -	
PS	XX	Claim 1; SEQ ID 203; 609pp + CD ROM; English.	
CC	XX	This invention relates to nucleic acid sequences AAF93744 - AAF93916	
CC	XX	which encode human secretory or membrane proteins represented by	
CC	XX	AAB88317 - AAB88419. Included in the invention are primers	
CC	XX	AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the	
CC	XX	cDNA sequences of the invention. The invention also includes methods for	
CC	XX	the production of antibodies directed against the proteins, and cDNA	
CC	XX	sequences, which can be used in vaccines. The polynucleotide sequences	
CC	XX	can be used in gene therapy. The polynucleotide sequences and the	
CC	XX	proteins they encode may be used in the prevention, treatment and	
CC	XX	diagnosis of diseases associated with inappropriate secretory	
CC	XX	protein/membrane protein expression. The nucleic acids and complementary	



Db 278 AGCATACGGCCATGTACACAAATCAGCCCTGGCCAGACAGCAGAGAGAGACA 219  
 QY 390 GAGAAAGAAAAACACAGCATGAGAAACACAGTAAATGATTAACCATTAATTTTAC 449  
 Db 218 GAGAAAGAAAAACACAGCATGAGAAACACAGTAAATGATTAACCATTAATTTTAC 159  
 QY 450 CCCCCTGTTCTGCTTACTGGCCAGGAAATGTTACCAATTTTTCAGTGTGACCTTGAC 509  
 Db 158 CCCCCTGTTCTGCTTACTGGCCAGGAAATGTTACCAATTTTTCAGTGTGACCTTGAC 99  
 QY 510 ACCTTCTTTGGCCAGAGAGAGATTTTAACTGTTTCAACCCCGGAGGAGTTGGC 569  
 Db 98 ACCTTCTTTGGCCAGAGAGAGATTTTAACTGTTTCAACCCCGGAGGAGTTGGC 39  
 QY 570 TGTGTTAAAGAAAGACATTAATGCTTTAGACAGTG 606  
 Db 38 TGTGTTAAAGAAAGACATTAATGCTTTAGACAGTG 2

RESULT 15  
 ABL79397  
 ID ABL79397 standard; cDNA; 558 BP.  
 AC ABL79397;  
 XX  
 DT 17-MAY-2002 (first entry)  
 DE Human ovarian cancer related cDNA clone SEQ ID NO:2375.  
 XX  
 KM Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192581-A2.  
 PD 06-DEC-2001.  
 XX  
 PF 29-MAY-2001; 2001WO-US17756.  
 XX  
 PR 26-MAY-2000; 2000US-207484P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Algate PA, Harlocker SL, Jones R;  
 XX  
 DR WPI: 2002-122075/16.  
 XX  
 PT Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide -  
 XX  
 PS Claim 1; SEQ ID 2375; 4899p; English.  
 XX  
 CC The present invention describes a composition (I) comprising: carriers  
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
 CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to  
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell  
 CC population of (II), or antigen presenting cells that express (II).  
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
 CC (SI) can be used for detecting ovarian cancer in a patient's biological  
 CC sample preferably serum or ovarian tissue. The method comprises  
 CC contacting a biological sample from a patient with (IV), detecting the  
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
 CC patient, where the amount of polynucleotide hybridising to (IV) is  
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
 CC specific for an ovarian tumour protein comprising contacting T cells  
 CC with (III) or (II). (III) is useful in design and preparation of  
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
 CC and proteins in tumour cells; and to isolate a full length gene from a

CC suitable library e.g., a tumour cDNA library using well known  
 CC techniques.

Sequence 558 BP; 147 A; 133 C; 166 G; 106 T; 6 other;

Query Match 69.3%; Score 433.2; DB 24; Length 558;

Best Local Similarity 95.6%; Pred. No. 5.9e-104;

Matches 539; Conservative 0; Mismatches 14; Indels 11; Gaps 9;

QY 1 AGTTCCTCTTGAGAGAGACTGGCCGGGACGCGGAAGACAGACAGGCGCTGCACAAAGC 60  
 Db 1 AGTTCCTCTTGAGAGAGACTGGCCGGGACGCGGAAGACAGACAGGCGCTGCACAAAGC 60  
 QY 61 GGGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120  
 Db 61 GGGCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 118  
 QY 121 CAGCAGACAGCGGCGGACAGACAGCCTGACAGAAACCCCGGAACTGCTGCGAGAGAC 180  
 Db 119 CAGCAGACAGCGGCGGAC--ACAGCAGCTGACAGAAACCCCGGAACTGCTGCGAGAGAC 176  
 QY 181 CAGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTGAGAAACGCTCCGAGAGGGAG 240  
 Db 177 CAGTACAGAGAGCGGGTGTGATGACCGAGCTGAGGTGAGAAACGCTCCGAGAGGGAG 236  
 QY 241 GAGGATCATGTAGC--CCCGAAGTAGGACCTGCTCAGTGTGGTGGTGGTGGTGGTGG 299  
 Db 237 GAGGATCATGTAGC--CCCGAAGTAGGACCTGCTCAGTGTGGTGGTGGTGGTGGTGG 296  
 QY 300 CCATGA--TCCTCCGAATCTGGTGGGATCCAGCATACGGCCAAATGTACACAAATCAGC 358  
 Db 297 CATTGATTCCTCGAATCTGTTGGGATCCAGCATACGGCCAAATGTACACAAATCAGC 356  
 QY 359 CCTGGGACAGACAGAGCAGC--AGGAGAGACAGAGAAAGAAACACACAGCATGAGAC 417  
 Db 357 CCTGGGACAGACAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416  
 QY 418 CAGTAAATGAATTAACCAATTAATTTAGCCCTCTGCTGTGCTTCTGCTGCTGCTGCT 477  
 Db 417 CAGTAAATGAAT--AAACCAATTAATTTAG--CCCTCTGCTGTGCTGCTGCTGCTGCT 474  
 QY 478 AATGTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCCACAGAGAGAGAA 537  
 Db 475 AATGTACCA--ATTTTTCAGTGTGAGCTTTCAGCTTCTTTGGCCACAGAGAGAG-A 532  
 QY 538 TTTAACAAGCTTTTCAACCCGGGG 561  
 Db 533 NTTAACAATTTTCAANCCGGGG 556

Search completed: November 7, 2002, 10:10:19

Job time : 135.06 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 ; Search time 1400.5 Seconds  
(without alignments)  
11220.326 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agttctctctgcagaggaact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 40582208

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents, NA, Main:\*

1: /cgn2\_6/ptodata/1/pna/US0600\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*  
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20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*  
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22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*  
23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*  
24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*  
25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*  
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31: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*  
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40: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*  
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43: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*

Result No.	Score	Query Match	Length	DB ID	Description
1	624	99.8	625	1	PCT-US01-45395-210 Sequence 210, App
2	624	99.8	625	31	US-09-825-294-210 Sequence 210, App
3	624	99.8	625	33	US-09-867-701-10876 Sequence 10876, A
4	624	99.8	625	36	US-09-970-966-210 Sequence 210, App
5	624	99.8	625	42	US-10-212-677-210 Sequence 210, App
6	624	99.8	1897	1	PCT-US01-45395-214 Sequence 214, App
7	624	99.8	1897	31	US-09-825-294-214 Sequence 214, App
8	624	99.8	1897	36	US-09-970-966-214 Sequence 214, App
9	624	99.8	1897	42	US-10-212-677-214 Sequence 214, App
10	616.4	98.6	1867	1	PCT-US02-29964-16 Sequence 16, App1
11	613	98.1	1619	1	PCT-US01-45395-205 Sequence 205, App
12	613	98.1	1619	28	US-09-713-550-205 Sequence 205, App
13	613	98.1	1619	31	US-09-825-294-211 Sequence 205, App
14	613	98.1	1619	33	US-09-825-294-205 Sequence 205, App
15	613	98.1	1619	36	US-09-970-966-205 Sequence 205, App
16	613	98.1	1619	36	US-09-970-966-205 Sequence 205, App
17	613	98.1	1619	36	US-09-970-966-211 Sequence 211, App
18	613	98.1	1619	42	US-10-212-677-205 Sequence 205, App
19	613	98.1	1619	42	US-10-212-677-211 Sequence 211, App
20	612.8	98.0	1918	17	US-09-397-022-4454 Sequence 4454, Ap
21	612.8	98.0	1918	31	US-09-808-385-4454 Sequence 4454, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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c 22 608 97.3 1714 17 US-09-359-922-11555 Sequence 11555, A
c 23 608 97.3 1714 17 US-09-359-922-11555 Sequence 11555, A
c 24 608 97.3 1714 34 US-09-919-002-11555 Sequence 11555, A
c 25 607 97.1 43729 70 US-60-261-974-9 Sequence 9, App1
c 26 606.6 97.1 1608 1 PCT-US01-18569-111 Sequence 111, App
c 27 606.6 97.1 1608 43 US-10-264-049-111 Sequence 111, App
c 28 606.6 97.1 1925 25 US-09-652-121-7293 Sequence 7293, Ap
c 29 606.6 97.1 1925 25 US-09-652-128-3375 Sequence 9375, Ap
c 30 606.6 97.1 1925 25 US-09-652-917-3346 Sequence 3346, Ap
c 31 606.6 97.1 1925 27 US-09-659-997-11085 Sequence 11085, A
c 32 606.6 97.1 1925 28 US-09-710-281-4458 Sequence 4458, Ap
c 33 606.6 97.1 1925 29 US-09-726-805-1608 Sequence 1608, Ap
c 34 606.6 97.1 1953 36 PCT-US00-09066-38 Sequence 38, App1
c 35 606.6 97.1 1953 36 US-09-950-083-1914 Sequence 1914, Ap
c 36 606.6 97.1 1953 40 US-10-105-299-2314 Sequence 2314, Ap
c 37 606.6 97.1 1956 1 PCT-US00-14973-23 Sequence 23, App1
c 38 606.6 97.1 1956 36 US-09-950-083-1915 Sequence 1915, Ap
c 39 606.6 97.1 1956 40 US-10-105-299-2415 Sequence 2415, Ap
c 40 605.4 96.9 1866 40 US-10-208-408-26 Sequence 26, App1
c 41 605.4 96.9 1866 73 US-60-295-262-26 Sequence 26, App1
c 42 605.4 96.9 1866 74 US-60-308-868-26 Sequence 26, App1
c 43 605.4 96.9 1917 17 US-09-371-168-7188 Sequence 7188, Ap
c 44 605.4 96.9 1917 25 US-09-644-873-9077 Sequence 9077, Ap
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## ALIGNMENTS

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RESULT 1
PCT-US01-45395-210
; Sequence 210, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
PCT-US01-45395-210
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Query Match          99.8%; Score 624; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGACAAAGGGCGCTGCACAAAGCG 60
DB 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGACAAAGGGCGCTGCACAAAGCG 60
QY 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATG 120
DB 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATG 120
QY 121 CAGCGACAGCGCGGAGCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
DB 121 CAGCGACAGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
QY 181 CGTGTACAGAGAGCGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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DB 181 CGTGTACAGAGAGCGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 GAGGATCATGTACAGCGCGGAGAGTAGAGTGTGATGATGATGATGATGATGATGATGAT 300
DB 241 GAGGATCATGTACAGCGCGGAGAGTAGAGTGTGATGATGATGATGATGATGATGATGAT 300
QY 301 CATGATCCTCCGATCTGTGTTGGGATCCAGCATACGCGCATGTACAAACATCAGGCC 360
DB 301 CATGATCCTCCGATCTGTGTTGGGATCCAGCATACGCGCATGTACAAACATCAGGCC 360
QY 361 TGGGACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420
DB 361 TGGGACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 420
QY 421 TAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
DB 421 TAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 481 GGTACCAATTTTTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GGTACCAATTTTTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600
DB 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600
QY 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
DB 601 ACAGTGNAAAAAAAAAAAAAAAAAAAA 625
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RESULT 2
US-09-825-294-210
; Sequence 210, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.4845
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210
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Query Match          99.8%; Score 624; DB 31; Length 625;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGACAAAGGGCGCTGCACAAAGCG 60
DB 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGGAAGACAAAGGGCGCTGCACAAAGCG 60
QY 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATG 120
DB 61 GGGCGTGTGCGTGTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATG 120
QY 121 CAGCGACAGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
DB 121 CAGCGACAGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
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Dp	181	CGTGCACGAGAGCGGGTTGATGACCCAGCTGAGTAAAGAAACGTCGCCAGAAAGGGAG	240
Qy	241	GAGGATCATGTAGCCCGCGGAAGTAGACCTGTCAGTCGTGTGGTTGGCCGAGC	300
Dp	241	GAGGATCATGTAGCCCGCGGAAGTAGACCTGTCAGTCGTGTGGTTGGCCGAGC	300
Qy	301	CATGATCCTCCGAMTCTGGTGTGGGCATCCAGCATAGCGCCCAATGTCCACATCCAGCCC	360
Dp	301	CATGATCCTCCGAAATCTGTGTTGGGCATCCAGCATAGCCCAATGTCCACAAATCCAGCCC	360
Qy	361	TGGGCAGACACGAGCAGAGGGAGAGACAGAGAAAAGAAAACACAGCATGAGAACACAG	420
Dp	361	TGGGCAGACACGAGCAGAGGGAGAGACAGAGAAAAGAAAACACAGCATGAGAACACAG	420
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Dp	421	TAAATGATTAAGACCATTAATATTAGCCCCCTGTCTGTGTGCTTACTGCGCAGGAAT	480
Qy	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTCCCAACAGCAGACAGATTT	540
Dp	481	GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTCCCAACAGCAGACAGATTT	540
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Dp	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGCATTAAATGCTTTAG	600
Qy	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	
Dp	601	ACAGTGNAAAAAAAAAAAAAAAAAAAA 625	

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RESULT 3
US-09-867-701-10876
: Sequence 10876, Application US/09867701
: GENERAL INFORMATION:
: APPLICANT: Aglate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlockner, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ ID NOS: 10912
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 10876
: LENGTH: 625
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 607
: OTHER INFORMATION: n = A,T,C or G
: US-09-867-701-10876

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QY 1	AGTTCCTCTTCAGAGGACTGGCGCCGGGACGCGAAGAGCACAAGGCGCGTGCACAAAGCG	60		
Db 1	AGTTCCTCTTCAGAGGACTGGCGCCGGGACGCGAAGAGCACAAGGCGCGTGCACAAAGCG	60		
QY 61	GGCGCTGTCGGGTGCTGGAGAGTGGGCATGTACGGCGGACAGCGCCTTCTCGTGGTTGGCGTGTG	120		
Db 61	GGCGCTGTCGGGTGCTGGAGAGTGGGCATGTACGGCGGACAGCGCCTTCTCGTGGTTGGCGTGTG	120		
QY 121	CAGCGACAGGGGGGACAGCAGACCTGGACAGCAACCCGGCGCAAACTGGTGAGAGACAC	180		
Db 121	CAGCGACAGGGGGGACAGCAGACCTGGACAGCAACCCGGCGCAAACTGGTGAGAGACAC	180		

QY	181	CGTGTACAGGAGCGGGTTGATGACCCGAGCTGAGTATAGAAAAACGTCCTCCGAGAAAGGGAG	240
Db	181	CGTGTACAGGAGCGGGTTGATGAGCCGAGCTGAGTATAGAAAAACGTCCTCCGAGAAAGGGAG	240
QY	241	GAGATCATGTAGCGCCCGGAAGTAGACCTGTGCACGTCTGTGGTTGGCCCGAGC	300
Db	241	GAGATCATGTAGACCCCGGAAGTAGAGCCTGTGCACGTCTGTGGTTGGCCCGAGC	300
QY	301	CATGATCCTCCGAATCTGTTGGGCAATCCAGCATATCGGCGCAATGTCAACAATCAGCCCC	360
Db	301	CATATCTCTCCGAATCTGTGTTGGGCAATCCAGCATATCGGCGCAATGTCAACAATCAGCCCC	360
QY	361	TGGGCAGACACGAGCAGAGGGAGGAGACAGAGAAAAAGAAAAACACACACATGAGAACACAG	420
Db	361	TGGGCACACACGAGCAGAGGGAGGAGACAGAGAAAAAGAAAAACACACACATGAGAACACAG	420
QY	421	TAAATGAAATAAACCAATAAATATTAGCCCCCTCTGTCTGTGCTTACTGTGCCAGGAAAT	480
Db	421	TAAATGAAATAAACCAATAAATATTATTTAGCCCCCTCTGTCTGTGCTTACTGTGCCAGGAAAT	480
QY	481	GGTACCAATTTTTCAGTGTGGATGTGACAGCTTCCTTTGCCCAACGACAGAGAAATTT	540
Db	481	GGTACCAATTTTTCAGTGTGGACTGTGACAGCTTCCTTTGCCCAACGACAGAGAAATTT	540
QY	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGCACTTAATGCTTTAG	600
Db	541	AACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTAAAGAAAGCACTTAATGCTTTAG	600
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RESULT 4
US-09-970-966-210
Sequence 210. Application US/09970966
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Molesh, David Alan
APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 210
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 607
OTHER INFORMATION: n = A,T,C or G
US-09-970-966-210

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Query Match	99.8%	Score 624	DB 36	Length 625
Best Local Similarity	100.0%	Pred. No. 5e-116		
Matches 625	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	AGTTCTCCTTTCAGAGGACTGGCCCGGAGCGGCAAGACAAAGCGCCCTGCACAAACG	60	
Db	1	AGTTCTCCTTTCAGAGGACTGGCCCGGAGCGGCAAGACAAAGCGCCCTGCACAAACG	60	
QY	61	GGCGCTGTGCGTGTGTGAGTGCACATGTACGCGCAGCGCTTTCGTTGTTGGCGTCTG	120	
Db	61	GGCGCTGTGCGTGTGTGAGTGCACATGTACCGCAGCGCTTTCGTTGTTGGCGTCTG	120	
QY	121	CAGGACAGAGCGGGAGCAGCAGACACCTGCAGCAAAACCCCGGAAACTCTCTCGAGGACAC	180	
Db	121	CAGGACAGAGCGGGAGCAGCAGACACCTGCAGCAAAACCCCGGAAACTCTCTCGAGGACAC	180	

```
QY 181 CGGTACAGAGACGGGTTGATGACCGAGCTGAGTAAAGAAACGTCTCCGAGAGGGGAG 240
DB 181 CCGTACAGAGACGGGTTGATGACCGAGCTGAGTAAAGAAACGTCTCCGAGAGGGGAG 240
QY 241 GAGGATCATGTACGCGCGGAGTAGGACCTGCTCCAGTGTGCTGGGTTGGCCGACG 300
DB 241 GAGGATCATGTACGCGCGGAGTAGGACCTGCTCCAGTGTGCTGGGTTGGCCGACG 300
QY 301 CATGATCTCCGAAATCTGGTGGGATCCAGCATACGCCAATGTCCAAATCAGCCC 360
DB 301 CATGATCTCCGAAATCTGGTGGGATCCAGCATACGCCAATGTCCAAATCAGCCC 360
QY 361 TGGGACAGACAGAGAGAGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TAAATGAATAAACATTAATATTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 480
DB 421 TAAATGAATAAACATTAATATTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 480
QY 481 GGTACCAATTTTTCAGTGTGAGCTTACAGCTTCTTTTGCACAGCAAGAGAGATTT 540
DB 481 GGTACCAATTTTTCAGTGTGAGCTTACAGCTTCTTTTGCACAGCAAGAGAGATTT 540
QY 541 AACACGTGTTTCAACCCGGGGAGGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
DB 541 AACACGTGTTTCAACCCGGGGAGGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
QY 601 ACAGTGNMAAAAAAAAAAAAAAAAA 625
DB 601 ACAGTGNMAAAAAAAAAAAAAAAAA 625
```

## RESULT 5

```
US-10-212-677-210
; Sequence 210, Application US/10212677
; GENERAL INFORMATION:
; APPLICANT: Chemault, Ruth A.
; APPLICANT: Xu, Jlangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 607
; OTHER INFORMATION: n = A,T,C or G
US-10-212-677-210
```

```
Query Match 99.8%; Score 624; DB 42; Length 625;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTCCTCTTGAGAGAGATGCGCGCGGAGACGGAAGAGACAGCGCGCTGCACAAAGG 60
DB 1 AGTTCCTCTTGAGAGAGATGCGCGCGGAGACGGAAGAGACAGCGCGCTGCACAAAGG 60
QY 61 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 61 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
QY 121 CAGGACAGAGGCGGACAGACAGCACTGACAGAAACCCGCGAAACTGCTGCGAGGACAC 180
```

```
DB 121 CAGGACAGAGGCGGACAGACAGCACTGACAGAAACCCGCGAAACTGCTGCGAGGACAC 180
QY 181 CCGTACAGAGAGCGGTTGATGACCGAGCTGAGTAAAGAAACGTCTCCGAGAGGGGAG 240
DB 181 CCGTACAGAGAGCGGTTGATGACCGAGCTGAGTAAAGAAACGTCTCCGAGAGGGGAG 240
QY 241 GAGGATCATGTACGCGCGGAGTAGGACCTGCTCCAGTGTGCTGGGTTGGCCGACG 300
DB 241 GAGGATCATGTACGCGCGGAGTAGGACCTGCTCCAGTGTGCTGGGTTGGCCGACG 300
QY 301 CATGATCTCCGAAATCTGGTGGGATCCAGCATACGCCAATGTCCAAATCAGCCC 360
DB 301 CATGATCTCCGAAATCTGGTGGGATCCAGCATACGCCAATGTCCAAATCAGCCC 360
QY 361 TGGGACAGACAGAGAGAGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TAAATGAATAAACATTAATATTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 480
DB 421 TAAATGAATAAACATTAATATTAGCCCTCTGTTCTGTGCTTACTGCGCAGGAAT 480
QY 481 GGTACCAATTTTTCAGTGTGAGCTTACAGCTTCTTTTGCACAGCAAGAGAGATTT 540
DB 481 GGTACCAATTTTTCAGTGTGAGCTTACAGCTTCTTTTGCACAGCAAGAGAGATTT 540
QY 541 AACACGTGTTTCAACCCGGGGAGGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
DB 541 AACACGTGTTTCAACCCGGGGAGGTTGGCTGTGTTAAAGAGACCATTAATGCTTTAG 600
QY 601 ACAGTGNMAAAAAAAAAAAAAAAAA 625
DB 601 ACAGTGNMAAAAAAAAAAAAAAAAA 625
```

## RESULT 6

```
PCT-US01-45395-214
; Sequence 214, Application PC/TUS0145395
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stoik, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Molesh, David Alan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-214
```

```
Query Match 99.8%; Score 624; DB 1; Length 1897;
Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGTTCCTCTTGAGAGAGATGCGCGCGGAGACGGAAGAGACAGCGCGCTGCACAAAGG 60
DB 1271 AGTTCCTCTTGAGAGAGATGCGCGCGGAGACGGAAGAGACAGCGCGCTGCACAAAGG 1330
QY 61 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 1331 GCGGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1390
QY 121 CAGGACAGAGGCGGACAGACAGCACTGACAGAAACCCGCGAAACTGCTGCGAGGACAC 180
```

```
Db 1391 CACGACAGGCGGCGACAGACACCTGACGAACACCCGCCGAAACTCTGCGAGAGACAC 1450
Qy 181 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGAG 240
Db 1451 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGAG 1510
Qy 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTCGTGCTTGGGTTTGGCCGACG 300
Db 1511 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTCGTGCTTGGGTTTGGCCGACG 1570
Qy 301 CATGATCTCCGAAATCTGTTGGGATCTCAGCATATGCGGCAATGTCAACAATCAGGCC 360
Db 1571 CATGATCTCCGAAATCTGTTGGGATCTCAGCATATGCGGCAATGTCAACAATCAGGCC 1630
Qy 361 TGGGACAGACGAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACAG 420
Db 1631 TGGGACAGACGAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACAG 1690
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAAAT 480
Db 1691 TAAATGAATAAACATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAAAT 1750
Qy 481 GTTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGAGAGAAATTT 540
Db 1751 GTTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGAGAGAAATTT 1810
Qy 541 AACACTGTTTCAAAACCCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
Db 1811 AACACTGTTTCAAAACCCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 1870
Qy 601 ACAGTGNAAAAAAGAAAAA 625
Db 1871 ACAGTGNAAAAAAGAAAAA 1895
```

```
RESULT 7
US-09-825-294-214
; Sequence 214, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stoik, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825.294
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214
```

```
Query Match 99.8%; Score 624; DB 31; Length 1897;
Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGTTTCCTTTCAGAGAGTGGCGCGGAGCGAAGAGCAAGGGCGCTGCACAAAGCG 60
Db 1271 AGTTTCCTTTCAGAGAGTGGCGCGGAGCGAAGAGCAAGGGCGCTGCACAAAGCG 1330
Qy 61 GCGGCTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCGTGTG 120
Db 1331 GCGGCTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCGTGTG 1390
Qy 121 CACGACAGGCGGCGACAGACACCTGACGAACAACCCGCCGAAACTCTGCGAGAGAC 180
```

```
Db 1391 CACGACAGGCGGCGACAGACACCTGACGAACACCCGCCGAAACTCTGCGAGAGACAC 1450
Qy 181 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGAG 240
Db 1451 CGGTACAGAGGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAAGGGAG 1510
Qy 241 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTCGTGCTTGGGTTTGGCCGACG 300
Db 1511 GAGGATCATGTACGCCCGGAAGTAGACCTGTCACAGTCGTGCTTGGGTTTGGCCGACG 1570
Qy 301 CATGATCTCCGAAATCTGTTGGGATCTCAGCATATGCGGCAATGTCAACAATCAGGCC 360
Db 1571 CATGATCTCCGAAATCTGTTGGGATCTCAGCATATGCGGCAATGTCAACAATCAGGCC 1630
Qy 361 TGGGACAGACGAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACAG 420
Db 1631 TGGGACAGACGAGAGGAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACAG 1690
Qy 421 TAAATGAATAAACATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAAAT 480
Db 1691 TAAATGAATAAACATTAATATTTAGCCCTCTGCTGTCTGCTTACTGGCCAGAAAT 1750
Qy 481 GTTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGAGAGAAATTT 540
Db 1751 GTTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGGCACAAGAGAGAAATTT 1810
Qy 541 AACACTGTTTCAAAACCCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
Db 1811 AACACTGTTTCAAAACCCCGGGGAGTGGCTGTGTTAAAGAAAGACATTAATGCTTTAG 1870
Qy 601 ACAGTGNAAAAAAGAAAAA 625
Db 1871 ACAGTGNAAAAAAGAAAAA 1895
```

```
RESULT 8
US-09-970-966-214
; Sequence 214, Application US/09970966
; GENERAL INFORMATION:
; APPLICANT: Stoik, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970.966
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-214
```

```
Query Match 99.8%; Score 624; DB 36; Length 1897;
Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGTTTCCTTTCAGAGAGTGGCGCGGAGCGGAGCAAGCAAGGGCGCTGCACAAAGCG 60
Db 1271 AGTTTCCTTTCAGAGAGTGGCGCGGAGCGGAGCAAGCAAGGGCGCTGCACAAAGCG 1330
Qy 61 GCGGCTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCGTGTG 120
Db 1331 GCGGCTGTGCGTGTGAGTGGCGCATGTACGCGAGGCGCTTCTGTTGGCGTGTG 1390
Qy 121 CACGACAGGCGGCGACAGACACCTGACGAACAACCCGCCGAAACTCTGCGAGAGAC 180
Db 1391 CACGACAGGCGGCGACAGACACCTGACGAACAACCCGCCGAAACTCTGCGAGAGAC 1450
```

QY 181 CGTGTACAGAGGAGGGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAGAGGGAG 240  
DB 1451 CGTGTACAGAGGAGGGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAGAGGGAG 1510  
QY 241 GAGGATCATGTACGCGCCGGAGTAGACCTGCTCCAGTCTGGGTTGGCCGACG 300  
DB 1511 GAGGATCATGTACGCGCCGGAGTAGACCTGCTCCAGTCTGGGTTGGCCGACG 1570  
QY 301 CATGATCTCCGAAATCTGGTGGGATCCAGATCCGCAATGTCACAAATCAGCCC 360  
DB 1571 CATGATCTCCGAAATCTGGTGGGATCCAGATCCGCAATGTCACAAATCAGCCC 1630  
QY 361 TGGGAGACACGACGAGAGGAGAGACAGAAAAACACAGATGAGAACAG 420  
DB 1631 TGGGAGACACGAGAGGAGAGAGACAGAAAAACACAGATGAGAACAG 1690  
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTGCTTACTGGCCAGAAAT 480  
DB 1691 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTGCTTACTGGCCAGAAAT 1750  
QY 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGCACAAAGAGAGAAAT 540  
DB 1751 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGCACAAAGAGAGAAAT 1810  
QY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600  
DB 1811 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 1870  
QY 601 ACAGTGNAAAAAAGAAAAA 625  
DB 1871 ACAGTGNAAAAAAGAAAAA 1895

## RESULT 9

US-10-212-677-214  
Sequence 214, Application US/10212677  
GENERAL INFORMATION:  
APPLICANT: Renault, Ruth A.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Fanger, Gary R.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.484C7  
CURRENT APPLICATION NUMBER: US/10/212,677  
CURRENT FILING DATE: 2002-08-02  
NUMBER OF SEQ ID NOS: 288  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 214  
LENGTH: 1897  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-212-677-214

Query Match 99.8%; Score 624; DB 42; Length 1897;  
Best Local Similarity 99.8%; Pred. No. 6, 3e-116;  
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACTTCTCTTGCAGAGAGACTGGCGCGGAGCGCAAGAGCAAGCGGCGCTGCACAAAGCG 60  
DB 1271 ACTTCTCTTGCAGAGAGACTGGCGCGGAGCGCAAGAGCAAGCGGCGCTGCACAAAGCG 1330  
QY 61 GCGCGTGTGGGTGGATGTGCGCATGTACGCGCAGCGCCCTTCTGTGTGGCGTGTG 120  
DB 1331 GCGCGTGTGGGTGGATGTGCGCATGTACGCGCAGCGCCCTTCTGTGTGGCGTGTG 1390  
QY 121 CAGCGACAGCGCGCAGACAGCAGCAGCAACACCGCCGCAAACTGTTGGAGGAGAC 180  
DB 1391 CAGCGACAGCGCGCAGACAGCAGCAGCAACACCGCCGCAAACTGTTGGAGGAGAC 1450  
QY 181 CGTGTACAGAGGAGGGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAGAGGGAG 240

DB 1451 CGTGTACAGAGGAGGGGTTGATGACCGAGCTGAGTAGAAAAAGCTCTCCGAGAGGGAG 1510  
QY 241 GAGGATCATGTACGCGCCGGAGTAGACCTGCTCCAGTCTGGGTTGGCCGACG 300  
DB 1511 GAGGATCATGTACGCGCCGGAGTAGACCTGCTCCAGTCTGGGTTGGCCGACG 1570  
QY 301 CATGATCTCCGAAATCTGGTGGGATCCAGATCCGCAATGTCACAAATCAGCCC 360  
DB 1571 CATGATCTCCGAAATCTGGTGGGATCCAGATCCGCAATGTCACAAATCAGCCC 1630  
QY 361 TGGGAGACACGACGAGAGGAGAGACAGAAAAACACAGATGAGAACAG 420  
DB 1631 TGGGAGACACGAGAGGAGAGAGACAGAAAAACACAGATGAGAACAG 1690  
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTGCTTACTGGCCAGAAAT 480  
DB 1691 TAAATGAATAAACCATTAATATTTAGCCCTCTGTTGCTTACTGGCCAGAAAT 1750  
QY 481 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGCACAAAGAGAGAAAT 540  
DB 1751 GGTACCAATTTTTCAGTGTGGACTTGACAGCTCTTTTGCACAAAGAGAGAAAT 1810  
QY 541 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 600  
DB 1811 AACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAATGCTTTAG 1870  
QY 601 ACAGTGNAAAAAAGAAAAA 625  
DB 1871 ACAGTGNAAAAAAGAAAAA 1895

## RESULT 10

PCT-US02-29964-16  
Sequence 16, Application PC/TUS0229964

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhang, Jie  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Wang, Dunrui  
APPLICANT: Ghosh, Malabika  
APPLICANT: Asundi, Vinod  
APPLICANT: Wehrman, Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle W.  
APPLICANT: Wang, Gezhi  
APPLICANT: Haley-Vicente, Dana  
APPLICANT: Drmanac, Radoje T  
TITLE OF INVENTION: Novel Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 809ACP PCT  
CURRENT APPLICATION NUMBER: PCT/US02/29964  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 60/323,739  
PRIOR FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: US 09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: US 09/496,914  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: US 09/560,875  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: PCT/US01/03800  
PRIOR FILING DATE: 2001-02-05

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:
:
: PRIOR APPLICATION NUMBER: US 09/515,126
:
: PRIOR FILING DATE: 2000-02-28
:
: Remaining Prior Application data removed - See File Wrapper or PALM
:
: NUMBER OF SEQ ID NOS: 992
:
: SOFTWARE: PL_Fl_genes Version 6.0
:
: SEQ ID NO: 16
:
: LENGTH: 1967
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (338)..(763)
:
PCT-US02-29964-16

```

Query Match	98.6%	Score 616.4	DB 1	Length 1967
Best Local Similarity	99.7%	Pred. No. 2.2e-114		
Matches 617; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY	1	AGTTCTCCTTGCAGAGAGACTGGGCGCCGGGACGCGAAGACACAAAGGCGCTGCACAAAGCG	60
Db	1349	AGTTCTCCTTGCAGAGAGACTGGGCGCCGGGACGCGAAGACAAAGGCGCGTGCACAAAGCG	1408
QY	61	GGCGCTGTCGAGTGGAGACTGGCCATGTACGGCAGGCGCTTCTCTGTGTTGGCGTCTG	120
Db	1409	GGCGCTGTCGAGTGGAGACTGGCCATGTACGGCAGGCGCTTCTCTGTGTTGGCGTCTG	1468
QY	121	CAGCGACAGGCGCGACAGCACTGTGCACGAACACCCGCGGAAACTGTGCAGAGACAC	180
Db	1469	CAGCGACAGGCGCGACAGCACTGTGCACGAACACCCGCGGAAACTGTGCAGAGACAC	1528
QY	181	GCTGTACAGAGACGGGTGTATGACGAGTGAAGTGAAGAAACGTCCTCCGAAAGGGGAG	240
Db	1529	GCTGTACAGAGACGGGTGTATGACGAGTGAAGTGAAGAAACGTCCTCCGAAAGGGGAG	1588
QY	241	GAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTCGTGTGGTTTGGCCGAGC	300
Db	1589	GAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTCGTGTGGTTTGGCCGAGC	1648
QY	301	CATGATCCCTCCGAATTTGGTTGGGATTCACAGCATATAGGGCCAAATGTCAACAATCACGCC	360
Db	1649	CATGATCCCTCCGAATTTGGTTGGGATTCACAGCATATAGGGCCAAATGTCAACAATCACGCC	1708
QY	361	TGGCGACAGACAGCAGAGAGGGAGAGACAGAGAAAAAACAACAGCATGAGAAACAG	420
Db	1709	TGGCGACAGACAGCAGAGAGGGAGAGACAGAGAAAAAACAACAGCATGAGAAACAG	1768
QY	421	TAAATGAATTAACAACCATTAATAATTATAGCCCTCTGTCTGTCTACTGTGCGCCAGGAAT	480
Db	1769	TAAATTAATAAACAACCATTAATAATTATAGCCCTCTGTCTGTCTACTGTGCGCCAGGAAT	1828
QY	481	GGTACCAATTTTTCAGTGTGGACTTGCAGCTTTCCTTTTGGCCACAAGCAAGAGAAATTT	540
Db	1829	GGTACCAATTTTTCAGTGTGGACTTGCAGCTTTCCTTTTGGCCACAAGCAAGAGAAATTT	1888
QY	541	AACACTGTGTTCAACCCGGGGGAGTTGGCGTGTTAAGAAGAACCTTAATAATGCTTTAG	600
Db	1889	AACACTGTGTTCAACCCGGGGGAGTTGGCGTGTTAAGAAGAACCTTAATAATGCTTTAG	1948
QY	601	ACAGTGNAAAAAAAAAAAAA 619	
Db	1949	ACAGTGTAAAAA 1967	

```

RESULT 1
PCT-US01-45395-205
: Sequence 205, Application PC/TUS0145395
: GENERAL INFORMATION:
: APPLICANT: Corixa Corporation
: APPLICANT: Xu, Jiaqichun
: APPLICANT: Stolk, John A.
: APPLICANT: Algate, Paul A.
: APPLICANT: Fling, Steven P.
: APPLICANT: Molesh, David Alan

```

```

? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.48401PC
? CURRENT APPLICATION NUMBER: PCT/US01/45395
? CURRENT FILING DATE: 2001-11-13
? NUMBER OF SEQ ID NOS: 215
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 205
? LENGTH: 1619
? TYPE: DNA
? ORGANISM: Homo sapiens
PCT-US01-45395-205

```

Query Match	98.1%	Score 613	DB 1	length 1619
Best Local Similarity	99.7%	Pred. No.	1e-113	
Matches 624	Conservative	0	Mismatches 1	Indels 1
				Gaps 1

OY	1	ATTTCACCTTGGACGAGAGACTGGCGCCGGGACGGGAACAGCAACGGGGCTCTACAAACG	60
Db	992	AATTTCCTCTTGACGAGAGACTGGCGCCGGGACGGGAACAGCAACGGGGCTCTACAAACG	1051
OY	61	GGCGCTGTGCGTGGTGGAGTGGCGCATGTACGGCAGGCGCTTCTGTGTGGCGTGTG	120
Db	1052	GGCGCTGTGCGTGGTGGAGTGGCGCATGTACGGCAGGCGCTTCTGTGTGGCGTGTG	1111
OY	121	CAGCGACAGCGCGGACACAGCAAC-7GCACGAAACACCCCGGAAACTGCTGCGAGGACA	179
Db	1112	CAGCGACAGCGCGGACACAGCAACCTTGCACGAAACACCCCGGAAACTGCTGCGAGGACA	1171
OY	180	CCGTGTACAGAGAGCGGGTGTGATACCGAGCTGTGAGTGTGAAATAACGTCTCCGAGAAGGGA	239
Db	1172	CCGTGTACAGAGAGCGGGTGTGATACCGAGCTGTGAGTGTGAAATAACGTCTCCGAGAAGGGA	1231
OY	240	GGAGGATCATGTATACGCCCGGAGTAGAGACTCGTCCAGTGTGCTTGGGTGGCCCGAG	299
Db	1232	GGAGGATCATGTATACGCCCGGAGTAGAGACTCGTCCAGTGTGCTTGGGTGGCCCGAG	1291
OY	300	CGATGATCCTCCGAATCTGTGGGATCCAGATACGGCCAAATGTACAAACATTCAGCC	359
Db	1292	CGATGATCCTCCGAATCTGTGGGATCCAGATACGGCCAAATGTACAAACATTCAGCC	1351
OY	360	CTGGCGACACGAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA	419
Db	1352	CTGGCGACACGAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACA	1411
OY	420	GTAATATGATTAATAACCATTAATAATTTAGGCCCTCTCTTCTGTGCTTACTGTGCCAGAGAA	479
Db	1412	GTAATATGATTAATAACCATTAATAATTTTAGGCCCTCTCTTCTGTGCTTACTGTGCCAGAGAA	1471
OY	480	TGTATCAATTTTTCAGTGTGTGGACTTGTGACAGCTTCTCTTGTGCCACAGCAAGAGAGAA	539
Db	1472	TGTATCAATTTTTCAGTGTGTGGACTTGTGACAGCTTCTCTTGTGCCACAGCAAGAGAGAA	1531
OY	540	TTACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACCATTTAAATGCTTTA	599
Db	1532	TTACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTAAAGAAAGACCATTTAAATGCTTTA	1591
OY	600	GACAGGNAAAAAAAAAAAAAAAAAAAAA 625	
Db	1592	GACAGGTATAAAAAAAAAAAAAAAAAAAAA 1617	

RESULT 12  
PCT-US01-45395-211  
; Sequence 211, Application PC/TUS0145395  
; GENERAL INFORMATION:  
; APPLICANT: Corixa Corporation  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Molesch, David Alan  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

```

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48401PC
; CURRENT APPLICATION NUMBER: PCT/US01/45395
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-45395-211

```

```

Query Match      98.1%; Score 613; DB 1; Length 1619;
Best Local Similarity 99.7%; Pred. No. 1e-113;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

QY 1 AGTTCTCCTTGCAGAGAGACTGGCCGGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 60
DB 992 AGTTCTCCTTGCAGAGAGACTGGCCGGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 1051
QY 61 GCGCGTGTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 1052 GCGCGTGTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
QY 121 CAGCGACAGCGCGGACAGACAGCACC-TGCAGCAACACCCCGGAAACTGCTGCGAGAGACA 179
DB 1112 CAGCGACAGCGCGGACAGACAGCACC-TGCAGCAACACCCCGGAAACTGCTGCGAGAGACA 1171
QY 180 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGCTCTCCGAGAAAGGGA 239
DB 1172 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGCTCTCCGAGAAAGGGA 1231
QY 240 GGAGGATCATGTACGCGCCGGAAGTAGAGACCTGCTCAGTGTGCTTGGGTTGGCCGAG 299
DB 1232 GGAGGATCATGTACGCGCCGGAAGTAGAGACCTGCTCAGTGTGCTTGGGTTGGCCGAG 1291
QY 300 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCCAATGTACAAACATCAGCC 359
DB 1292 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCCAATGTACAAACATCAGCC 1351
QY 360 CTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 1352 CTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 420 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTGCTTACTTGCCAGAGAA 479
DB 1412 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTGCTTACTTGCCAGAGAA 1471
QY 480 TGGTACCAATTTTTCAGTGTGAGTGTGAGCTTCTTTTGCACAGCAAGAGAGAAAT 539
DB 1472 TGGTACCAATTTTTCAGTGTGAGTGTGAGCTTCTTTTGCACAGCAAGAGAGAAAT 1531
QY 540 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599
DB 1532 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591
QY 600 GACAGTGNAAAAAAAAAAAAAAAAAAAA 625
DB 1592 GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617

```

```

RESULT 13
US-09-713-550-205
; Sequence 205, Application US/09713550
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09-713, 550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-713-550-205

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Query Match      98.1%; Score 613; DB 28; Length 1619;
Best Local Similarity 99.7%; Pred. No. 1e-113;
Matches 624; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

QY 1 AGTTCTCCTTGCAGAGAGACTGGCCGGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 60
DB 992 AGTTCTCCTTGCAGAGAGACTGGCCGGGAGCGGAAGACAGCGGGCGCTGCACAAAGCG 1051
QY 61 GCGCGTGTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120
DB 1052 GCGCGTGTGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1111
QY 121 CAGCGACAGCGCGGACAGACAGCACC-TGCAGCAACACCCCGGAAACTGCTGCGAGAGACA 179
DB 1112 CAGCGACAGCGCGGACAGACAGCACC-TGCAGCAACACCCCGGAAACTGCTGCGAGAGACA 1171
QY 180 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGCTCTCCGAGAAAGGGA 239
DB 1172 CCGTGTACAGAGAGCGGGTGTGATGACCGAGCTGAGTGAAGAAAACGCTCTCCGAGAAAGGGA 1231
QY 240 GGAGGATCATGTACGCGCCGGAAGTAGAGACCTGCTCAGTGTGCTTGGGTTGGCCGAG 299
DB 1232 GGAGGATCATGTACGCGCCGGAAGTAGAGACCTGCTCAGTGTGCTTGGGTTGGCCGAG 1291
QY 300 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCCAATGTACAAACATCAGCC 359
DB 1292 CCATGATCTCTCCGAATCTGTTGGGATCCAGCATACGGCCCAATGTACAAACATCAGCC 1351
QY 360 CTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 1352 CTGGGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 420 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTGCTTACTTGCCAGAGAA 479
DB 1412 GTAATGATTAATAACCATTAATATTATTAGCCCTCTGTCTGTGCTTACTTGCCAGAGAA 1471
QY 480 TGGTACCAATTTTTCAGTGTGAGTGTGAGCTTCTTTTGCACAGCAAGAGAGAAAT 539
DB 1472 TGGTACCAATTTTTCAGTGTGAGTGTGAGCTTCTTTTGCACAGCAAGAGAGAAAT 1531
QY 540 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 599
DB 1532 TAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACCATTAATGCTTTA 1591
QY 600 GACAGTGNAAAAAAAAAAAAAAAAAAAA 625
DB 1592 GACAGTGNAAAAAAAAAAAAAAAAAAAA 1617

```

```

RESULT 14
US-09-825-294-205
; Sequence 205, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825, 294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619

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272

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 17.4612 Seconds  
(without alignments)  
3937.596 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625

Sequence: 1 agtctctctgcagagact.....gnaaaaaaaaaaaaaa 625

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 193892 segs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_MA\_New.\*  
1: /cgn2\_6/pdata1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/pdata1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/pdata1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/pdata1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/pdata1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/pdata1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/pdata1/pna/US10\_NEW\_COMB.seq.\*

#### SUMMARIES

Result No.	Score	Query #	Match	Length	DB	ID	Description
1	393	62.9	1524	6	US-10-230-437-15		Sequence 15, Appl
2	46	7.4	2136	6	US-10-270-333-38		Sequence 38, Appl
3	46	7.4	6472	7	US-10-270-333-37		Sequence 37, Appl
4	45	7.2	667	7	US-60-416-172-67		Sequence 67, Appl
5	38.6	6.2	1032	1	PCT-US02-12342-2		Sequence 2, Appl
6	38.6	6.2	1149	1	PCT-US02-12342-1		Sequence 1, Appl
7	38.6	6.2	1376	1	PCT-US02-12342-4		Sequence 4, Appl
8	38	6.1	1251	6	US-10-270-333-98		Sequence 98, Appl
9	38	6.1	9268	6	US-10-270-333-97		Sequence 97, Appl
10	37.4	5.8	5927	6	US-10-270-333-115		Sequence 115, Appl
11	36.4	5.8	990	6	US-10-270-333-116		Sequence 116, Appl
12	36.2	5.8	852	6	US-10-267-255-36		Sequence 36, Appl
13	36.2	5.8	53500	6	US-10-267-255-76		Sequence 76, Appl
14	35.8	5.7	1285	1	PCT-US02-32094-2		Sequence 2, Appl
15	35.8	5.7	1285	6	US-10-265-872-2		Sequence 2, Appl
16	34.4	5.5	1248	6	US-10-272-983-11		Sequence 11, Appl
17	33.6	5.4	3829	6	US-10-240-425-1329		Sequence 1329, Ap
18	33.6	5.4	828	6	US-10-267-255-35		Sequence 35, Appl
19	33.4	5.3	535	5	US-09-513-999C-11576		Sequence 11576, A
20	33.4	5.3	1696	6	US-10-240-965-97		Sequence 97, Appl
21	33.2	5.3	15825	6	US-10-270-333-193		Sequence 193, Appl
22	33.2	5.3	135259	6	US-10-240-485-111		Sequence 111, Appl
23	33.2	5.3	2889	6	US-10-240-425-1585		Sequence 1585, Ap
24	33	5.3	23683	6	US-10-240-965-256		Sequence 256, Appl
25	32.8	5.2	246	5	US-10-240-485-176		Sequence 176, Appl
26	32.8	5.2	246	5	US-09-513-999C-14062		Sequence 14062, A

27	32.8	5.2	473	5	US-09-513-999C-14061	Sequence 14061, A
28	32.8	5.2	1024	6	US-10-270-377-1	Sequence 1, Appl
29	32.8	5.2	1201	6	US-10-240-425-334	Sequence 334, Appl
30	32.8	5.2	1242	7	US-60-417-298-5	Sequence 5, Appl
31	32.8	5.2	1772	5	US-09-674-988A-3	Sequence 3, Appl
32	32.6	5.2	1926	6	US-10-194-046-3	Sequence 3, Appl
33	32.4	5.2	3096	1	PCT-US02-06147-9	Sequence 9, Appl
34	32.4	5.2	3949	1	PCT-US02-06147-7	Sequence 7, Appl
35	32.2	5.2	415	5	US-09-513-999C-1158	Sequence 1158, Ap
36	32	5.1	1335	6	US-10-282-958-3	Sequence 3, Appl
37	32	5.1	2689	6	US-10-282-958-1	Sequence 1, Appl
38	31.8	5.1	308	5	US-09-513-999C-18015	Sequence 18015, A
39	31.8	5.1	831	6	US-10-272-490-3	Sequence 3, Appl
40	31.8	5.1	2739	6	US-10-264-237-553	Sequence 553, Appl
41	31.6	5.1	2080	6	US-10-257-022-30	Sequence 30, Appl
42	31.6	5.1	2158	6	US-10-264-237-1227	Sequence 1277, Ap
43	31.6	5.1	2845	6	US-10-131-813A-207	Sequence 207, Appl
44	31.6	5.1	2845	6	US-10-131-819A-207	Sequence 207, Appl
45	31.6	5.1	2845	6	US-10-131-823A-207	Sequence 207, Appl

#### ALIGNMENTS

RESULT 1  
US-10-230-437-15  
Sequence 15, Application US/10230437  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C94  
CURRENT FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO: 15  
LENGTH: 1524  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-230-437-15  
Query Match 62.9%; Score 393; DB 6; Length 1524;

Best Local Similarity 100.0%; Pred. No. 4.3e-96;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTTCCTTGAGAGAGTGGCGCGGAGCCGAGACAGACAGCGGCGCTGCACAAAGCG 60  
 DB 1132 AGTTTCCTTGAGAGAGTGGCGCGGAGCCGAGACAGACAGCGGCGCTGCACAAAGCG 1191  
 QY 61 GCGCGTGTGCTGTGAGTGGCATGTACGGCAGCGCCCTTCTGCTGTTGGCGTGTG 120  
 DB 1192 GCGCGTGTGCTGTGAGTGGCATGTACGGCAGCGCCCTTCTGCTGTTGGCGTGTG 1251  
 QY 121 CAGCGACAGCGCGAGACAGACAGTGTGACGAAACCCCGGAACTGCTGCGAGAGAC 180  
 DB 1252 CAGCGACAGCGCGAGACAGACAGTGTGACGAAACCCCGGAACTGCTGCGAGAGAC 1311  
 QY 181 CGTGTACAGAGCGGGTTGATGACGAGCTGAGGTGAGAAAACGTTCCGAGAGAGGAG 240  
 DB 1312 CGTGTACAGAGCGGGTTGATGACGAGCTGAGGTGAGAAAACGTTCCGAGAGAGGAG 1371  
 QY 241 GAGGATCATGTACGCGCGGAGTAGGACCTGCTCCAGTGTGCTGTTGGCGCAGC 300  
 DB 1372 GAGGATCATGTACGCGCGGAGTAGGACCTGCTCCAGTGTGCTGTTGGCGCAGC 1431  
 QY 301 CATGATCTCCGAATCTGTTGGCATCCAGATACGGCCAAATGTACAAATCAGCCC 360  
 DB 1432 CATGATCTCCGAATCTGTTGGCATCCAGATACGGCCAAATGTACAAATCAGCCC 1491  
 QY 361 TGGGACAGACGAG 393  
 DB 1492 TGGGACAGACGAG 1524

# RESULT 2 US-10-270-333-38/c

; Sequence 38, Application US/10270333  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cravchik, Anibal  
 ; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES  
 ; FILE REFERENCE: THEREOF AS INSECTICIDAL TARGETS  
 ; CURRENT APPLICATION NUMBER: US/10/270,333  
 ; PRIOR FILING DATE: 2002-10-15  
 ; PRIOR APPLICATION NUMBER: 60/168,677  
 ; PRIOR FILING DATE: 1999-12-03  
 ; PRIOR APPLICATION NUMBER: 60/175,691  
 ; PRIOR FILING DATE: 2000-01-12  
 ; PRIOR APPLICATION NUMBER: 60/191,638  
 ; PRIOR FILING DATE: 2000-03-23  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 38  
 ; LENGTH: 2196  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila  
 US-10-270-333-38

Query Match 7.4%; Score 46; DB 6; Length 2196;  
 Best Local Similarity 52.6%; Pred. No. 0.0025;  
 Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 63 CGCTTCGCTGTGAGTGGCATGTACGCGAGCGCTTCTGCTGTTGGCGTGTGCA 122  
 DB 1888 CGCTTCGCTGTGAGTGGCATGTACGCGAGGATGTGATGTGATGTGCGCGTT 1829  
 QY 123 GCGACAGCGCGAGACAGACAGTGTGACGAAACCCCGGAACTGCTGCGAGACCG 182  
 DB 1828 GCGCGACAGCAAGTGTGAGACAGCGCGCGGAGAGCGCGCTGCGAAATTTGAGACATCAGGT 1769  
 QY 183 TGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAGTCTCCGAGAGGAGAGA 242  
 DB 1768 TGTACAGAGAGCGGTTGATGACCGAGCTGAGTGAAGCAATGAAGCGGAGAGATACAGCA 1709

QY 243 GGATCATGTA 252  
 DB 1708 GGTTGTAGTA 1699

# RESULT 3 US-10-270-333-37/c

; Sequence 37, Application US/10270333  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cravchik, Anibal  
 ; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES  
 ; FILE REFERENCE: THEREOF AS INSECTICIDAL TARGETS  
 ; CURRENT APPLICATION NUMBER: US/10/270,333  
 ; PRIOR FILING DATE: 2002-10-15  
 ; PRIOR APPLICATION NUMBER: 60/168,677  
 ; PRIOR FILING DATE: 1999-12-03  
 ; PRIOR APPLICATION NUMBER: 60/175,691  
 ; PRIOR FILING DATE: 2000-01-12  
 ; PRIOR APPLICATION NUMBER: 60/191,638  
 ; PRIOR FILING DATE: 2000-03-23  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 37  
 ; LENGTH: 6472  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila  
 US-10-270-333-37

Query Match 7.4%; Score 46; DB 6; Length 6472;  
 Best Local Similarity 52.6%; Pred. No. 0.0041;  
 Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 63 CGCTTCGCTGTGAGTGGCATGTACGCGAGCGCTTCTGCTGTTGGCGTGTGCA 122  
 DB 5164 CGCTTCGCTGTGAGTGGCATGTACGCGAGGATGTGATGTGATGTGCGCGTT 5105  
 QY 123 GCGACAGCGCGAGACAGACAGTGTGACGAAACCCCGGAACTGCTGCGAGACAGC 182  
 DB 5104 GCGCGACAGCAAGTGTGAGACAGCGCGCGGAGAGAGCGCGTGGAAATTTGAGAGATCAGGT 5045  
 QY 183 TGTACAGAGCGGTTGATGACCGAGCTGAGTGAAGAAAGTCTCCGAGAGGAGAGA 242  
 DB 5044 TGTACAGAGCGGTTGATGACCGAGCTGAGTGAAGCAATGAAGCGGAGAGATACAGCA 4985  
 QY 243 GGATCATGTA 252  
 DB 4984 GGTTGTAGTA 4975

# RESULT 4 US-60-416-172-67

; Sequence 67, Application US/60416172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chang, Hwai Wen  
 ; APPLICANT: Felts, Katherine A.  
 ; APPLICANT: Warren, Amy J.  
 ; APPLICANT: Cooper, Judith R.  
 ; TITLE OF INVENTION: Genes from Human Cancer Cells and Human Tumors  
 ; FILE REFERENCE: 216019-153  
 ; CURRENT APPLICATION NUMBER: US/60/416,172  
 ; PRIOR FILING DATE: 2002-10-04  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 67  
 ; LENGTH: 667  
 ; TYPE: DNA  
 ; ORGANISM: Gallus gallus  
 ; NAME/KEY: misc\_feature  
 ; FEATURE:  
 ; OTHER INFORMATION: Human extended sequence for VOG3\_71  
 US-60-416-172-67

Query Match	7.28: Score	45: DB	7: Length	667: Best Local Similarity	46.88: Pred. No.	0.0026: Matches	141: Conservative	0: Mismatches	160: Indels	0: Gaps
Qy	46	GCCTGCACAAAGCGGGCGCTGTGCGTGTGAGTGGCGCATGTACGCGCAGCGCTTCTC	105							
Db	187	GCGGCAAGACAGACGACGCCGTACGGGGTGGCCGGGGCGCTCCACAGCCTTTCAGCGGGA	246							
Qy	106	GTTGTGGCGCTGCTCAGCGACAGCGCGGCGACACAGCACACTTCACAGACACCCGCCGAA	165							
Db	247	GTTGGTGGAGTGTCCGGGCACGGCTTGGGCGACGCCGCGCCCGCGGATGTCAGCGCGA	306							
Qy	166	CTGCTGCGAGGACCCGTGTACAGAGCGGGTGTGATGACCGATGAGTAAAGAAACGT	225							
Db	307	GTACAGAGCACTTCATGTGAGTGCATGCACCGCACACCAAGCTGGCTCTCTGGGTTGAAAAAGAT	366							
Qy	226	CTTCCGAGAAGGAGAGAGATCATGTACGCCCGGAAGTAGAGACCTTCGTCAGTGTGCTTT	285							
Db	367	CCTGGAGCAGAGAGGACCAAGATGATCAAGAGGGGAAGTACACCCGCCGAGATCACCAA	426							
Qy	286	GGGTTTGGCCCGACGCATATCTCCGAATCTGTGTTGGGCAATCCACATAGGGCCAAATG	345							
Db	427	GGGTGAGAGGACACCCGCCCTTGAAGCACAGGGACTCTCAGGGACCCGACAGCGCTCGT	486							
Qy	346	C 346								
Db	487	C 487								

```

RESULT 5
PCT-US02-12342-2/c
: Sequence 2, Application PC/TUS0212342
: GENERAL INFORMATION:
: APPLICANT: Chu, Peter
: APPLICANT: Jiang, Yingling
: APPLICANT: Li, Congfen
: APPLICANT: Liao, X. Charlene
: APPLICANT: Masuda, Esteban
: APPLICANT: Pardo, Jorge
: APPLICANT: Spencer, Colin
: APPLICANT: Zhao, Haoran
: APPLICANT: Rigel Pharmaceuticals, Inc.
: TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
: FILE REFERENCE: 021044-000310PC
: CURRENT APPLICATION NUMBER: PCT/US02/12342
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: US 60/284,763
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: US 09/971,228
: PRIOR FILING DATE: 2001-10-03
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1032
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: mutant #1, C-terminally truncated variant of
: OTHER INFORMATION: human endothelial differentiation G-protein
: OTHER INFORMATION: coupled receptor (GPCR) 1 (EDG1)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (9)..(1031)
: OTHER INFORMATION: mutant #1 human EDG1
PCT-US02-12342-2

```

[illegible]

Db 1004 CCGGCACCTTGCACGACGACATGATCCGGATTAAGGCCGACGCACTTCCTGTGTGTAC 945

Qy 181 CGTGTACAGAGCGGGTTGATGACCGAGCTGAG 213

Db 944 AGGTAAATGATGGGGTTGGTCCGGAGTTGAG 912

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RESULT 6
PCT-US02-12342-1/c
: Sequence 1, Application PC/TUS0212342
: GENERAL INFORMATION:
: APPLICANT: Chu, Peter
: APPLICANT: Jjiang, Yingping
: APPLICANT: Li, Congfen
: APPLICANT: Liao, X. Charlene
: APPLICANT: Masuda, Esteban
: APPLICANT: Pardo, Jorge
: APPLICANT: Spencer, Colin
: APPLICANT: Zhao, Haoran
: APPLICANT: Rigel Pharmaceuticals, Inc.
: TITLE OF INVENTION: EDS: Modulators of Lymphocyte Activation and Migration
: FILE REFERENCE: 021044-000310PC
: CURRENT APPLICATION NUMBER: PCT/US02/12342
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: US 60/284,763
: PRIOR FILING DATE: 2001-04-18
: PRIOR APPLICATION NUMBER: US 09/971,228
: PRIOR FILING DATE: 2001-10-03
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1149
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: wild-type human endothelial differentiation
: OTHER INFORMATION: G-protein coupled receptor (GPCR) 1 (EDG1)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1149)
: OTHER INFORMATION: wild type human EDG1
: PCT-US02-12342-1

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Query Match	6.2%	Score 38.6	DB 1	Length 1149
Best Local Similarity	63.4%	Pred. No. 0.17		
Matches	59	Conservative	0	Mismatches 34
			Indels	0
			Gaps	0

QY	121	CACGACAGCGCGGCACACAGCAGCCTGACAGACACGCCGCCGAAATCGTCGAGACAC	180
DB	996	CGGGCACTTCACACAGACACATGATCCGGATGAGAGCGCCGACGCGATCTCTTGTGTGCAG	937
QY	181	CGTGTACAGAGCGCGGTGATGACACAGCTGAG	213
DB	936	AGGTAAATGATGAGGTGTGTGCGGAGGTGAG	904

RESULT 7  
PCT-US02-12342-4/C  
; Sequence 4, Application PC/TUS0212342  
; GENERAL INFORMATION:  
; APPLICANT: Chu, Peter  
; APPLICANT: Jiang, Yingsheng  
; APPLICANT: Li, Congfen  
; APPLICANT: Liao, X. Charlene  
; APPLICANT: Masuda, Esteban  
; APPLICANT: Pardo, Jorge  
; APPLICANT: Spencer, Collin  
; APPLICANT: Zhao, Haoran  
; APPLICANT: Rigel Pharmaceuticals, Inc.  
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration  
; FILE REFERENCE: 021044-000310PC  
; CURRENT APPLICATION NUMBER: PCT/US02/12342  
; CURRENT FILING DATE: 2002-08-26

;; PRIOR APPLICATION NUMBER: US 60/284,763  
;; PRIOR FILING DATE: 2001-04-18  
;; PRIOR APPLICATION NUMBER: US 09/971,228  
;; PRIOR FILING DATE: 2001-10-03  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 4  
;; LENGTH: 1376  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: mutant #3, C-terminally truncated variant of  
;; OTHER INFORMATION: human endothelial differentiation G-protein  
;; OTHER INFORMATION: coupled receptor (GPCR) 1 (EDG1)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (338)..(1375)  
;; OTHER INFORMATION: mutant #3 human EDG1  
PCT-US02-12342-4

Query Match  
Best Local Similarity 6.2%; Score 38.6; DB 1; Length 1376;  
Matches 59; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 121 CAGGACAGCGCGCAGACACCTGCGAGACACCCCGGAAACTGCTGCGAGACAC 180  
Db 1333 CGGCGACTTCCAGACAGACATGATCCGATGAAGCCCGGACGATCTGTTGTGTCAG 1274  
QY 181 CGTGTACAGGAGCGGCTGTGATGACCGAGCTGAG 213  
Db 1273 AGTGTAAATGATGGGGTGTGGTCCGAGATTGAG 1241

RESULT 8  
US-10-270-333-98/c  
; Sequence 98, Application US/10270333  
; GENERAL INFORMATION:  
; APPLICANT: Cravchik, Anibal  
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES  
; FILE REFERENCE: CL000733CON  
; CURRENT APPLICATION NUMBER: US/10/270,333  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/168,677  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 60/175,691  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/191,638  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 198  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 1251  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-10-270-333-98

Query Match  
Best Local Similarity 6.1%; Score 38; DB 6; Length 1251;  
Matches 59; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 124 CGACGAGCGCGCAGACACCTGCGAGACACCCCGGAAACTGCTGCGAGACACCGT 183  
Db 1221 CGAATAGCGCGCAGACACCTTCTTGAAGCGCTGCCGGAACACCTTGTGAATGAT 1162  
QY 184 GTACGAGCGCGCTGTGATGACGAGCTGAGTAG 217  
Db 1161 GTAGAGATGGGCTTCCACCATGAGACTAGCGTAG 1128

RESULT 9  
US-10-270-333-97/c

;; Sequence 97, Application US/10270333  
;; GENERAL INFORMATION:  
;; APPLICANT: Cravchik, Anibal  
;; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES  
;; FILE REFERENCE: CL000733CON  
;; CURRENT APPLICATION NUMBER: US/10/270,333  
;; CURRENT FILING DATE: 2002-10-15  
;; PRIOR APPLICATION NUMBER: 60/168,677  
;; PRIOR FILING DATE: 1999-12-03  
;; PRIOR APPLICATION NUMBER: 60/175,691  
;; PRIOR FILING DATE: 2000-01-12  
;; PRIOR APPLICATION NUMBER: 60/191,638  
;; PRIOR FILING DATE: 2000-03-23  
;; NUMBER OF SEQ ID NOS: 198  
;; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 9268  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-10-270-333-97

Query Match  
Best Local Similarity 6.1%; Score 38; DB 6; Length 9268;  
Matches 59; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 124 CGACGAGCGCGCAGACACCTGCGAGACACCCCGGAAACTGCTGCGAGACACCGT 183  
Db 8238 CGAATAGCGCGCAGACACCTTCTTGAAGCGCTGCCGGAACACCTTGTGAATGAT 8179  
QY 184 GTACGAGCGCGCTGTGATGACCGAGCTGAGTAG 217  
Db 8178 GTAGAGATGGGCTTCCACCATGAGACTAGCGTAG 8145

RESULT 10  
US-10-270-333-115  
; Sequence 115, Application US/10270333  
; GENERAL INFORMATION:  
; APPLICANT: Cravchik, Anibal  
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES  
; FILE REFERENCE: CL000733CON  
; CURRENT APPLICATION NUMBER: US/10/270,333  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/168,677  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 60/175,691  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/191,638  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 198  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 5927  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-10-270-333-115

Query Match  
Best Local Similarity 6.0%; Score 37.4; DB 6; Length 5927;  
Matches 71; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 142 CACCTGCAGACACACCCCGGAAACTGCTGCGAGACACCTGTAAGAGCGGCTTGTAT 201  
Db 1371 CACCTGTGAAGAGCGCTTCCGGAATCTCGGAGAGGAGCGGTAGACAGCGGATGAT 1430  
QY 202 GACCGAGCTGAGGTAGAAAACGCTCCGAGAGGAGGAGAGATCATGTACCCCGGAA 261  
Db 1431 ACAGAGCTGCTGTAGCCAGAGATGCGGCGGTGACCTGAGATGACTTGTGTAGGAT 1490

OY 262 GTAGAC 268  
DB 1491 GTTCGTC 1497

## RESULT 11

US-10-270-333-116/C

; Sequence 116, Application US/10270333  
; GENERAL INFORMATION:  
; APPLICANT: Cravchik, Anibal  
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES  
; TITLE OF INVENTION: THEORETICAL AS INSECTICIDAL TARGETS  
; FILE REFERENCE: C000733CON  
; CURRENT APPLICATION NUMBER: US/10/270,333  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/168,677  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 60/175,691  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/191,638  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 198  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 116  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-10-270-333-116

## Query Match

Best Local Similarity 5.8%; Score 36.4; DB 6; Length 990;  
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

OY 135 AGCAGACACCTGCAGCAACCCGCCGAACCTGCTGCGAGAGACACCGTACAGGAGCG 194  
DB 988 AGAATTCGCTTGTAGAGAGCGCTCCGGAATTTCTCGAGAGAGAGCGTACAGGAGCG 929  
OY 195 GGTGATGACCGAGCTGAGTGAAGAAACCTCTCCGAGAGAGGAGAGATCATCTAGC 254  
DB 928 GATGATACACGAGCTGCTGTAGGCGCAGAGTCTGGCGGTGACTGATGACTGCTGG 869  
OY 255 CCGGAGTAGGAC 268  
DB 868 TGAGGCTGTCGTC 855

## RESULT 12

US-10-267-255-36/C

; Sequence 36, Application US/10267255  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D  
; APPLICANT: Mao, Y  
; APPLICANT: Varoglu, M  
; APPLICANT: He, M  
; APPLICANT: Sheldon, P  
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
; FILE REFERENCE: 600,456US1  
; CURRENT APPLICATION NUMBER: US/10/267,255  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 09/266,965  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: US 08/624,447  
; PRIOR FILING DATE: 1996-08-19  
; PRIOR APPLICATION NUMBER: PCT/US94/11279  
; PRIOR FILING DATE: 1994-10-06  
; PRIOR APPLICATION NUMBER: US 08/133,963  
; PRIOR FILING DATE: 1993-10-07  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 852  
; TYPE: DNA

; ORGANISM: Streptomyces lavendulae  
US-10-267-255-36

## Query Match

Best Local Similarity 5.8%; Score 36.2; DB 6; Length 852;  
Matches 104; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

OY 98 CGCTTCGCTGCTGGGTGCTGCGAGCAGAGGCGGACAGACAGCAGCAGCAGCAGCAGC 157  
DB 539 CGCTCGAAGAGTGTGAGAGAGCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
OY 158 CGCCGAAGCTGCTCGAGAGACCGGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAG 217  
DB 479 GCGAGCACCTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420  
OY 218 AAAAGCTGCTCGAAGAGGAGGAGAGATCATGTACAGCGCCGGAAGTACAGCCTGCTCAG 277  
DB 419 AAGCTTCGCTCTGAGAGGAGGAGGCTCCATCCGCTGCGGCGGCGGCGGCGGCGGCGG 360  
OY 278 TCGTCTTGGGTTGGCGGCGAGCCCATGATCCCGAA 314  
DB 359 GCGAGCGCGGCGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 323

## RESULT 13

US-10-267-255-76

; Sequence 76, Application US/10267255  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D  
; APPLICANT: Mao, Y  
; APPLICANT: Varoglu, M  
; APPLICANT: He, M  
; APPLICANT: Sheldon, P  
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
; FILE REFERENCE: 600,456US1  
; CURRENT APPLICATION NUMBER: US/10/267,255  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 09/266,965  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: US 08/624,447  
; PRIOR FILING DATE: 1996-08-19  
; PRIOR APPLICATION NUMBER: PCT/US94/11279  
; PRIOR FILING DATE: 1994-10-06  
; PRIOR APPLICATION NUMBER: US 08/133,963  
; PRIOR FILING DATE: 1993-10-07  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 53500  
; TYPE: DNA  
; ORGANISM: Streptomyces lavendulae  
US-10-267-255-76

## Query Match

Best Local Similarity 5.8%; Score 36.2; DB 6; Length 53500;  
Matches 104; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

OY 98 CGCTTCGCTGCTGGGTGCTGCGAGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 157  
DB 7046 CGCTCGAAGAGTGTGAGAGAGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7105  
OY 158 CGCCGAAGCTGCTCGAGAGACCGGTGACAGAGAGCGGTTGATGACCGAGCTGAGTAG 217  
DB 7106 GCGAGCACCTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7165  
OY 218 AAAAGCTGCTCGAAGAGGAGGAGAGATCATGTACAGCGCCGGAAGTACAGCCTGCTCAG 277  
DB 7166 AAGCTTCGCTCTGAGAGGAGGAGGCTCCATCCGCTGCGGCGGCGGCGGCGGCGGCGG 7225  
OY 278 TCGTCTTGGGTTGGCGGCGAGCCCATGATCCCGAA 314  
DB 7226 GCGAGCGCGGCGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7262





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 ; Search time 837.306 Seconds  
(without alignments)  
12088.985 Million cell updates/sec

Title: US-09-970-966-210

Perfect score: 625  
Sequence: 1 agtctctcttcagagact.....gnaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_estlum:\*  
3: em\_estlu:\*  
4: em\_estlu:\*  
5: em\_estlu:\*  
6: em\_estlu:\*  
7: em\_estlu:\*  
8: em\_estlu:\*  
9: em\_estlu:\*  
10: em\_estlu:\*  
11: em\_estlu:\*  
12: em\_estlu:\*  
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25: em\_estlu:\*  
26: em\_estlu:\*  
27: em\_estlu:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	622.4	99.6	702	14	BQ006545 UI-H-E11-
C 2	621.4	99.4	627	13	BM669397 UI-E-DW1-
C 3	610.4	97.7	696	13	BM547680 AGENCOURT
C 4	603.4	96.5	678	9	AT936826 wp69h10.x
C 5	601.2	96.2	616	9	AT990500 ws40d07.x
C 6	601.2	96.2	649	10	AM590950 hg51e12.x

Result No.	Score	Query Match	Length	ID	Description
C 7	600.8	96.1	696	12	BF439382
C 8	599.4	95.9	690	10	AM149665 x440h5.x
C 9	583.8	93.4	645	12	BF432379
C 10	548.4	87.7	551	12	BE588216
C 11	538.4	86.1	540	12	BF939693
C 12	537	85.9	537	12	BF994242
C 13	532.8	85.2	538	13	BF594242
C 14	531.2	85.0	537	12	BF667957
C 15	525.8	84.1	561	10	AM150789
C 16	524.4	83.9	527	10	AM338938
C 17	523.8	83.8	359	9	AM859538
C 18	512.4	82.0	515	9	AM133688
C 19	495.6	79.3	676	10	BE385990
C 20	494.2	79.1	500	10	AM075558
C 21	485.4	77.7	640	10	AM148557
C 22	472.6	75.6	480	9	AM142316
C 23	472	75.5	510	12	BF726459
C 24	466	74.6	475	9	AM133261
C 25	451.8	72.3	456	9	AM1765236
C 26	451.6	72.3	843	12	BF125134
C 27	445.4	71.3	591	9	AM1884686
C 28	444.4	71.1	463	9	AM1202043
C 29	443	70.9	442	9	AM1391683
C 30	443	70.9	454	10	AM191974
C 31	443	70.9	814	9	AL567376
C 32	440.6	70.5	578	9	AM1742092
C 33	439.4	70.3	759	12	BF126050
C 34	433.2	69.3	558	9	AM173383
C 35	427.4	68.4	432	10	AM087372
C 36	427.4	68.4	499	10	AM075549
C 37	424	67.8	452	9	AA626797
C 38	424	67.8	467	9	AM150931
C 39	401.4	64.2	420	9	AM1566797
C 40	401	64.2	412	9	AA084249
C 41	398.6	63.8	564	14	BM687629
C 42	396	63.3	396	9	AA613995
C 43	395.4	63.3	409	9	AA419229
C 44	390	62.4	396	9	AM499630
C 45	390	62.4	534	10	BE350014

# ALIGNMENTS

RESULT 1  
LOCUS BQ006545/c 702 bp mRNA linear EST 26-MAR-2002  
DEFINITION UI-H-E11-aza-n-21-0-UI-s1 NCL\_CGAP\_E11 Homo sapiens cDNA clone  
IMAGE:5846228 3', mRNA sequence.  
ACCESSION BQ006545  
VERSION BQ006545.1 GI:19731445  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 702)  
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
JOURNAL Unpublished (1997)  
COMMENT Tumor Gene Index  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Dr. Jose Mercende  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Seq primer: M13 FORWARD  
POLA-yes.  
FEATURES  
Location/Qualifiers  
I. .702

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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:5846228"
/clone_lib="NCL_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pRT3-Pac (Pharmacia) with a modified polylinker. Site_1: EcoR I; Site_2: Not I; NCL_CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGCGAC.
TAG_LIB=UI-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTGCGAC"
BASE COUNT 137 a 200 c 163 g 202 t
ORIGIN

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Query Match 99.6%; Score 622.4; DB 14; Length 702;
Best Local Similarity 99.7%; Pred. No. 1.1e-102;
Matches 623; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCGCTGCACAAAGCG 60
DB 625 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCGCTGCACAAAGCG 566
OY 61 GCGCTGTGCTGTGAGAGTGCAGTACGCGCAGCGCGCTTCTGCTGGTGGCTGCTG 120
DB 565 GCGCTGTGCTGTGAGAGTGCAGTACGCGCAGCGCGCTTCTGCTGGTGGCTGCTG 506
OY 121 CAGGACAGAGGCGGAGCAGCAGCAGCAGCAACCGCGGCAATGCTGCGAGAGCAGC 180
DB 505 CAGGACAGAGGCGGAGCAGCAGCAGCAGCAACCGCGGCAATGCTGCGAGAGCAGC 446
OY 181 CGTGTACAGAGCAGCGGCTGTGATGACCGAGCTGAGTAAAGAAAGCGTCTCCGAGAGGAG 240
DB 445 CGTGTACAGAGCAGCGGCTGTGATGACCGAGCTGAGTAAAGAAAGCGTCTCCGAGAGGAG 386
OY 241 GAGGATCATGTACGCGCGGAGTACGCTGCTCCAGTCTGCTGGTGGTGGCGGAGC 300
DB 385 GAGGATCATGTACGCGCGGAGTACGCTGCTCCAGTCTGCTGGTGGTGGCGGAGC 326
OY 301 CATGATCCCTCCGAATCTGGTGGGATCCAGCATACGGCCATGTCACAAATCAGGCC 360
DB 325 CATGATCCCTCCGAATCTGGTGGGATCCAGCATACGGCCATGTCACAAATCAGGCC 266
OY 361 TGGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 265 TGGGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206
OY 421 TAAATGAATAAACCATTAATATTAGCCCTCTGCTGTGCTTACCTGCGCAGAGAAAT 480
DB 205 TAAATGAATAAACCATTAATATTAGCCCTCTGCTGTGCTTACCTGCGCAGAGAAAT 146
OY 481 GGTACCAATTTTTCAGTGTGAGCTTGCAGCTCTTTTGCACAAAGAGAGAAAT 540
DB 145 GGTACCAATTTTTCAGTGTGAGCTTGCAGCTCTTTTGCACAAAGAGAGAAAT 86
OY 541 AACACTGTTTCAACCCGGGAGAGTGGCTGTAAAGAGAGACATTAAATGCTTTAG 600
DB 85 AACACTGTTTCAACCCGGGAGAGTGGCTGTAAAGAGAGACATTAAATGCTTTAG 26
OY 601 ACAGTGNAAAAAAAAAAAAA 625
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DB 25 ACAGTGTAAAAAAAAAAAAAAA 1
RESULT 2
LOCUS BM669397/c 627 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-DW1-shd-c-11-0-UI-s1 UI-E-DW1 Homo sapiens cDNA clone
ACCESSION BM669397
VERSION UI-E-DW1-shd-c-11-0-UI 3', mRNA sequence.
KEYWORDS EST.
SOURCE BM669397.1 GI:18979294
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iuiwee.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLY-A-Tes.
Location/Qualifiers
1..627
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="UI-E-DW1-shd-c-11-0-UI"
/clone_lib="UI-E-DW1"
/tissue_type="lens"
/dev_stage="adult"
/note="Organ: Eye; Vector: pRT3-Pac (Pharmacia) with a modified polylinker. Site_1: EcoR I; Site_2: Not I; UI-E-DW1 is a normalized cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATGTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-DW1
TAG_TISSUE=human lens
TAG_SEQ=CGATTAGCGA"
BASE COUNT 118 a 180 c 145 g 183 t 1 others
ORIGIN

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Query Match 99.4%; Score 621.4; DB 13; Length 627;
Best Local Similarity 99.5%; Pred. No. 1.7e-102;
Matches 622; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCGCTGCACAAAGCG 60
DB 625 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCAGCAAGAGCAGCGCGCTGCACAAAGCG 566
||||| ||||||| |||||||

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QY 61 GGGCTGTCGGTGGTGGATGCGATGACGCGAGCGGCTTCTGCTGGTGGCGTGC 120
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Db 565 GGGGCTTCGGTGGTGGATGCGATGACGCGAGCGGCTTCTGCTGGTGGCGTGC 506
QY 121 CAGCGACAGCGCGGAGACAGACACCTGACAGACACCGCGGAAACCTCTGCGAGACAC 180
    |||
Db 505 CAGCGACAGCGCGGAGACAGACACCTGACAGACACCGCGGAAACCTCTGCGAGACAC 446
QY 181 CGGTACAGAGCGGGTGGATGACGCGATGAGTAAAGAAACGCTCTCGAGAGAGGAG 240
    |||
Db 445 CGGTACAGAGCGGGTGGATGACGCGATGAGTAAAGAAACGCTCTCGAGAGAGGAG 386
QY 241 GAGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGGTGGCGGAGC 300
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Db 385 GAGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGGTGGCGGAGC 326
QY 301 CATGATCTCTCCGAATCTGCTGGGATCAGCATACGCGCAATGTACACAAATCAGCC 360
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Db 325 CATGATCTCTCCGAATCTGCTGGGATCAGCATACGCGCAATGTACACAAATCAGCC 266
QY 361 TGGGACAGACAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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Db 265 TGGGACAGACAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTGCTGCTGCTTACTGGCCAGGAAT 480
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Db 205 TAAATGAATAAACCATTAATATTTAGCCCTGCTGCTGCTTACTGGCCAGGAAT 146
QY 481 GGTACCAATTTTTCAGTGTGGATGACAGCTTCTTGGCCACAGAGAGAGAAAT 540
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Db 145 GGTACCAATTTTTCAGTGTGGATGACAGCTTCTTGGCCACAGAGAGAAAT 86
QY 541 AATACCTTTTCAAAACCGGGGAGTGGCTGTAAAGAAAGACATTAATGCTTAG 600
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Db 85 AATACCTTTTCAAAACCGGGGAGTGGCTGTAAAGAAAGACATTAATGCTTAG 26
QY 601 ACAGTGNAAAAAAGAAAAA 625
    |||
Db 25 ACAGTGNAAAAAAGAAAAA 1

RESULT 3
BM547680 696 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727798
DEFINITION 5', mRNA sequence.
ACCESSION BM547680
VERSION BM547680.1 GI:18781656
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 696)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcrfemail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
http://image.llnl.gov
Plate: LLM12722 row: h column: 07
High quality sequence stop: 641.
Location/Qualifiers
1..696
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/cldone="IMAGE:5727798"
/cldone_1lb="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pCMV-Sport6; Site:1: EcoRV
(deleted); Site:2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT 188 a 160 c 197 g 134 t 17 others
ORIGIN
QY 1 AGTTCTCCTGCAAGAGAGCGGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 60
    |||
Db 65 AGTTCTCCTGCAAGAGAGCGGCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 124
QY 61 GGGCTGTCGGTGGTGGATGCGATGACGCGAGCGGCTTCTGCTGGTGGCGTGC 120
    |||
Db 125 GGGCTGTCGGTGGTGGATGCGATGACGCGAGCGGCTTCTGCTGGTGGCGTGC 184
QY 121 CAGCGACAGCGCGGAGACAGACCTGACAGACACCGCGGAAACCTCTGCGAGACAC 180
    |||
Db 185 CAGCGACAGCGCGGAGACAGACCTGACAGACACCGCGGAAACCTCTGCGAGACAC 244
QY 181 CGGTACAGAGCGGGTGGATGACGCGATGAGTAAAGAAAGCTCTCGAGAGGAG 240
    |||
Db 245 CGGTACAGAGCGGGTGGATGACGCGATGAGTAAAGAAAGCTCTCGAGAGGAG 304
QY 241 GAGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGGTGGCGGAGC 300
    |||
Db 305 GAGATCATGTACGCGCGGAGAGTACGCTGCTGCTGCTGGTGGCGGAGC 364
QY 301 CATGATCTCTCCGAATCTGCTGGGATCAGCATACGCGCAATGTACACAAATCAGCC 360
    |||
Db 365 CATGATCTCTCCGAATCTGCTGGGATCAGCATACGCGCAATGTACACAAATCAGCC 424
QY 361 TGGGACAGACAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||
Db 425 TGGGACAGACAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
QY 421 TAAATGAATAAACCATTAATATTTAGCCCTGCTGCTGCTTACTGGCCAGGAAT 480
    |||
Db 485 TAAATGAATAAACCATTAATATTTAGCCCTGCTGCTGCTTACTGGCCAGGAAT 544
QY 481 GGTACCAATTTTTCAGTGTGGATGACAGCTTCTTGGCCACAGAGAGAAAT 540
    |||
Db 545 GGTACCAATTTTTCAGTGTGGATGACAGCTTCTTGGCCACAGAGAGAAAT 604
QY 541 AACACTGTTTCAAAACCGGGGAGTGGCTGTAAAGAAAGCAATTAATGCTTAG 600
    |||
Db 605 AACACTGTTTCAAAACCGGGGAGTGGCTGTAAAGAAAGCAATTAATGCTTAG 664
QY 601 ACAGTGNAAAAAAGAAAAA 621
    |||
Db 665 ACAGTGNAAAAAAGAAAAA 685

RESULT 4
A1936826 678 bp mRNA linear EST 08-MAR-2000
LOCUS wp69h10.x1 NCI CGAP Brnz2 Homo sapiens cDNA clone IMAGE:2467075 3'
DEFINITION similar to SW:GP39 HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GP39 ; mRNA sequence.
ACCESSION A1936826
VERSION A1936826.1 GI:5675696
KEYWORDS EST.

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Source	Organism	Human
REFERENCE	1 (bases 1 to 678)	
AUTHORS	NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGP), Tumor Gene Index	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.	
FEATURES	cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo, Ph.D. cdna Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www.bio.lnl.gov/dbrr/image/image.html Insert length: 1143 Std Error: 0.00 Seq primer: ~40up from Gbpco High quality sequence stop: 454. Location/Qualifiers	
Source	1. 678 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2467075" /clone_lib="NCI-CGAP_Brn25" /russue_type="anaplastic oligodendroglioma" /lab_host="DH10B" /note="Organ: Brain; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cdna was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTGGAGGCGGCGCAATGATTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cdna was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bernaldo."	
BASE COUNT	133 a 199 c 161 g 182 t 3 others	
ORIGIN		
Query Match	96.5%; Score 603.4; DB 9; Length 678;	
Best Local Similarity	99.7%; Pred. No. 2.9e-92;	
Matches 604; Conservative	0; Mismatches 9; Indels 0; Gaps 0;	
OY	1 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGCAAGAGACAGGGCGCTGCACAAAGCG 60	
DB	606 AGTTCTCCTTGAGAGAGACTGGCGCGGAGCGCGCAAGAGACAGGGCGCTGCACAAAGCG 547	
OY	61 GGCCTGTGCGGTGTGAGAGTGGCATGTACGGCGAGCGCTTCTGCGTGGCTGCTG 120	
DB	546 GGCCTGTGCGGTGTGAGAGTGGCATGTACGGCGAGCGCTTCTGCGTGGCTGCTG 487	
OY	121 CAGGACAGGGCGGAGACAGCACTGGACAGCAACCCGGCGAATCTGTGGAGAGAC 180	
DB	486 CAGGACAGGGCGGAGACAGCACTGGACAGCAACCCGGCGAATCTGTGGAGAGAC 427	
OY	181 CGTGTACAGGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGTCCTCGAAGAGGAG 240	
DB	426 CGTGTACAGGAGCGGGTGTATGACCGAGCTGAGTAGAAAAACGTCCTCGAAGAGGAG 367	
OY	241 GAGGATCATGTATGCGCCCGAAGTAGACTCTGCAGTCGTGCTTGGGTTGGCGGAGC 300	
DB	366 GAGGATCATGTATGCGCCCGAAGTAGACTCTGCAGTCGTGCTTGGGTTGGCGGAGC 307	
OY	301 CATGATCTCTCGAATCTGTTGGGATCATCAGATTCAGGCCCAATGTCAACAATCAGCCC 360	
DB	306 CATGATCTCTCGAATCTGTTGGGATCATCAGATTCAGGCCCAATGTCAACAATCAGCCC 247	
OY	361 TGGCGACAGACAGCAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACAG 420	

Db	246	TGGCGACAGCAGCAGGAGGAGACAGAAAGAAAAACACATGAGAACACAG	187
Oy	421	TAATTCGAATTAAACCATATAAATATTACCCCTCTGTCTGTACTGCCTCAAGAAAT	480
Db	186	TAAATTAATTAAMACCATTAATATTACCCCCCTCTGTCTGTACTGCCTCAAGAAAT	127
Oy	481	GGTACCAATTTTTCGTGTGACTTGACAGCTTTTTCGCACACAGAAGAGAAATTT	540
Db	126	GGTACCAATTTTTCGTGTGACTTGACAGCTTTTTCGCACACAGAAGAGAAATTT	67
Oy	541	AACACTGTTTCAAACCCGGGGAGTGTCTGTTTAAAGAAACCATTTAAATGCTTAG	600
Db	66	AACACTGTTTCAAACCCGGGGAGTGTCTGTTTAAAGAAACCATTTAAATGCTTAG	7
Oy	601	ACAGTG 606	
Db	6	ACAGTG 1	
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RESULT 5			
AI990500/c 616 bp mRNA linear EST_08-MAR-2000			
LOCUS DEFINITION ws40d07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:249661 3' similar to SW:G939_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39.; , mRNA sequence.			
ACCESSION AI990500			
VERSION AI990500.1 GI:5837381			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1 (bases 1 to 616)			
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
JOURNAL Unpublished (1997)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: www-bio.lnlnl.gov/dbrr/image/image.html Insert length: 1212 Std Error: 0.00 Seq primer: -40np from Gibco High quality sequence stop: 459. Location/Qualifiers 1..616 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:249661" /clone_lib="NCI CGAP GC6" /tissue_type="pooled germ cell tumors" /lab_host="DH10B" /note="Vector: pYT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HMP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."			
FEATURES			
source			
<hr/>			
BASE COUNT 120 a 182 c 147 g 167 t			
ORIGIN			
<hr/>			
Query Match 96.2%, Score 601.2; DB 9; Length 616;			

Best Local Similarity 99.5%: Pred. No. 7.4e-99;  
Matches 603; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 AGTTCCTCTGACAGAGACTGGCCGCGAGCGCAAGACAGCGGCGCTGCACAAAGCG 60
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Db 607 AGTTCCTCTGACAGAGACTGGCCGCGAGCGCAAGACAGCGGCGCTGCACAAAGCG 548
QY 61 GCGGCTGTGCGTGGTGGAGTGGCGCATGTAGCGGCGCGCTTCTGTGGTGGCGTGTG 120
    |||||||
Db 547 GCGGCTGTGCGTGGTGGAGTGGCGCATGTAGCGGCGCGCTTCTGTGGTGGCGTGTG 488
QY 121 CAGGACAGAGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
    |||||||
Db 487 CAGGACAGAGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 428
QY 181 CGGTACAGAGAGCGGCTGTGATGACCGAGCTGAGTAAAGAAAGCGTCCGAGAGGCGAG 240
    |||||||
Db 427 CGGTACAGAGAGCGGCTGTGATGACCGAGCTGAGTAAAGAAAGCGTCCGAGAGGCGAG 368
QY 241 GAGGATCATGTAGCGCCCGGAAGTAGGACCTGCTCAGTCTGTGGTGGCGCGCAGC 300
    |||||||
Db 367 GAGGATCATGTAGCGCCCGGAAGTAGGACCTGCTCAGTCTGTGGTGGCGCGCAGC 308
QY 301 CATGATCTCTCCGATCTGTGGTGGCGATCCAGCATACGCCAATGTACACAAATCAGCCC 360
    |||||||
Db 307 CATGATCTCTCCGATCTGTGGTGGCGATCCAGCATACGCCAATGTACACAAATCAGCCC 248
QY 361 TGGGACAGACAGCAGAGGAGGAGAGACAGAGAAAGAAAGACAGCATGAGAACAGAG 420
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Db 247 TGGGACAGACAGCAGAGGAGGAGAGACAGAGAAAGAAAGACAGCATGAGAACAGAG 188
QY 421 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCT 480
    |||||||
Db 187 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 128
QY 481 GGTACCAATTTTACAGTGTGAGCTTGACACTTCTTTTGCACAAAGCAAGAGAAATTT 540
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Db 127 GGTACCAATTTTACAGTGTGAGCTTGACACTTCTTTTGCACAAAGCAAGAGAAATTT 68
QY 541 AACACTGTTTCAAAACCGGCGGAGTGTGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
    |||||||
Db 67 AACACTGTTTCAAAACCGGCGGAGTGTGCTGTGTTAAAGAAAGACATTAATGCTTTAG 8
QY 601 ACAAGTG 606
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Db 7 ACAAGTG 2

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RESULT 6  
AM590950/c 649 bp mRNA linear EST 22-MAR-2000  
LOCUS hg51612.x1 NCI-CGAP GC6 Homo sapiens cDNA clone IMAGE:2949166 3'  
DEFINITION similar to SW:GP39, HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR  
GPR39, mRNA sequence.

ACCESSION AM590950  
VERSION AM590950.1 GI:7278094  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 649)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonafide, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILUML at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

Possible reversed clone: similarity on wrong strand  
Seq primer: -400P from Gibco  
High quality sequence stop: 457.  
Location/Qualifiers

FEATURES  
source

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/db\_xref="taxon:9606"  
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/clone\_1bp="NCI-CGAP GC6"  
/issue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"

/note="Vector: pT73D-Pac (pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
from the normalized library NCI-CGAP GC4 was prepared, and  
ss circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneds  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonafide."

BASE COUNT 132 a 189 c 155 g 173 t  
ORIGIN

Query Match 96.2%: Score 601.2; DB 10; Length 649;  
Best Local Similarity 99.5%: Pred. No. 7.3e-99;  
Matches 603; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 AGTTCCTCTGACAGAGACTGGCCGCGAGCGCAAGACAGCGGCGCTGCACAAAGCG 60
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Db 607 AGTTCCTCTGACAGAGACTGGCCGCGAGCGCAAGACAGCGGCGCTGCACAAAGCG 548
QY 61 GCGGCTGTGCGTGGTGGAGTGGCGCATGTAGCGGCGCGCTTCTGTGGTGGCGTGTG 120
    |||||||
Db 547 GCGGCTGTGCGTGGTGGAGTGGCGCATGTAGCGGCGCGCTTCTGTGGTGGCGTGTG 488
QY 121 CAGGACAGAGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
    |||||||
Db 487 CAGGACAGAGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 428
QY 181 CGGTACAGAGAGCGGCTGTGATGACCGAGCTGAGTAAAGAAAGCGTCCGAGAGGCGAG 240
    |||||||
Db 427 CGGTACAGAGAGCGGCTGTGATGACCGAGCTGAGTAAAGAAAGCGTCCGAGAGGCGAG 368
QY 241 GAGGATCATGTAGCGCCCGGAAGTAGGACCTGCTCAGTCTGTGGTGGCGCGCAGC 300
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Db 367 GAGGATCATGTAGCGCCCGGAAGTAGGACCTGCTCAGTCTGTGGTGGCGCGCAGC 308
QY 301 CATGATCTCTCCGATCTGTGGTGGCGATCCAGCATACGCCAATGTACACAAATCAGCCC 360
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Db 307 CATGATCTCTCCGATCTGTGGTGGCGATCCAGCATACGCCAATGTACACAAATCAGCCC 248
QY 361 TGGGACAGACAGCAGAGGAGGAGAGACAGAGAAAGAAAGACAGCATGAGAACAGAG 420
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QY 421 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCT 480
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Db 187 TAAATGAATAAAACCATTAATATTTAGCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 128
QY 481 GGTACCAATTTTACAGTGTGAGCTTGACACTTCTTTTGCACAAAGCAAGAGAAATTT 540
    |||||||
Db 127 GGTACCAATTTTACAGTGTGAGCTTGACACTTCTTTTGCACAAAGCAAGAGAAATTT 68
QY 541 AACACTGTTTCAAAACCGGCGGAGTGTGCTGTGTTAAAGAAAGACATTAATGCTTTAG 600
    |||||||
Db 67 AACACTGTTTCAAAACCGGCGGAGTGTGCTGTGTTAAAGAAAGACATTAATGCTTTAG 8
QY 601 ACAAGTG 606

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Db      7 ACAGTG 2
|||||
RESULT 7
LOCUS   BF439382/c 696 bp mRNA linear EST 30-MAR-2001
DEFINITION ncbi39382.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3272627 3' similar to SW:GP39_HUMAN O43194 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR39. ; mRNA sequence.
ACCESSION BF439382
VERSION   BF439382.1 GI:11451899
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           This clone is available royalty-free through LNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Seq primer: -40UP from Gibco
           High quality sequence stop: 459.
FEATURES
   source
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       /organism="Homo sapiens"
       /db_xref="taxon:9606"
       /clone="IMAGE:3272627"
       /clone_1lb="Soares_NSF_F8_9W_OT_PA_P_S1"
       /lab_host="DH10B"
       /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
       a modified polylinker; Site_1: Not I; Site_2: Eco RI;
       Equal amounts of plasmid DNA from five normalized
       libraries were mixed, and ss circles were made in vitro.
       Following HAP purification, this DNA was used as tracer in
       a subtractive hybridization reaction. The driver was
       PCR-amplified cDNAs from pools of 5,000 clones made from
       the same 5 libraries. The pools consisted of the following
       libraries and cloneIDs: Soares NBHSF pool 1:
       309384-310919, 323208-325895 Soares NB2HP pool 1:
       145032-147335, 147720-148103, 148872-149255, 15002 -
       150407, 151176-152327 Soares NB2HP-9W pool 1:
       758280-760583, 772104-774407 Soares NBHPA pool 1:
       304776-306311, 320136-322823, 326280-326663 Soares NBHOT
       pool 1: 723720-726407, 739080-740999 Subtraction by Bento
       Soares and M. Fatima Bonaldo."
BASE COUNT 138 a 202 c 164 g 192 t
ORIGIN
Query Match 96.1%; Score 600.8; DB 12; Length 696;
Best Local Similarity 99.5%; Pred. No. 8.3e-99;
Matches 602; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 8 CTTGCAGAGAGCTGGCGCCGCGGAGAGAGACGAGCGGCGCTGCACAAAGCGGCGTG 67
DB 1 CTTGCAGAGAGCTGGCGCCGCGGAGAGAGACGAGCGGCGCTGCACAAAGCGGCGTG 67
DB 605 CCTGCAGAGAGCTGGCGCCGCGGAGAGAGACGAGCGGCGCTGCACAAAGCGGCGTG 546
QY 68 TCGGTGATGATGCGCATGTACGCGCGAGCGGCTTCTCGGTGCGGTGCGTCCAGCGAC 127
DB 545 TCGGTGATGATGCGCATGTACGCGCGAGCGGCTTCTCGGTGCGGTGCGTCCAGCGAC 486
QY 128 AGCGCGACACAGACACCTGCAGAGAACACCCGCGAAGCTGTGCGAGAGACACCGTGTAC 187
DB 485 AGCGCGACACAGACACCTGCAGAGAACACCCGCGAAGCTGTGCGAGAGACACCGTGTAC 426
QY 188 AGGAGCGGTTGATGACCGAGCTGAGGTGAGAAAACGCTCCGAGAGAGGAGGAGATC 247
DB 425 AGGAGCGGTTGATGACCGAGCTGAGGTGAGAAAACGCTCCGAGAGAGGAGGAGATC 366

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QY 248 ATGTACCGCCGGAAGTAGACCTCTCTCAGTCGCTGGGTTTGGCCGAGCCATGATC 307
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DB 305 CTCGCAATCTGTTGGGCATCCAGCATACGCGCCATATGTCACAACATCAGCCCTGGCGAG 246
QY 368 ACACGAGCAGAGGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGACACAGTAATATG 427
DB 245 ACACGAGCAGAGGAGGAGAGACAGAGAAAAGAAAACACAGCATGAGACACAGTAATATG 186
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QY 488 ATTTTCAGTGTGGACCTTGACAGCTTCTTTTGGCCACAGCAAGAGAGATTTTACACTG 547
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QY 548 TTTCAACCCGCGGAGGAGTGGCTGTGTTAAAGAACATTAATGCTTTAGACAGTG 607
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QY 608 AAAAA 612
DB 5 AAAAA 1
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DEFINITION x440h05.x1 NCI CGAP Brn50 Homo sapiens cDNA clone IMAGE:2620569 3'
similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39. ; mRNA sequence.
ACCESSION AM149665
VERSION   AM149665.1 GI:6197561
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 690)
AUTHORS  NCI/NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute / National Institute of Neurological
           Disorders and Stroke, Brain Tumor Genome Anatomy Project
           (CGAP/BRGAP), Tumor Gene Index
JOURNAL   Unpublished (1998)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.
           CDNA library Preparation: M. Bento Soares, Ph.D.
           CDNA library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           www.bio.llnl.gov/bbrp/image/image.html
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       /clone="IMAGE:2620569"
       /clone_1lb="NCI CGAP Brn50"
       /tissue_type="medulloblastoma"
       /lab_host="DH10B (phage resistant)"
       /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
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       medulloblastoma tumor tissue, and was then primed with a

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Db 123 GGTACCAATTTTTCAGTGTGGAGCTTGACAGCTTTTTCGCCAAGCAAGAGAGATTT 64
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Db 63 AACACTGTTTCAACCCGGGGAGATTGCTGTGTTAAAGAACATTAATGCTTTAA 4
Oy 601 ACA 603
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Db 3 ACA 1

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DEFINITION similar to SW:GP9_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.; mRNA sequence.
ACCESSION BE858216 GI:10372861
VERSION BE858216
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 551)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL, send email to:
info@image.llnl.gov
Seq primer: -400p from Glibco
High quality sequence stop: 490.
Location/Qualifiers
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/clone="IMAGE:3306972"
/clone_lib="NCI-CGAP_Brn23"
/tissue_type="gliblastoma (pooled)"
/lab_host="DH10B"
/note="organ: brain; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTATCAATCTGAGTGTGAGCGCGCCCATATCTTTTCTTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia); digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 110 a 161 c 128 g 152 t
ORIGIN

Query Match 87.7%; Score 548.4; DB 12; Length 551;
Best Local Similarity 99.8%; Pred. No. 2.5e-89;
Matches 549; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 57 ACCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 116
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Db 551 ACCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
Oy 117 GCTGACGACAGCGGCGGACGACACCTGACGACGACGACGACGACGACGACG 176

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Db 491 GCTGACGACAGCGGCGGACAGACAGCTTGACAGAACCCGCCGAACCTGCTGCGAG 432
Oy 177 AACACCTGTACAGAGAGCGGCTTATACCCGAGTGAAGTAAAGAAACGCTCCGAAAG 236
Db 431 AACACCTGTACAGAGAGCGGCTTATACCCGAGTGAAGTAAAGAAACGCTCCGAAAG 372
Oy 237 GGAGAGAGATCATGTACGCGCCGGAATAGACCTCCAGTCTGCTTGGGTTGGCCG 296
Db 371 GGAGAGAGATCATGTACGCGCCGGAATAGACCTCCAGTCTGCTTGGGTTGGCCG 312
Oy 297 CAGCCATGATCTCTCGAATCTGCTTGGCATCCAGATACGGCCAAATGTCACAAATCA 356
Db 311 CAGCCATGATCTCTCGAATCTGCTTGGCATCCAGATACGGCCAAATGTCACAAATCA 252
Oy 357 GCCCTGGCAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Db 251 GCCCTGGCAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
Oy 417 ACAGTAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAG 476
Db 191 ACAGTAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGTCTTACTGCGCAG 132
Oy 477 AATGCTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCGACAGAGAGAGA 536
Db 131 AATGCTACCAATTTTTCAGTGTGAGCTTGACAGCTTCTTTGCGACAGAGAGAGA 72
Oy 537 ATTATACACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCT 596
Db 71 ATTATACACTGTTTCAACCCGGGGAGTGGCTGTGTTAAAGAAACCATTAATGCT 12
Oy 597 TTAGACAGTG 606
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Db 11 TTAGACAGTG 2

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LOCUS nacb0b12.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:340591.3'
DEFINITION similar to SW:GP9_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
GPR39.; mRNA sequence.
ACCESSION BF939693 GI:12357104
VERSION BF939693
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 540)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL, send email to:
info@image.llnl.gov
Seq primer: -400p from Glibco
High quality sequence stop: 467.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:340591"

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RESULT	13	
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VERSION	U1-E-DW0-aggm-j-01-0-U1.3'	
KEYWORDS	BM667957	Homo sapiens cDNA clone
SOURCE	BM667957.1	GI:18975788
ORGANISM	EST.	
	human.	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 538)	
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.	
TITLE	Normalization and subtraction: two approaches to facilitate gene	
	discovery	
JOURNAL	Genome Res.	6 (9), 791-806 (1996)
MEDLINE	97044477	
COMMENT	Contact: Soares, MB	



Fri Nov 8 18:56:56 2002

us-09-970-966-210.std.rst

Page 12

Search completed: November 7, 2002, 15:02:36  
Job time : 843.306 secs

942

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 16:56:48 ; Search time 418.22 Seconds

(without alignments)  
11441.218 Million cell updates/sec

Title: US-09-970-966-211

Perfect score: 1619

Sequence: 1 ggcacatttcgcgactgt.....aaaaaaaaaaaaaaaaaaaaa 1619

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2108461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hlg\_hum:\*

31: em\_hlg\_inv:\*

32: em\_hlg\_other:\*

33: em\_hlg\_mus:\*

34: em\_hlg\_pin:\*

35: em\_hlg\_rod:\*

36: em\_hlg\_mam:\*

37: em\_hlg\_vrt:\*

38: em\_sy:\*

39: em\_hgo\_hum:\*

40: em\_hgo\_mus:\*

41: em\_hgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1427	88.1	1832	9	AK094501
2	1310	80.9	129676	9	AC079773
3	1264	78.1	1524	6	AX358762
4	1264	78.1	1524	6	AX362255
5	1149	71.0	2528	6	AX319944
6	1014	62.6	1890	6	AX136281
7	648	40.0	946	6	BC017318
8	541	33.4	826	6	BC011449
9	386	23.8	1362	6	AX319942
10	386	23.8	1362	9	AF034633
11	364	22.6	587	6	AX136698
12	364	22.5	444	6	AX150120
13	315	19.5	369	6	AX093381
14	310	19.1	396	6	AX093191
15	250	15.4	591	6	AX136556
16	142	8.8	14731	9	AC010974
17	47	2.9	209885	2	AC124493
18	38	2.3	1797	10	AB041649
19	30	1.9	125703	2	AC123338
20	27	1.7	487	9	AF150733
21	27	1.7	1086	8	AF082874
22	27	1.7	1114	3	AY118358
23	27	1.7	1368	6	AX285020
24	27	1.7	1614	9	AK026521
25	27	1.7	2625	9	BC028978
26	27	1.7	3155	3	AY094780
27	27	1.7	48206	10	AL645986
28	27	1.7	92874	2	AC112072
29	27	1.7	127524	2	AL807806
30	27	1.7	138851	10	AL645938
31	27	1.7	151602	2	AC126321
32	27	1.7	170255	9	AC027118
33	27	1.7	179364	2	AC074245
34	27	1.7	195782	9	AC074389
35	27	1.7	209572	2	AC099615
36	27	1.7	212690	2	AC110232
37	27	1.7	214411	2	AC069297
38	27	1.7	217929	9	AL133395
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40	26	1.6	1409	8	AF176571
41	26	1.6	2481	6	AX056994
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43	26	1.6	3889	9	BC034500
44	26	1.6	7940	9	AF044209
45	26	1.6	94336	9	AC005250

# ALIGNMENTS

RESULT 1

LOCUS AK094501 1832 bp mRNA PRI 15-JUL-2002

DEFINITION Homo sapiens cDNA FLJ37182 f1s, clone BRAL22001350, weakly similar to Homo sapiens Gz-selective GTPase-activating protein (RGS20) mRNA.

ACCESSION AK094501

VERSION AK094501.1 GI:21753575

KEYWORDS OLIGO capping; f1s (full insert sequence).

SOURCE Homo sapiens alzheimer cortex cDNA to mRNA, clone\_1ib:BRAL22

ORGANISM Homo sapiens

REFERENCE 1

Maruyama; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Primates; Catarrhini; Homnidae; Homo.

AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,  
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,  
Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,  
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,  
Matsushima, M., Murakawa, K., Kanehori, K., Takahashi, F., A.,  
Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuko, Y., Nagai, K.,  
and Isogai, T.

TITLE NEDO human cDNA sequencing project

REFERENCE Unpublished

AUTHORS 2 (bases 1 to 1832)

TITLE Isogai, T. and Yamamoto, J.

JOURNAL Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FUJ Project(HRI Team); 2-6-7  
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
(E-mail:genomshri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: HRI and RAB.

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/note="Cloning vector: PME18SFL3"  
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CDS  
BASE COUNT 411 a 501 c 513 g 407 t

ORIGIN

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Matches 1597; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db CCAACCCCTCCGCAATGTTGTTTCCAGCCCTGGCCCCCAACCCCACTCCCTAGTGA 714  
Qy 481 GTTCTCTCGGGTGTCTCTTATTTCTGAGTGAAGAGCGAGTCCGTCTCTTTGTT 540  
Db GTTCTCTCGGGTGTCTCTTATTTCTGAGTGAAGAGCGAGTCCGTCTCTTTGTT 774  
Qy 541 CCTGTGCAATATATGAAAGAGCTCGGTAAAGCAATTTCTGATTAATTTACCTGAT 600  
Db CCTGTGCAATATATGAAAGAGCTCGGTAAAGCAATTTCTGATTAATTTACCTGAT 834  
Qy 601 TTTTCAATATGTTGAAAGAGAGTGTGAGAAAGTTCAACCCCATGTCTGTATAC 660  
Db TTTTCAATATGTTGAAAGAGAGTGTGAGAAAGTTCAACCCCATGTCTGTATAC 894  
Qy 661 CGAGTCAAGGCCAGGCTGGCAGAGTCACTCTTAGAAGTCACTGAGTGGGCATCTGCC 720  
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Qy 841 ACATTCAAACTTCATGCTCTCTGAAAAACATTTCTGACAGAGAAATGCTGTGCTGCC 900  
Db ACATTCAAACTTCATGCTCTCTGAAAAACATTTCTGACAGAGAAATGCTGTGCTGCC 1134  
Qy 901 CTGAGTTGGGCTCTATGATCTGAGACATCAATGACGAGGAACTTAGCTGGGCTGGCCT 960  
Db CTGAGTTGGGCTCTATGATCTGAGACATCAATGACGAGGAACTTAGCTGGGCTGGCCT 1194  
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Db CCCTGGAAGAGTCTTAAAGAAATCTTCTCAGTTCTCTTCCAGAGAGTGGCGCGGG 1254  
Qy 1021 ACGGAGAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGCTGTGAGTGGCATGTA 1080  
Db ACGGAGAGAGCAACGGGCGCTGCACAAAGCGGGCGCTGTGCTGTGAGTGGCATGTA 1314  
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Db CTGAGTGAAGAAAGCTCTCCGAGAAAGGAGAGGATATGATGACCCCGGAATGAGAC 1493  
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Db CCCCTGTGTTGCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1733

OY 1501 CAGCTTCTTTGCCAAGCAGAGACATTTAACTGTTTCAAAACCCGGGGAGTTGG 1560  
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 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 AUTHORS Sulston, J.E. and Waterston, R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 98063792  
 PUBMED 9847074

REFERENCE  
 AUTHORS Shah, N., Meyer, R., Boyer, E. and Dignan, G.  
 TITLE The sequence of Homo sapiens BAC clone RP11-258B17  
 JOURNAL Unpublished (2001)  
 REFERENCE  
 AUTHORS Waterston, R.H.  
 TITLE Submitted (10-SEP-2000) Genome Sequencing Center, Washington  
 JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE  
 AUTHORS Waterston, R.H.  
 TITLE Submitted (09-AUG-2001) Genome Sequencing Center, Washington  
 JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA

REFERENCE  
 AUTHORS Waterston, R.H.  
 TITLE Submitted (09-JAN-2002) Department of Genetics, Washington  
 JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Aug 9, 2001 this sequence version replaced gi:14488388.

COMMENT  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: W0GSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@wustl.edu](mailto:sapiens@wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_NH0258B17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis

MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://pacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-1122; the clone sequenced to the right is RP11-159N20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-258B17; actual end is at base position 60003 of RP11-159N20.

#### FEATURES

##### SOURCE

RP11-258B17 contains a single plasmid region from 1230 to 1239.  
 Location/Qualifiers

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 /db\_xref="taxon:9606"  
 /chromosome="2"  
 /map="2"  
 /clone="RP11-258B17"  
 /clone\_1bp="RPCT-11"  
 488..779  
 /rpt\_family="MER2\_type"  
 941..1253  
 /note="match to EST BF804362 (NID:gi2133351)"  
 1388..1412  
 /rpt\_family="AT-rich"  
 1397..3331  
 /rpt\_family="L1"  
 2346..2370  
 /rpt\_family="(TTTG)n"  
 9444..9466  
 /rpt\_family="AT-rich"  
 11961..11969  
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 12697..12739  
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 14016..14171  
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 14175..14337  
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 15532..15842  
 /rpt\_family="Alu"  
 16269..16605  
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 16629..16712  
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 16810..16939  
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 17238..17381  
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 17508..17966  
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 18190..18453  
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 18933..19074  
 /rpt\_family="ERV1"  
 19144..19250  
 /rpt\_family="ERV1"  
 19260..19628  
 /rpt\_family="ERV1"  
 20104..20145  
 /rpt\_family="(TG)n"  
 20170..20305

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/rpt_family="MERL_type"
20618..20756
repeat_region /rpt_family="MERL_type"
21300..21325
repeat_region /rpt_family="(A)n"
21428..21796
misc_feature /note="match to EST BF821779 (NID:g12161303)"
23084..23328
repeat_region /rpt_family="MIR"
23667..24256
repeat_region /rpt_family="Alu"
25108..25208
repeat_region /rpt_family="MIR"
25485..25805
repeat_region /rpt_family="MALR"
26417..26463
repeat_region /rpt_family="ERV1"
26466..26655
repeat_region /rpt_family="MER2_type"
26656..27047
repeat_region /rpt_family="MALR"
27048..27149
repeat_region /rpt_family="MER2_type"
27246..27403
repeat_region /rpt_family="(TA)n"
27309..27380
repeat_region /rpt_family="L1"
27403..27671
repeat_region /rpt_family="Alu"
27698..27749
repeat_region /rpt_family="MER2_type"
27750..27904
repeat_region /rpt_family="(TA)n"
27926..28052
repeat_region /rpt_family="L2"
28052..28667
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28834..28958
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29414..29696
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29727..30221
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30363..30543
repeat_region /rpt_family="MERL_type"
30738..30919
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31494..31783
repeat_region /rpt_family="Alu"
32028..32488
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32053..32080
repeat_region /rpt_family="(GA)n"
32667..32787
repeat_region /rpt_family="MIR"
34079..34164
repeat_region /rpt_family="L2"
34271..34348
repeat_region /rpt_family="MERL_type"
34409..34703
misc_feature /note="match to EST BG956501 (NID:g14374672)"
35346..35374
repeat_region /rpt_family="(TTTGG)n"
35361..35676
repeat_region /rpt_family="Alu"

Query Match 80.9%: Score 1310; DB 9; Length 129676;
Best Local Similarity 99.9%: Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 230 TACAGTCCCTTGTGCTCCCGACGGAAGTGAAGTGAAGTTCATGAGTGTGCAACACC 289
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Db 120681 TACAGTCCCTTGTGCTCCCGACGGAAGTGAAGTGAAGTTCATGAGTGTGCAACACC 120682

QY 230 CCTCTTTGTAAAGGGGCAAGGGCCCAAGAAAGGGAAGTTGTGCTCGGCTCAGGCCA 349
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Db 120621 CCTCTTTGTAAAGGGGCAAGGGCCCAAGAAAGGGAAGTTGTGCTCGGCTCAGGCCA 120662

QY 350 GGGCTCCGACACCATCCTGTCTGCTCAAAATTAAGCCCTCTTGGGCACTGCTGAAGC 409
|||||
Db 120561 GGGCTCCGACACCATCCTGTCTGCTCAAAATTAAGCCCTCTTGGGCACTGCTGAAGC 120502

QY 410 TGAAGAGATGCGACCCCTCCCTGCAATGCTTCAGCCCTCGGCCCAACCCCAACC 469
|||||
Db 120501 TGAAGAGATGCGACCCCTCCCTGCAATGCTTCAGCCCTCGGCCCAACCCCAACC 120442

QY 470 TCCCTGAGTGAATTTCTCTGCTGCTCTTTTATCTGGGTAGGAGCGGAGTCCGTGT 529
|||||
Db 120441 TCCCTGAGTGAATTTCTCTGCTGCTCTTTTATCTGGGTAGGAGCGGAGTCCGTGT 120382

QY 530 TCTCTTTTGTCTCTGCAAAATTAAGAGAGCTCGCTTAAGCATTCGTAATTAATTCG 589
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Db 120381 TCTCTTTTGTCTCTGCAAAATTAAGAGAGCTCGCTTAAGCATTCGTAATTAATTCG 120322

QY 590 CCTGACTGAATTTTCAATGATGATGATGAAGAGAGTGAAGTGAAGTGAAGTGAAGT 649
|||||
Db 120321 CCTGACTGAATTTTCAATGATGATGATGAAGAGAGTGAAGTGAAGTGAAGTGAAGT 120262

QY 650 GTCTGTGTAAACCGAGTCAAGGCCAGGCTGCGAGAGTCAAGTCTTGAAGTCAAGT 709
|||||
Db 120261 GTCTGTGTAAACCGAGTCAAGGCCAGGCTGCGAGAGTCAAGTCTTGAAGTCAAGT 120202

QY 710 GGGCATCTGCTCTTTGTAAAGCTCCAGTGCATTCATTCCTGCTGAGGGCATAGTT 769
|||||
Db 120201 GGGCATCTGCTCTTTGTAAAGCTCCAGTGCATTCATTCCTGCTGAGGGCATAGTT 120142

QY 770 GAGACTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 829
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Db 120141 GAGACTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120082

QY 830 TCCCTGCTTGAACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 889
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Db 120081 TCCCTGCTTGAACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 120022

QY 890 TGGTTTCGGCGCTGAGTGGGCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 949
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Db 120021 TGGTTTCGGCGCTGAGTGGGCTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 119962

QY 950 GGGCTGCGGCTGCTCTGAAAGTGTGAAGAAATCTTCTGAGTCTCTCTGACAGAGA 1009
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Db 119961 GGGCTGCGGCTGCTCTGAAAGTGTGAAGAAATCTTCTGAGTCTCTCTGACAGAGA 119902

QY 1010 CTGGCGCGCGGAGCGGAAGAGCAAGCGGCTGCAAAACCGGGGCTCTGCTGCTGGA 1069
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Db 119901 CTGGCGCGCGGAGCGGAAGAGCAAGCGGCTGCAAAACCGGGGCTCTGCTGCTGGA 119842

QY 1070 GTGGCGATGATGCGCGAGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129
|||||
Db 119841 GTGGCGATGATGCGCGAGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119782

QY 1130 CAGCACCTTGAACAGAACACCGCGGAATCTGCGAGAGACACCGTGAACAGAGCGGT 1189
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Db 119781 CAGCACCTTGAACAGAACACCGCGGAATCTGCGAGAGACACCGTGAACAGAGCGGT 119723

QY 1190 TGATGACCAAGCTGAGTGAAGAAAGCTCTCGAAGAAAGGAGAGAGATGATGATGATG 1249
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Db 119722 TGATGACCAAGCTGAGTGAAGAAAGCTCTCGAAGAAAGGAGAGAGATGATGATGATG 119663

QY 1250 GGAAGTAGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1309
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Db 119662 GGAAGTAGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119603
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QY	1310	GGGGGCAATCCACATTCATGGCCAAATGCACAAATACACCCGCGGCGACAGACGAGCAG	1369
Db	119602	GTTTGGGCATCCACATTCATGGCCAAATGCACAAATACACCCGCGGCGACAGACGAGCAG	119543
QY	1370	GAGGAGAGACAGAGAAAAAACAACACAGCATGAGACACAGTAAATGAATAAACCAT	1429
Db	119542	GAGGAGAGACAGAGAAAAAACAACACAGCATGAGAAACACAGTAAATGAATAAACCAT	119483
QY	1430	AAATATTTTACCCCTCTGTTCTGCTTACTGGCCAGAAATGTTCCCAATTTTCAGT	1489
Db	119482	AAATATTTTACCCCTCTGTTCTGCTTACTGGCCAGAAATGTTCCCAATTTTTCAGT	119423
QY	1490	GTTGGACTTGCACAGCTTCTTTTGCACACAGACAGAGAAATTTAACACTGTTTCAAAACC	1549
Db	119422	GTTGGACTTGCACAGCTTCTTTTGCACACAGACAGAGAAATTTAACACTGTTTCAAAACC	119363
QY	1550	GGGGGAGTTCGCTGTGTTAAAGAANAACATTAATGCTTTAGACAGTGA	1600
Db	119362	GGGGGAGTTCGCTGTGTTAAAGAANAACATTAATGCTTTAGACAGTGA	119312

### RESULT 3

LOCUS	AX558762	1524 bp	DNA
DEFINITION	Sequence 15 from Patent WO0139383.		linear
ACCESSION	AX558762		
VERSION	AX558762.1	GI:18675282	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		

## AUTHORS

**TITLE** Secreted and transmembrane polypeptides and nucleic acids encoding the same

**JOURNAL** Patent: WO 01/3983-A 15 13-DEC-2001;

## FEATURES

Location/Qualifiers  
1. .1524

**ORIGIN**

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321 a      433 c      435 g      335 t
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
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Query Match

Query Match	78.18;	Score 1264;	DB 6;	Length 1524;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 1384;	Conservative	0;	Mismatches 0;	Indels 1;
				Gaps 1

Oy	1	GGCAACCTTTTGGCGAATGTTCTTGCTCCAGGCTTGGACCTGCAATTCAGAGTCACCA	60
Db	141	GGCAACCTTTTGGCGAATGTTCTTGCTCCAGGCTTGGACCTGCAATTCAGAGTCACCA	200
Oy	61	GTGTGAAGAATTCACGCTGAAACAACGACCTGCTCCCGGAGTTCATTTGAAATTGCAC	120
Db	201	GTGTGAAGAATTCACGCTGAAACAACGACCTGCTCCCGGAGTTCATTTGAAATTGCAC	260
Oy	121	GGTGAACCTTTAAAGCATGTGTCAAGAAAGATATGGAGCAAAAGTCCGGGATCATGTA	180
Db	261	GGTGAACCTTTAAAGCATGTGTCAAGAAAGATATGGAGCAAAAGTCCGGGATCATGTA	320
Oy	181	CCGCAAGTCTGTGATCATATAGGGGGCTGTCTATGCGCTCGCGGGTACCAAGTCCTT	240
Db	321	CCGCAAGTCTGTGATCATATAGGGGGCTGTCTATGCGCTCTGCGGGTACCAAGTCCTT	380
Oy	241	CTGCTCCCCAGGGAACCTGAACCTCAGTTTGATCAGCTGTGCAACACCCCTCTTTGTAA	300
Db	381	CTGCTCCCCAGGGAACCTGAACCTCAGTTTGATCAGCTGTGCAACACCCCTCTTTGTAA	440
Oy	301	CGGGCCAAAGGCCCAAGAAAGGGAAGTCTGCTCGGGCCCTCAGGCCAAGGCTCCGGCAC	360

Db	441	CGGGCCAA6GCCCAAGAAAAGGGAAGTTCTGGCTGGGCCCTCAGGGCAGGGCTCCGGAC	500
Qy	361	CACCATCTCTGTTCTCTCAAAATTAAGCCCTCTTCCTGGCACACTGCTGAAGCTGAAGAGATG	420
Db	501	CACCATCTCTGTTCTCTCAAAATTAAGCCCTCTTCCTGGCACACTGCTGAAGCTGAAGAGATG	560
Qy	421	CCACCCTCCCGAANTGTTCTTCCAGGCCCTGGCCCCCAACCCCGCACCTCCCTGAGTGA	480
Db	561	CCACCCTCCCGAANTGTTCTTCCAGGCCCTGGCCCCCAACCCCGCACCTCCCTGAGTGA	620
Qy	481	GTTTCTTCGGGTGTCCTTTTAATTCGGGTAGGGAGCCGGAGTCGGTGTCTCTTTTGT	540
Db	621	GTTTCTTCGGGTGTCCTTTTAATTCGGGTAGGGAGCCGGAGTCGGTGTCTCTTTTGT	680
Qy	541	CCTGTGCAAAATTAATGAAGAAGCTCGGTAAAGCAATTCGTGATAAATTCAGCCTCACTGAAT	600
Db	681	CCTGTGCAAAATTAATGAAGAAGCTCGGTAAAGCAATTCGTGATAAATTCAGCCTCACTGAAT	740
Qy	601	TTTTCAGTATGTACTTGAAGGAAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC	660
Db	741	TTTTCAGTATGTACTTGAAGGAAGAGAGTGAAGTGAAGTTCACCCCATCTCTGTGAAC	800
Qy	661	CGGAGTCAGAGCCAGGCTGGCAGAGTCAGTCCTTAAGAACACACCTGAGAGTGGGCACTCGCC	720
Db	801	CGGAGTCAGAGCCAGGCTGGCAGAGTCAGTCCTTAAGAACACACCTGAGAGTGGGCACTCGCC	860
Qy	721	TTTTGTAAAGCCCTCAGTGTCCATTCCTCATCCCTGATGGGGGCAATGTTTGAAGCTGAGA	780
Db	861	TTTTGTAAAGCCCTCAGTGTCCATTCCTCATCCCTGATGGGGGCAATGTTTGAAGCTGAGA	920
Qy	781	GTGAGAGTACGTTTTTCTTAAGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGTTG	840
Db	921	GTGAGAGTACGTTTTTCTTAAGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGTTG	980
Qy	841	ACATTCAAACTTCATGCTCTCTGAAAAACAATTCCTGAGAGAGAAATTTGGTTTCGCG	900
Db	981	ACATTCAAACTTCATGCTCTCTGAAAAACAATTCCTGAGAGAGAAATTTGGTTTCGCG	1040
Qy	901	CTGAGTTGGGCTCTAGTGACTCGAGACTCAATGACTGGGACTTGAAGCTGGGGCTCGGCT	960
Db	1041	CTGAGTTGGGCTCTAGTGACTCGAGACTCAATGACTGGGACTTGAAGCTGGGGCTCGGCT	1100
Qy	961	CGCTCTGAAAAGTCTTAAAGAAATTTCTCAATTCCTCTTGCAGAGGACTGGCGCCGGG	1020
Db	1101	CGCTCTGAAAAGTCTTAAAGAAATTTCTCAATTCCTCTTGCAGAGGACTGGCGCCGGG	1160
Qy	1021	ACGGGAAGAGCAACGGGGCCCTGCACAAAGGGGGCGCTGTCGGGTGGAGTGGCCATGTA	1080
Db	1161	ACGGGAAGAGCAACGGGGCCCTGCACAAAGGGGGCGCTGTCGGGTGGAGTGGCCATGTA	1220
Qy	1081	CGCGCAGCGCTTCCTGTGGTTGGCTGTGCGACAGCGACAGGCGGACACAGCACTCTTGC	1140
Db	1221	CGCGCAGCGCGCTTCCTGTGGTTGGCTGTGCGACAGCGACAGGCGGACACAGCACTCTTGC	1279
Qy	1141	ACGAACACCCCGGAAACTGTCTGAGAGACACCGTGTACAGGAGCGGGTTGATACCGAG	1200
Db	1280	ACGAACACCCCGGAAACTGTCTGAGAGACACCGTGTACAGGAGCGGGTTGATACCGAG	1359
Qy	1201	CTGAGGTAGAAAACGTCTCCGGAAGGGGAGGAGATCTATACGCCCGGAAGTAAAGAC	1260
Db	1340	CTGAGGTAGAAAACGTCTCTCCGGAAGGGGAGGAGATCTATACGCCCGGAAGTAAAGAC	1399
Qy	1261	CTGCTTCACATCGTGTGGGTTTGGCGCGACGATGATCTCCGAATCTGGTTGGGATC	1320
Db	1400	CTGCTTCACATCGTGTGGGTTTGGCGCGACGATGATCTCCGAATCTGGTTGGGATC	1459
Qy	1321	CAGCATACGGCCAATGTCAACAACATCAGCCCTGGGCGACACGAGCAGAGAGGAGAGAC	1380
Db	1460	CAGCATACGGCCAATGTCAACAACATCAGCCCTGGGCGACACGAGCAGAGAGGAGAGAC	1519
Qy	1381	AGAGA 1385	
Db	1520	AGAGA 1524	

RESULT 4  
AX362255 1524 bp DNA linear PAT 15-FEB-2002  
LOCUS Sequence 15 from Patent WO0208288.  
DEFINITION AX362255  
ACCESSION AX362255.1 GI:18694585  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
1 Baker, K.P., Desnoyers, L., Gerltzen, M.E., Goddard, A.,  
Godoski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Matenabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0208288-A 15 31-JAN-2002;  
Genentech, Inc. (US)  
Location/Qualifiers  
1. 1524  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

FEATURES  
source

BASE COUNT 321 a 433 c 435 g 335 t

ORIGIN

Query Match 78.1%; Score 1264; DB 6; Length 1524;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1344; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGACCTTTTGGGATTTGCTTGTCCAGGCTTTGCGCTCAAAATCCAGTGTACCA 60  
DB 141 GCGACCTTTTGGGATTTGCTTGTCCAGGCTTTGCGCTCAAAATCCAGTGTACCA 200

QY 61 GTGTGAAGATTCAGCTGAAACAACAGCTCTCTCCCGAGTTCATTGTGAATGAC 120  
DB 201 GTGTGAAGATTCAGCTGAAACAACAGCTCTCTCCCGAGTTCATTGTGAATGAC 260

QY 121 GTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAGTCCGGATCATGTA 180  
DB 261 GTGAAGCTTCAAGACATGTGTGAGAAAGATGATGAGCAAGTCCGGATCATGTA 320

QY 181 CGCGAAGTCTGTGATCATCAGCGGCTGTCTCATCGCCCTGCGGGATACAGTCTT 240  
DB 321 CGCGAAGTCTGTGATCATCAGCGGCTGTCTCATCGCCCTGCGGGATACAGTCTT 380

QY 241 CTGCTCCCGAGGAAATGAACTGATTTGATCAGCTGCTGCAACACCCCTTTGTAA 300  
DB 381 CTGCTCCCGAGGAAATGAACTGATTTGATCAGCTGCTGCAACACCCCTTTGTAA 440

QY 301 CGGGCCCAAGGCCCAAGAAAGGGAGTTCTGCTCGGCCCTAGAGGCGAGGGCTCCGCAC 360  
DB 441 CGGGCCCAAGGCCCAAGAAAGGGAGTTCTGCTCGGCCCTAGAGGCGAGGGCTCCGCAC 500

QY 361 CACCATCTGTTCTCTCAAAATAGCCCTCTCTGCGACACATGCTGAAGCTGAAGAGATG 420  
DB 501 CACCATCTGTTCTCTCAAAATAGCCCTCTCTGCGACACATGCTGAAGCTGAAGAGATG 560

QY 421 CCAACCCCTCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCACTCTCTGATGTA 480  
DB 561 CCAACCCCTCTGATTTGTTCTTCCAGCCCTGCGCCCAACCCCACTCTCTGATGTA 620

QY 481 GTTCTTCTGAGTCTCTTTTATTTCTGGGATGAGGAGCGGAGTCCGTTCTTTGTT 540  
DB 621 GTTCTTCTGAGTCTCTTTTATTTCTGGGATGAGGAGCGGAGTCCGTTCTTTGTT 680

QY 541 CCTGTGCAATAATGAAGAAGCTCGGTAAGAATTCGTAATAATTCAGCTGACTGAAT 600  
DB 681 CCTGTGCAATAATGAAGAAGCTCGGTAAGAATTCGTAATAATTCAGCTGACTGAAT 740

QY 601 TTTCAATATGTAAGAGAGAGGTGAGTGAAGAGTTCCACCCCAATGCTGTGTAAAC 660

DB 741 TTTCAATATGTAAGAGAGAGGTGAGTGAAGAGTTCCACCCCAATGCTGTGTAAAC 800

QY 661 CGGAGTCAAGGCCAGGCTGCGACAGTCAATCTTGAAGTCACTAGAGTGGGATCTGCC 720  
DB 801 CGGAGTCAAGGCCAGGCTGCGACAGTCAATCTTGAAGTCACTAGAGTGGGATCTGCC 860

QY 721 TTTTGAAGGCTCCAGTGTGATTCATTCATCCCTGATGGGGGATAGTTGATGATGAGA 780  
DB 861 TTTTGAAGGCTCCAGTGTGATTCATTCATCCCTGATGGGGGATAGTTGATGATGAGA 920

QY 781 GTGAGTGAAGTCTTCTTGAAGGCTGAGGAGGCCAGTTCCACTCAAGCTCCCTGCTG 840  
DB 921 GTGAGTGAAGTCTTCTTGAAGGCTGAGGAGGCCAGTTCCACTCAAGCTCCCTGCTG 980

QY 841 ACATTCAACTTCAATGCTCTGTAAGAACCAATCTCTGAGCAGAAATTTGGCTTCCGC 900  
DB 981 ACATTCAACTTCAATGCTCTGTAAGAACCAATCTCTGAGCAGAAATTTGGCTTCCGC 1040

QY 901 CTGAGTGGGCTCTAGTCACTGAGACTCAATGACTGGGAGTCTGAGTGGGCTCGGCT 960  
DB 1041 CTGAGTGGGCTCTAGTCACTGAGACTCAATGACTGGGAGTCTGAGTGGGCTCGGCT 1100

QY 961 CGCTCTGAAAAAGTCTTGAAGAAATCTTCAATCTCTGAGCAGAAATTTGGCTTCCGC 1020  
DB 1101 CGCTCTGAAAAAGTCTTGAAGAAATCTTCAATCTCTGAGCAGAAATTTGGCTTCCGC 1160

QY 1021 ACCGGAAGACACACGGGCGCTGCAACAAAGGGGCGCTGTGTGTGATGAGTGGCATGTA 1080  
DB 1161 ACCGGAAGACACACGGGCGCTGCAACAAAGGGGCGCTGTGTGTGATGAGTGGCATGTA 1220

QY 1081 CGGCGAGGCGCTCTCTGAGTGGGCTGAGCAGCAGAGCGGCGACAGCACTTGC 1140  
DB 1221 CGGCGAGGCGCTCTCTGAGTGGGCTGAGCAGCAGAGCGGCGACAGCACTTGC 1279

QY 1141 ACGAACACCCCGGAAATCTCTGAGAGACACCGTGTACAGAGCGGGTGTATGACCGAG 1200  
DB 1280 ACGAACACCCCGGAAATCTCTGAGAGACACCGTGTATGAGAGCGGGTGTATGACCGAG 1339

QY 1201 CTGAGGTAGAAAAACGCTCTCGAAGAGGAGGAGGATCTGTAACGCCCGAATGAGAC 1260  
DB 1340 CTGAGGTAGAAAAACGCTCTCGAAGAGGAGGAGGATCTGTAACGCCCGAATGAGAC 1399

QY 1261 CTGCTCAGTCTGCTTGGGCTTGGCGCAGCCATGATCTCCGAATCTGTTGGCATC 1320  
DB 1400 CTGCTCAGTCTGCTTGGGCTTGGCGCAGCCATGATCTCCGAATCTGTTGGCATC 1459

QY 1321 CACGATACGGCAATGTCACACAATACAGCCCTGCGACACAGACAGAGAGAGAGAC 1380  
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QY 1381 AGAGA 1385  
DB 1520 AGAGA 1524

RESULT 5  
AX319944/c 2528 bp DNA linear PAT 14-DEC-2001  
LOCUS Sequence 3 from Patent WO0181634.  
DEFINITION AX319944  
ACCESSION AX319944  
VERSION AX319944.1 GI:17901491  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
1 Galvin, K.A. and Rudolph-Owen, L.A.  
Methods and compositions for the diagnosis and treatment of  
cardiovascular and tumorigenic disease using 4941  
Patent: WO 0181634-A 3 01-NOV-2001;  
Millennium Pharmaceuticals, Inc. (US)